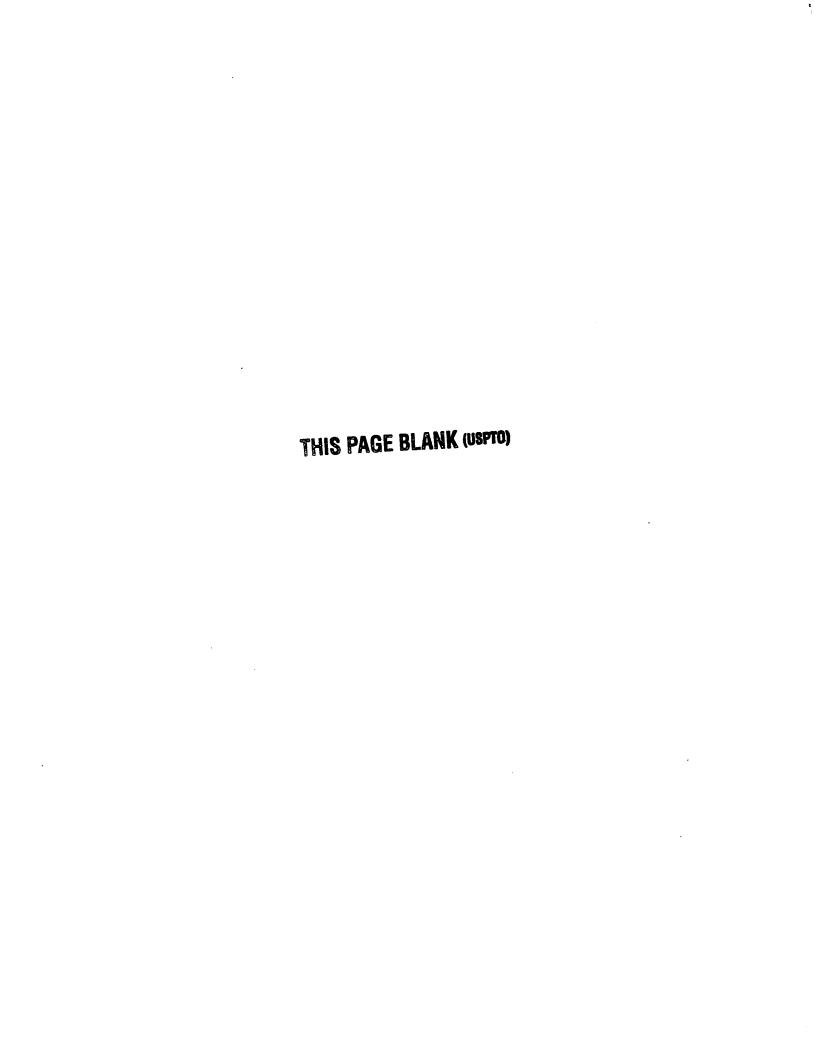
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Description	Complementary dete	neavy chain compie Variable heavy cha	Antiqen-binding pr	Antigen-binding pr	Humanised antibody	VEGF antagonist an	Heavy chain comple	Humanised antibody	VEGF antagonist an
SUMMARIES		AAY97235	AAU74412	AAU74419	AAE13138	AAB82704	AAU74416	AAE13143	AAB82709
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AAU74417 AAE13145 AAAB4201 AAAW9162 AAX70794 AAX39531 AAX39538 AAX39538 AAX39538 AAX39538 AAX39538 AAX39538 AAX39538 AAX39538 AAX39541 AAX39542 AAX39543 AAX39543 AAX39543 AAX39543 AAX79543	ALIGNMENTS 1230 AAY97230 standard; Protein; 17 AA. AAY97230; 19-DEC-2000 (first entry) Complementary determining region (CDRH2) of anti-service insert domain containing receptor; KDR; kinase insert domain containing receptor; MULLival humanised antibody; chimeric antibody; tumour; diseglioblastoma multiforme; hemangioblastoma; ALDS; central nervous system neoplasms; ALDS associated acquired immune deficiency syndrome; ALDS; human. Homo sapiens. Synthetic. WO200044777-A1. 03-AUG-2000. 28-JAN-1999; 99US-0117726. 29-JAN-1999; 99US-0117726. 29-JAN-1999; 99US-0117726. Zhu Z, Witte L;
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444400000000000000000000000000000000000	T 1 230 AAY97230 standan AAY97230; 19-DEC-2000 (f: Complementary de Immunoglobulin; VEGF; vascular Kinase insert di Humanised antibo gliobbastoma mui central arryous acquired immune Homo sapiens. Synthetic. WO200044777-A1. 03-AUG-2000. 28-JAN-1999; 29-JAN-1999; (IMCL-) IMCLONE
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Claim 55; Page 56; 64pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New immunoglobulin molecules are described that bind kinase insert domain-containing receptor (KDR) with a comparable affinity to human vascular enotations receptor (KDR) with a comparable affinity to human vascular enotation. The immunoglobulin may be a multivalent single chain antibody, a monovalent single chain antibody, a diabody, a chimarised antibody, a diabody, a chimarised antibody, a diabody, a crimabody, a chimarised antibody.

The immunoglobulin molecules bind specifically to an extracelfular domain of the KDR receptor with the same affinity as VEGF. Overexpression of VEGF has been immulationme, of human tumour cell lines including glioblastoma multiforme, hemangloblastoma, central nervous system neoplasms and AIDS associated Karposi's sarcoma. The antibodies therefore have applications in treating these conditions. This sequence encodes a firm than the complementary determining region of the
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                                                                                                                                                                                        Novel immunopobulin molecules binding kinase insert domain-containing receptor with the same affinity as vascular endothelial growth factor,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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                                                                                                                                                                                                                                                                                            used to reduce tumour growth
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                                    WPI; 2000-505966/45.
N-PSDB; AAA53762.
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The invention describes an antigen-binding protein (I) comprising a complex of two polypeptides (P1) and two second polypeptides (P2) which are stably associated in an immunoglobulin like complex. Pl has an antigen-binding site located to the N terminus of immunoglobulin (Ig) light chain constant domain (CL domain), and P2 has an antigen-binding site located to the N terminus of the CHI domain. (I) is useful for: neutralising the activation of a vascular endothelial growth factor (VEGF) receptor; reducing tumour growth; inhibiting angiogenesis; ceducing endothelial cell proliferation; inhibiting angiogenesis; ceducing endothelial cell proliferation; inhibiting useful for: migration of human leukaemia cells; blocking interaction of a protein and its ligand; promoting interactions between immune cells and target cells; can in vivo and in vitro for investigative, diagnostic or treatment methods. The design of (I) provides for efficient production so that substantially all of the antigen-binding proteins produced are assembled in the desired configuration. (I) is bivalent and bispecific, homogeneous and in tetrameric form. The heavy chain constant domains which constitute the Fc region (e.g., CH2 and CH3 for an ig6 molecule) of a natural antibody and which provide other antibody functions can be present.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          is no requirement for processing in vitro to obtain the complete product. This peptide sequence represents the heavy chain variable domain complementarity determining region H2 (CDRH2) version #1 incorporated into an antigen-binding protein described in the method of the invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      VEGF; vascular endothelial growth factor; KDR;
kinase insert domain containing receptor; multivalent; monovalent;
humanised antibody; chimeric antibody; tumour; diabody; triabody;
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100.0%; Pred. No. 8.6e-09;
ive 0; Mismatches 0;
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Matches 17; Conservative
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29-JAN-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                33-AUG-2000.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAY97235;
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                                                                      New immunoglobulin molecules are described that bind kinase insert conclaining receptor (KDR) with a comparable affinity to human vascular endothelial growth factor (VEGF). The antibodies neutralise KDR activation. The immunoglobulin may be a multivalent single chain antibody, a monovalent single chain antibody, a diabody, a crimabody, a monovalent single chain antibody, a diabody, a triabody, a monovalent single chain antibody, a diabody, a triabody, a monovalent single chain antibody. The immunoglobulin molecules bind specifically to an extracellular domain of the KDR receptor with the same affinity as VEGF. Overexpression of VEGF has been implicated in a number of human tumour cell lines including glioblastoma multiforme, hemangloblastoma, central nervous system neoplasms and AIDS associated Karposi's sarcoma. The antibodies therefore have applications in treating these conditions. This sequence encodes a preferred heavy chain complementary determining region of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New bispecific immunoglobulin-like antigen-binding protein for reducing tumour growth and for inhibiting angiogenesis, comprises a complex of two polypeptides and two second polypeptides \cdot
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The invention describes an antigen-binding protein (1) comprising a complex of two polypeptides (P1) and two second polypeptides (P2) which
Novel immunoglobulin molecules binding kinase insert domain-containing receptor with the same affinity as vascular endothelial growth factor,
                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Antigen-binding protein; antibody heavy chain variable domain; cytostatic; angiogenesis inhibitor; tumour; leukaemia; antibody; vascular endothelial growth factor receptor; VEGF; cell proliferation inhibitor.
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                                                                                                                                                                                                                                                                                                     Length 117;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Antigen-binding protein heavy chain variable domain (VH) #1.
                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                   100.0%; Score 101; DB 21; 100.0%; Pred. No. 6.7e-08;
                                                                                                                                                                                                                                                                                                                              0; Mismatches
                                                 Claim 4; Page 50-51; 55pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                            AAU74412 standard; peptide; 117 AA.
                                                                                                                                                                                                                                       preferred heavy chain complementa-
immunoglobulins of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 57; Page 57; 64pp; English.
                        used to reduce tumour growth
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  24-MAY-2001; 2001WO-US16924.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         24-MAY-2000; 2000US-206749P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (IMCL-) IMCLONE SYSTEMS INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (first entry)
                                                                                                                                                                                                                                                                                                                                                                    1 WIDPENGDSGYAPKFQG 17
                                                                                                                                                                                                                                                                                                                            17; Conservative
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                                                                                                                                                                                                                                                                                                                Local Similarity
                                                                                                                                                                                                                                                                            117 AA
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                                                                                                                                                                                                                                                                                                     Query Match
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antigen-binding site located to the N terminus of immunoglobulin (1g)

light chain constant domain (CL domain), and P2 has an antigen-binding

site located to the N terminus of the CH1 domain. (I) is useful for:

constant domain (CL domain), and P2 has an antigen-binding

site located to the N terminus of the CH1 domain. (I) is useful for:

constant of the activation of a vascular endothelial growth factor

(VEGF) receptor; reducing tumour growth; inhibiting angiogenesis;

reducing endothelial cell proliferation; inhibiting vEGF induced

migration of human leukaemia cells; blocking interaction of a protein and

its ligand; promoting interactions between immune cells and target cells;

and in vivo and in vitro for investigative, diagnostic or treatment

methods. The design of (I) provides for efficient production so that

substantially all of the antigen-binding proteins produced are assembled

in the desired configuration. (I) is bivalent and bispecific, homogeneous

and in tetrameric form. The heavy chain constant domains which constitute

the Fc region (e.g., CH2 and CH3 for an IgG molecule) of a natural

cantibody and which provide other antibody functions can be present. There

so no requirement for processing in vitro to obtain the complete product.

This sequence represents a heavy chain variable domain (VH) incorporated

into Fv, an engineered protein containing a heavy chain variable domain

and a light chain variable domain in one polypeptide chain, described in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Antigen-binding protein, single chain variable fragment version #1.
stably associated in an immunoglobulin like complex. Pl has an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note- "Heavy chain variable domain. Specifically claimed in claim 57"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /label= VL
/note= "Light chain variable domain. Specifically
claimed in claim 57"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     cytostatic; angiogenesis inhibitor; tumour; leukaemia; antibody; vascular endothelial growth factor receptor; VEGF; cell proliferation inhibitor.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 117;
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100.0%; Pred. No. 6.7e-08;
ive 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAU74419 standard; Protein; 240 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          the method of the invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 WIDPENGDSGYAPKFQG 17
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   117 AA;
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Synthetic.
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Region
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Rafii S;
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                                                                               N-PSDB; AAD21664
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                                       Witte L,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The invention describes an antigen-binding protein (I) comprising a complex off two polypeptides (P1) and two second polypeptides (P2) which are stably associated in an immunoglobulin like complex. Pl has an antigen-binding site located to the N terminus of immunoglobulin (Ig) in coated to the N terminus of immunoglobulin (Ig) is useful for: Iight chain constant domain (CL domain), and P2 has an antigen-binding cs site located to the N terminus of the CH1 domain. (I) is useful for: neutralising the activation of a vascular endothelial growth factor (VEGF) receptor; reducing tumour growth; inhibiting angiogenesis, reducing endothelial cell proliferation; inhibiting vEGF induced migration of human leukaemia cells; blocking interaction of a protein and its ligand; promoting interactions between immune cells and target cells; and in vivo and in viro for investigative, diagnostic or treatment can in vivo and in viro for investigative, diagnostic or treatment companies, The design of (I) provides for efficient production so that csubstantially all of the antigen-binding proteins production so that csubstantially all of the antigen-binding proteins production so that can in the desired configuration. (I) is bivalent and bispecific, homogeneous can din tetrament for processing in vitro to obtain the complete product. This is the amino acid sequence of a single chain variable fragment (SCF), an engineered protein containing a variable light and variable fragment containing a variable light and variable fragment contains the complete product.
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                                                                                          New bispecific immunoglobulin-like antigen-binding protein for reducing tumour growth and for inhibiting angiogenesis, comprises a complex of two polypeptides and two second polypeptides
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            cytostatic; heavy chain hypervariable region; VH; myelocytic leukaemia; lymphocytic; erythrocytic; monocytic; multiple myeloma; lymphoid cell; Hodgkin's disease; complementarity determining region-2; CDR-2; mouse.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               endothelial growth factor receptor; VEGFR; antagonist; tumour;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Humanised antibody murine heavy chain hypervariable region (VH) CDR2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  100.0%; Score 101; DB 23; Length 240; 100.0%; Pred. No. 1.4e-07;
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                                                                                                                                                  Claim 63; Page 62; 64pp; English.
            (IMCL-) IMCLONE SYSTEMS INC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               13; Conservative
                                                                 WPI; 2002-106189/14:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         240 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               invention
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The invention relates to a method for inhibiting the growth of non-solic tumour cells that are stimulated by a ligand of vascular endothelial growth factor receptor (VEGFR) in mammals particularly humans. The method involves treating the mammals with humanised VEGFR monoclonal antibodies (antagonists). Humanised monoclonal antibody comprises humanised mouse variable region joined to human constant region, where the humanised mouse variable region contains mouse complementarity determining region (CDR) grafted into human ontains mouse complementarity determining region (CDR) grafted into human variable region. The method is useful for treating leukaemias such as acute or chronic myelocytic leukaemia, acute or chronic lymphocytic leukaemia, erythrocytic or monocytic leukaemia, multiple myelomas and lymphoid cells, particularly those related to non-Hodgkin's and Hodgkin's disease. The present sequence is humanised antibody murine heavy chain hypervariable region (VH) CDR-2 used in the
                                                                                                                                                                                                                                                                                                                                                  Inhibiting growth of non-solid tumor cells useful to treat bone marrow
                                                                                                                                                                                                                                                                                                                                                                                      tumors such as leukemias or multiple myeloma comprises treatment with an antagonist of a vascular endothelial growth factor receptor - \,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                IMC-1C11; chimeric antibody; mouse; human; antagonist; VEGF; vascular endothelial growth factor; anglogenesis; antiangiogenic; antitumour; neoplasm; collagen-vascular disease; autoimmune disea tumour; breast carcinoma; lung carcinoma; prostate carcinoma;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ;
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glioblastoma multiforme; melanoma; therapy; heavy chain; CDR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 94; DB 22; Length 17; Pred. No. 1e-07;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 8; Page 14; 68pp; English.
(IMCL-) IMCLONE SYSTEMS INC. (CORR ) CORNELL RES FOUND INC.
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31-MAR-2000; 2000US-0539692.
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Best Local Similarity 94.1
Matches 16; Conservative
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Rafii S;
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                                                                                                                                                                                                                                           The present sequence is that of complementarity determining region of the heavy chain variable region (see also AAB82701) of IMC-1C11, a mouse-human chinneric antibody that has vascular endothelial growth factor (VEGF) antagonist activity. The antibody, or a fragment of it, can be used as an anti-angiogenic molecule, together with a chemotherapeutic acid, for the treatment of an angiogenic dependent condition in a mammal, especially a human. The invention relates generally to a method of treating or controlling an angiogenic dependent condition by administering an anti-angiogenic molecule and a chemotherapeutic agent, to produce a controlling as ignificant toxicity of the chemotherapeutic agent. The anti-angiogenic molecule inhibits or blocks the action of a preventing significant toxicity of the chemotherapeutic agent. The anti-angiogenic molecule inhibits or blocks the action of a vascular endothelium survival factor such as VEGF or its receptor, and is especially IMC-1C11. Conditions that can be treated include a neoplasm, a colladen-vascular disease or an autoimmune disease, especially a soild tumour, including breast carcinoma, lung carcinoma, prostate carcinoma, covarian carcinoma, neuroblastoma, central nervous system tumour, covarian carcinoma, entitiorme or melanoma (all claimed).
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                                                                                       Treating or controlling an angiogenic dependent condition (e.g. neoplasm, collagen-vascular or autoimmune disease) in mammal by administering a combination of an antiangiogenic molecule and a chemotherapeutic agent
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Pred. No. 1e-07;
0; Mismatches 1; Indels
                                                                                                                                                                                                         Disclosure; Page 37; 42pp; English.
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94.1%;
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Matches 16; Conservative
                                              WPI; 2001-514531/56
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AAU74416
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The invention describes an antigen-binding protein (I) comprising a complex of two polypeptides (P1) and two second polypeptides (P2) which are stably associated in an immunoglobulin like complex. Pl has an antigen-binding site located to the N terminus of immunoglobulin (Ig) light chain constant domain (CL domain), and P2 has an antigen-binding site located to the N terminus of the CHI domain. (I) is useful for: site located to the N terminus of the CHI domain. (I) is useful for: neutralising the activation of a vaccular endothelial growth factor (VEGF) receptor; reducing tumour growth; inhibiting vEGF induced migration of human leukaemia cells; blocking interaction of a protein and invivo and in vitro for investigative, diagnostic or treatment methods. The design of (I) provides for efficient production so that substantially all of the antigen-binding proteins produced are assembled in the desired configuration. (I) is bivalent and bispecific, homogeneous and in tetrameric form. The heavy chain constant domains which constitute antibody and which provide other antibody functions can be present. There is no requirement for processing in vitro to obtain variable domain and in committees the heavy chain variable domain and in the committees the heavy chain variable domain and in the committees the heavy chain variable domain and the committees the committees the heavy chain variable domain and the committees 
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            complementarity determining region H2 (CDRH2) version #2 incorporated into an antigen-binding protein described in the method of the invention.
New bispecific immunoglobulin-like antigen-binding protein for reducing tumour growth and for inhibiting angiogenesis, comprises a complex of two polypeptides and two second polypeptides
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Pred. No. 1e-07;
0; Mismatches 1; Indels
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                                                                                                                                                                                                                                Claim 59; Page 60; 64pp; English.
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94.1%;
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Best Local Similarity 94.1'
Matches 16, Conservative
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Chimeric - Mus sp.
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31-MAR-2000; 2000US-0539692
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                                                                                                                The invention relates to a method for inhibiting the growth of non-solid tumour cells that are stimulated by a ligand of vascular endothelial growth factor receptor (VBGFR) in mammals particularly humans. The method involves greating the mammals with humanised VBGFR monoclonal antibodies (antagoniĝis). Humanised monoclonal antibody comprises humanised mouse
                                                                                                                                                                                     variable region joined to human constant region, where the humanised mouse variable region contains mouse complementarity determining region (CDR) grafted into human variable region. The method is useful for treating leukaemias such as acute or chronic myelocytic leukaemia, acute
                                                                                                                                                                                                                                        or chronic lymphocytic leukaemia, erythrocytic or monocytic leukaemia, multiple myelomas and lymphoid cells, particularly those related to non-Hodgkin's and Hodgkin's disease. The present sequence is humanised antibody heavy chain fragment used in the exemplification of the
                                     Inhibiting growth of non-solid tumor cells useful to treat bone marrow tumors such as leukemias or multiple myeloma comprises treatment with an antagonist of a vascular endothelial growth factor receptor
                                                                                                                                                                                                                                                                                                                                                                            Gaps
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Pred. No. 8e-07;
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                                                                                           Claim 8; Bage 15; 68pp; English.
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/label= CDR-H2
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/label- CDR-H1
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94.1%;
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Homo sapiens.
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 2001-662942/76
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Matches 16; Conserv
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             N-PSDB; AAD21669
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Chimeric
                                                                                                                                                                                                                                                                                                 Invention
                                                                                                                                                                                                                                                                                                                        Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 10
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The present sequence is that of the heavy chain variable region of IMC-1C11, a mouse-human chimeric antibody that has vascular endothelial growth factor (VEGF) antegonist activity. The antibody, or a fragment of it, can be used as an anti-angiogenic molecule, together with a chemotherapeutic acid, for the treatment of an angiogenic dependent condition in a mammal, especially a human. The invention relates generally to a method of treating or controlling an angiogenic dependent condition by administering an anti-angiogenic molecule and a chemotherapeutic agent, to produce a controlling significant toxicity of the commontant angiogenic molecule inhibits or blocks the action of a rarest of molecule inhibits or blocks the action of a characterial angiogenic molecule inhibits or blocks the action of a characterial and a characterial factor such as VEGF or its receptor, and action of a characterial and a characterial cha
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      and is especially IMC-ICII. Conditions that can be treated include a neoplasm, a collagen-vascular disease or an autoimmune disease, especially a solid tumour, including breast carcinoma, lung carcinoma, prostate carcinoma, colon carcinoma, prostate carcinoma, ochon carcinoma, contral nervous system tumour, neuroblastoma, glioblastoma multiforme or melanoma (all claimed).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The antibody,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Antigen-binding protein; antibody heavy chain variable domain; cytostatic; angiogenesis inhibitor; tumour; leukaemia; antibody; vascular endothelial growth factor receptor; VBGF; cell proliferation inhibitor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Treating or controlling an angiogenic dependent condition (e.g. neoplasm, collagen-vascular or autoimmune disease) in mammal by administering a combination of an antiangiogenic molecule and a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 94; DB 22; Length 117; Pred. No. 8e-07;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0; Mismatches
(SUNN-) SUNNYBROOK HEALTH SCI CENT. (IMCL-) IMCLONE SYSTEMS INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Disclosure; Page 38; 42pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAU74417 standard; peptide; 117 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  93.1%;
94.1%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             24-MAY-2000; 2000US-206749P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 WIDPENGDSGYAPKFQG 17
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             chemotherapeutic agent
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Best Local Similarity
"hes 16; Conserve
                                                                                                                                                                                                                                                                                                WPI; 2001-514531/56.
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N-PSDB; AAD21682
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   Region
                                                                                                                        Region
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                                                                                                                                                                                    The invention describes an antigen-binding protein (I) comprising a complex of two polypeptides (P1) and two second polypeptides (P2) which are stably associated in an immunoglobulin like complex. Pl has an antigen-binding site located to the N terminus of immunoglobulin (Ig) antigen-binding site located to the N terminus of immunoglobulin (Ig) is useful for:

COURTY (MECE) receptor; reducing tumour growth; inhibiting angiogenesis; reducing endothelial cell proliferation; inhibiting angiogenesis; reducing endothelial cells; blocking interaction of a protein and its ligand; promoting interactions between immune cells and target cells; and in vivo and in vito for investigative, diagnostic or treatment complexiant of human leurals endothelial part of investigative, diagnostic or treatment complexiantially all of the antigen-binding proteins produced are assembled in the desired configuration. (I) is bivalent and bispecific, homogeneous and in tetrameric form. The heavy chain constant domains which constitute the region (e.g., CL2 and CH3 for an igd molecule) of a natural antibody and which provide other antibody functions can be present. There is no requirement for processing in vitro to obtain the complete product. This sequence represents a heavy chain variable domain and a light chain variable domain in one polypeptide chain, described in the method of the invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        cytostatic; heavy chaín; myelocytic leukaemia; lymphocytíc; erythrocytic; monocytic; multiple myeloma; lymphoid cell; Hodgkin's disease; chimeric;
                                                                                                  New bispecific immunoglobulin-like antigen-binding protein for reducing tumour growth and for inhibiting angiogenesis, comprises a complex of two polypeptides and two second polypeptides
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Vascular endothelial growth factor receptor; VEGFR; antagonist; tumour;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note= "Mature chimeric plCll heavy chain fragment"
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Pred. No. 8e-07;
0; Mismatches 1; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Chimeric plC11 heavy chain fragment.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAE13145 standard; Protein; 136 AA.
                                                                                                                                                                Claim 61; Page 60; 64pp; English.
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/label= CDR_Hî
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               93.18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              94.18;
(IMCL-) IMCLONE SYSTEMS INC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             16; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    - Homo sapiens
- Unidentified
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Local Similarity
                                                         WPI; 2002-106189/14.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   human; plC11 vector
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 117 AA;
                                                                        N-PSDB; AAS20288.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             28-JAN-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAE13145;
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The invention relates to a method for inhibiting the growth of non-solid tumour cells that are stimulated by a ligand of vascular endothelial cy growth factor receptor (VEGFR) in mammals particularly humans. The method involves treating the mammals with humanised VEGFR monoclonal antibodies (antagonists). Humanised monoclonal antibody comprises humanised mouse (ariable region ofoliaed to human constant region, where the humanised mouse variable region contains mouse complementarity determining region (CDR) grafted into human variable region. The method is useful for treating leukaemias such as acute or chronic myelocytic leukaemia, acute or chronic lymphocytic leukaemia, erythrocytic or monocytic leukaemia, acute or chronic lymphocytic leukaemia, erythrocytic or monocytic leukaemia, multiple myelomas and lymphod cells, particularly those related to non-Hodgkin's and Hodgkin's disease. The present sequence is chimeric picli leavy chain fragment which is used for the construction of chimeric picli ligo expression vector. Chimeric picli heavy chain contains cloned and account of the construction of chimeric picli ligo expression vector. Chimeric picli heavy chain (VH) and human IgGI (gamma) heavy chain constant
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Inhibiting growth of non-solid tumor cells useful to treat bone marrow tumors such as leukemias or multiple myeloma comprises treatment with an antagonist of a vascular endothelial growth factor receptor -
                                                                                in the
                                                                                                                                                                                           in the
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vascular endothelial growth factor; angiogenesis; antianglogenic;
                                                             /note= "Residue 'O' is present at this location sequence shown in fig-11 of the specification"
                                                                                                                                                                                /note= "Residue 'O' is present at this location sequence shown in fig-11 of the specification" 119..125
/label= CDR_H3
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Pred. No. 9.4e-07;
); Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAB82701 standard; Protein; 136 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Example 3; Fig 11; 68pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ;
/label- CDR_H2
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94.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               31-MAR-2000; 2000US-0540770.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          30-MAR-2001; 2001WO-US10504.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 WIDPENGDSGYAPKFQG 17
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 2001-662942/76.
                                                                                                                                                 Misc-difference 101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
Matches 16; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Witte L, Rafii S;
                                          Misc-difference 84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 136 AA;
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1 WIDPENGDSGYAPKFQG 17

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The present sequence is that of the heavy chain variable region of IMC-ICILE a mouse-human chimeric antibody that has vascular endotheldal growth factor (VEGF) antagonist activity. The antibody, or a fragment of it, can be used as an anti-anglogenic molecule, copether with a chemotherapeutic acid, for the treatment of an angiogenic dependent condition in a mammal, especially a human. The invention relates generally to a method of treating or controlling an angiogenic dependent condition by administering an anti-anglogenic molecule and a chemotherapeutic agent.

The anti-anglogenic molecule and a chemotherapeutic agent.

The anti-anglogenic molecule inhibits or blocks the action of a vascular andothelium survival factor such as VEGF or its receptor, and is especially IMC-ICIL. Conditions that can be treated include a neoplasm, a collagen-vascular disease or an autoimmune disease, especially a solid tumour, including breast carcinoma, lung contain prostate carcinoma, prostate carcinoma, prostate carcinoma, carcinoma, prostate carcinoma, colon carcinoma, prostate carcinoma, colon carcinoma, prostate carcinoma, contain contain the contain contains that can be created and contains colon carcinoma, prostate carcinoma, colon carcinoma, prostate carcinoma, colon carcinoma prostate carcinoma, colon carcinoma prostate carcinoma, colon carcinoma prostate carcinoma colon carcinoma prostate carcinoma colon carci
antitumour; neoplasm; collagen-vascular disease; autoimmune disease; tumour; breast carcinoma; lung carcinoma; prostate carcinoma; colon carcinoma; ovarian carcinoma; neuroblastoma; glioblastoma; multiforme; melanoma; therapy; heavy chain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ovarian carcinoma, neuroblastoma, central nervous system tumour, neuroblástoma, glioblastoma multiforme or melanoma (all claimed).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Treating for controlling an angiogenic dependent condition (e.g. neoplasm collagen-vascular or autoimmune disease) in mammal by administering a combination of an antiangiogenic molecule and a chemotherapeutic agent
                                                                                                                                                                                                                                                                                                                                                                                 'note= "complementarity determining region 1"
                                                                                                                                                                                                                                                                                                                                                                                                                                        //note="complementarity determining region 2"
118..125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /label- CDR-H3
/note- "complementarity determining region 3"
                                                                                                                                                                                                                                                    /label= Signal_peptide
                                                                                                                                                                                                                                                                            10..136
| Jabel = Mature_protein
                                                                                                                                                                                                        Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (SUNN-) SUNNYBROOK HEALTH SCI CENT. (IMCL-) IMCLONE SYSTEMS INC.
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                                                                                                                                                                                                                                                                                                                                15..54
/label= CDR-H1
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/label= CDR-H2
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31-MAR-2000; 2000US-0539692
                                                                                                                          Chimeric - Mus sp.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence
                                                                                                                                                                                                                             Peptide
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The invention describes an antigen-binding protein (I) comprising a complex of two polypeptides (Pl) and two second polypeptides (P2) which are stably associated in an immunoglobulin like complex. Pl has an artispen-binding site located to the N terminus of immunoglobulin (Ig) light chain constant domain (CL domain), and P2 has an antigen-binding site located to the N terminus of the CH1 domain. (I) is useful for: neutralising the activation of a vascular endothelial growth factor (VEGF) receptor; reducing tumour growth; inhibiting angiogenesis; reducing endothelial cell proliferation; inhibiting vEGF induced migration of human leukaemia cells; blocking interaction of a protein and its ligand; promoting interactions between immune cells and target cells; and in vivo and in vitro for investigative, diagnostic or treatment substantially all of the antigen-binding proteins production so that substantially all of the antigen-binding proteins production so that the desired configuration. (I) is bivalent and bispecific, homogeneous
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                comprising a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New bispecific immunoglobulin-like antigen-binding protein for reducing tumour growth and for inhibiting anglogenesis, comprises a complex of two polypeptides and two second polypeptides .
                                                                                                                                                                                                                    Antigen-binding protein; single chain variable fragment; svFv; antigen; cytostatic; angiogenesis inhibitor; tumour; leukaemia; antibody; vascular endothelial growth factor receptor; VEGF; cell proliferation inhibitor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Antigen-binding protein, single chain variable fragment version #2.
                                                                                                                                                                                                                                                                                                                                                                                               /note- "Heavy chain variable domain. Specifically claimed in claim 61"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 63; Page 62-63; 64pp; English.
                                                                                                                                                                                                                                                                                                                                                  Location/Qualifiers
                                                                                           AAU74420 standard; Protein; 238 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                               /label- Linker
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      24-MAY-2000; 2000US-206749P.
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                                                                                                                                                          (first entry)
69 WIDPENGDSDYAPKFOG 85
                                                                                                                                                                                                                                                                                                                                                                                                                              118..132
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Synthetic.
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                                                           RESULT 14
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Gaps

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93.1%; Score 94; DB 22; Length 136; 94.1%; Pred. No. 9.4e-07; ive 0; Mismatches 1; Indels

16; Conservative

e.

Best Local Similarity

Matches

Query Match

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anti-tumour immunity; to elicit an increased immune response to tumour associated antigen (TAA) and/or to induce an immune response to tumour associated antigen (TAA) and/or to induce an immune response to mutant or wild-type forms of TAA in mammals. (A) is: (i) a monoclonal antibody (MAb) to TAA, or its fragment; (ii) a peptide based on a CDR (abble to elicit antibodies to TAA); or (iii) a DNA that encodes the variable (V) region of MAb, in a gene delivery vehicle. The present sequence represents a peptide based on CDR2 of the heavy chain of anti-DNA antibodies (Ab) by immunising a mammal with a MAb directed to a domain containing a DNA-binding site of a DNA-binding protein (A) is used to treat a wide variety of primary and metastatic cancers, particularly those where p53 is involved. Ab are used for diagnosis (e, g to determine critical sequences in animal or plant breeding); to identify bacteria and other parasites; to determine
                                                                                                                                                                                                                                                 ó
and in tetrameric form. The heavy chain constant domains which constitute the Fr region (e.g., CHZ and CH3 for an 196 molecule) of a natural antibody and which provide other antibody functions can be present. There is no requirement for processing in vitro to obtain the complete product. This is the amino acid sequence of a single chain variable fragment (scFV), an engineered protein containing a variable light and variable heavy domain on one polypeptide, described in the method of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The present invention describes the use of an immunogen (A) to induce
                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Anti-p53; monoclonal antibody 240; immunogen; anti-tumour; immunity; immune response; tumour associated antigen; metastatic cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Use of a monoclonal antibody to a tumour-associated antigen - to induce anti-tumour immunity or elicit an increased immune response
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Anti-p53 monoclonal antibody 421 CDR2 heavy chain based peptide.
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                                                                                                                                                                                                            Length 238;
                                                                                                                                                                                                        Score 94; DB 23; Length 23
Pred. No. 1.7e-06;
0; Mismatches 1; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Herkel J,
                                                                                                                                                                                                                                                                                                                                                                                                                 AAW89162 standard; peptide; 17 AA.
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                                                                                                                                                                                                            93.1%;
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                                                                                                                                                                                                                                                                                                    11111111 | 1111111 | 50 WIDPENGDSDYAPKFQG 66
                                                                                                                                                                                                        Query Match 93.1
Best Local Similarity 94.1
Matches 16; Conservative
                                                                                                                                                                                                                                                                                  1 WIDPENGDSGYAPKFQG 17
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                                                                                                                                                                       238 AA;
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Synthetic.
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parentage; in forensic science; to isolate specific genes for DNA vaccination; in gene sequencing and cloning; also possibly for activation of selected therapeutic genes in plants, animals and humans. (A) induce an effective anti-tumour response without causing harm to the patient. The method uses (A) to generate anti-TAA by exploiting the anti-idiotype
                                                                                                                                                                                         Gaps
                                                                                                                                                                                         ;
                                                                                                                                                       Length 17;
                                                                                                                                    Score 90; DB 20; Length 17, Pred. No. 4.3e-07;
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88.2%;
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                                                                                                                                                                       Local Similarity
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                                                                                                                      17 AA;
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Sequence Sequence

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; MOLECULE TYPE: protein US-08-017-570-4
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Matches 15; Conser
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CITY: Midland
STATE: MI
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Query Match
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163.250 Million cell updates/sec
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/cgn2_6/ptodata/1/laa/5B_COMB.pep:*
/cgn2_6/ptodata/1/laa/AA_COMB.pep:*
/cgn2_6/ptodata/1/laa/6B_COMB.pep:*
/cgn2_6/ptodata/1/laa/PCTUS_COMB.pep:*
/cgn2_6/ptodata/1/laa/PCTUS_COMB.pep:*
             GenCore version 5.1.3
Copyright (c) 1993 - 2002 Compugen Ltd.
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5-09-025-403A-9
5-09-025-403A-10
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US-08-471-426-6
US-09-672-609-1
US-09-672-609-4
US-09-672-609-5
US-09-672-609-6
US-09-672-609-6
US-09-672-609-8
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US-09-025-403A-6
US-09-025-403A-7
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-09-025-403A-12
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                                                                                                                     December 23, 2002, 07:20:23
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Maximum Match 100%
Listing first 45 summaries
                                                                                     protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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1 WIDPENGDSGYAPKFQG 17
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Maximum DB seq length: 2000000000
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Perfect score:
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APPLICANT: GOURLIE, BRIAN B
APPLICANT: RIXON, MARK W
APPLICANT: MEZES, PETER S
APPLICANT: RAPLAN, DONALD A
APPLICANT: SCHLOM, JEFFREY
TITLE OF INVENTION: A NOVEL FAMILY OF ANTI-CARCINOEMBRYONIC
TITLE OF INVENTION: ANTIGEN CHIMERIC ANTIBODIES
NUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 124;
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US-08-652-507-2
US-08-681-35A-38
US-08-681-052-16
US-09-188-082-16
US-09-18-082-16
US-09-171-945-31
US-09-171-945-55
US-09-171-945-55
US-09-171-945-79
US-09-171-945-81
US-09-171-945-81
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US-09-171-945-85
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Pred. No. 4e-07;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 4, Application US/08017570 Patent No. 5472693
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADDRESSEE: Duane C. Ulmer STREET: P.O. Box 1967
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   89.1%;
88.2%;
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SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/471,426
FILING DATE: 06-JUN-1995
CLASSIFICATION 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/017,570
FILING DATE: 16-FEB-1993
ATTORNEY/AGENT INFORMATION:
NAME: ULAGRAPHEN UMBER: 34,941
REGISTRATION NUMBER: 34,941
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADDRESSEE: Duane C. Ulmer
STREET: P.O. Box 1967
CITY: Midland
STARE: MI
COUNTRY: US
ZIP: 48641-1967
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
COMPUTER: IBM PC COMPATIBLE
COMPUTER: IBM PC COMPATIBLE
COMPATIBLE SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        REFERENCE/DOCKET NUMBER: C-38,777
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 6, Application US/08471426
Patent No. 5808033
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: GOURLIE, BRIAN B
APPLICANT: RIXON, MARK W
APPLICANT: RIXON, MARK W
APPLICANT: RAPLAN, DONALD A
APPLICANT: SCHLOM, JEFFREY
TITLE OF INVENTION: A NOVEL FA
TITLE OF INVENTION: ANTIGEN CH
NUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                    NAME: ULMER, DUANE C
REGISTRATION NUMBER: 34,941
REPERENCE/DOCKET NUMBER: C-:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (517) 636-8104
INFORMATION FOR SEQ ID NO: 4:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   89.1%;
88.2%;
                                                                                                                                                                                                                                                                                                                                                                                                        : 124 amino acids
amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             50 WIDPENGDTEYAPKFQG 66
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Best Local Similarity 88.2
Matches 15; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 WIDPENGDSGYAPKFQG 17
                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY: linear

MOLECULE TYPE: protein
US-08-471-426-4
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US-08-471-426-6
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APPLICANT: MEZES, PPTER S

APPLICANT: MEZES, PPTER S

APPLICANT: SCHLOM, DONALD A

APPLICANT: SCHLOM, BY NOVEL FAMILY OF ANTI-CARCINOEMBRYONIC

TITLE OF INVENTION: A NOVEL FAMILY OF ANTI-CARCINOEMBRYONIC

TITLE OF INVENTION: ANTIGEN CHIMERIC ANTIBODIES

NUMBER OF SEQUENCES: 24

CORRESPONDENCE ADDRESS:

ADDRESSEE: Danne C. Ulman-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
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                                                                                                                                                                                                                                                                                                                                            CITX: FILLING
STATE: MI
COUNTRY; US
ZIP: 48641-1967
COMPUTER; US
COMPUTER; ENDANGLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER; IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/017,570
FILLING DATE: 19930216
CLASSIPLATION: 424
ATTORNEY,AGENT INFORMATION:
NAME: ULIME UNMBER: 34,941
REFERENCE/DOCKET NUMBER: 34,941
REFERENCE/DOCKET NUMBER: C-38,777
TELEPHONE: (517) 636-8104
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE/CHARACTERISTICS:
FOWCHH # 124 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 90; DB 1;
Pred. No. 4e-07;
1; Mismatches
                 US/080175.

LACANT RIXON:

LICANT RIXON MARK W
APPLICANT RIXON MARK W
APPLICANT RAPLAN, DONALD A
TITLE OF INVENTION: A NOVEL FAMILY OF A
TITLE OF INVENTION: A NOVEL FAMILY OF A
TITLE OF INVENTION: A NOVEL FAMILY OF A
TITLE OF INVENTION: ANTIGEN CHIMERIC ANT.
NUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESSE:
ADDRESSEE: Duane C. Ulmer
STREET: P.O. Box 1967
CITY: Midland
STATE: MI
               US-08-017-570-6
Sequence 6, Application US/08017570
Patent No. 5472693
CENERAL INFORMATION:
APPLICANT F GOURLIE, BRIAN B
APPLICANT RIXON, MARK W
APPLICANT RIXON, MARK W
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AMINO ACID
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Best Local Similarity 88.2
Matches 15; Conservative
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US-08-471-426-4
RESULT 2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 90; DB 1; Length 124; Pred. No. 4e-07;
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: The PC compatible
COMPUTER: The PC compatible
COMPUTER: The PC compatible
COMPUTER: Patentin Release #1.0, Version #1.25
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/471,426
FILING DATE: 06-JUN-1995
PRIOR APPLICATION NUMBER: 08/017,570
FILING DATE: 16-FEB-1993
ATTOMNEY/AGENT INFORMATION:
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LENGTH: 124
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Best Local
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US-09-672-609-3
Sequence 3, Application US/09672609
Patent No. 6333405
GENERAL INFORMATION:
APPLICANT: Anderson, W.H. Kerr
APPLICANT: Tempest, Philip R.
APPLICANT: Tempest, Philip R.
APPLICANT: Arank J.
APPLICANT: Arank J.
APPLICANT: Arank J.
APPLICANT: Arank Milliam J.
APPLICANT: Arank J.
APPLICANT: Arank Milliam J.
APPLICANT: Arank J
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APPLICANT: Tempest, Philip R.
APPLICANT: Tempest, Philip R.
APPLICANT: Tempest, Philip R.
APPLICANT: Tempest, Philip R.
APPLICANT: Harris, William J.
APPLICANT: Harris, William J.
APPLICANT: Armour, Kathryn
TITLE OF INVENTION: High Affinity Humanized Anti-CEA Monoclonal Antibodies
FILE REPERENCE:
CURRENT APPLICATION NUMBER: US/09/672,609
PRIOR APPLICATION NUMBER: 09/025,403
PRIOR FILING DATE: 1998-02-18
NUMBER: OF SEQ ID NOS: 50
SOFTWARE: Microsoft Word 97 SR-2
SEQ ID NO 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
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Pred. No. 4e-07;
1; Mismatches 1; Indels
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Pred. No. 4e-07;
.; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-09-672-609-1; Sequence 1, Application US/09672609; Sequence 1, Application US/09672609; Patent No. 6333405; CENERAL INFORMATION:
TELEPHONE: (517) 636-8104
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 124 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                      89.1%;
88.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              89.1%;
88.2%;
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                                                                                                                                                                                                          ; MOLECULE TYPE: protein US-08-471-426-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: PRT
ORGANISM: Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
                                                                                                                                                                                    linear
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Best Local Similarity
Matches 15; Conserv
                                                                                                                                                                             TOPOLOGY:
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LOCATION: 1..124
CTHER INFORMATION: Humanized heavy chain variable region containing human OTHER INFORMATION: NEWM VH FRS, murine COL-1 VH CDRS, and Ala-24, Phe-27, Asn-28, COTHER INFORMATION: Ile-29, Lys-30, Asn-97, and Thr-98
US-09-672-609-4
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APPLICANT: Anderson, W.H. Kerr
APPLICANT: Tempest, Philip R.
APPLICANT: Carr, Frank J.
APPLICANT: Harris, William J.
APPLICANT: Harris, William J.
APPLICANT: Harris, William J.
APPLICANT: Amour, Kathryn
TITLE OF INVENTION: High Affinity Humanized Anti-CEA Monoclonal Antibodies
FILE REFERENCE:
CURRENT APPLICATION NUMBER: US/09/672,609
CURRENT FILING DATE: 2000-09-28
PRIOR FILING DATE: 1998-02-18
PRIOR FILING DATE: 1998-02-18
NUMBER OF SEQ ID NOS: 50
SOFTWARE: Microsoft Word 97 SR-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
APPLICANT: Tempest, Philip R.
APPLICANT: Carr, Frank J.
APPLICANT: Harris, William J.
APPLICANT: Harris, William J.
APPLICANT: Armour, Kathryn
TILE OF INVENTION: High Affinity Humanized Anti-CEA Monoclonal Antibodies
FILE REFERENCE:
                   FEATURE:
MAME/KEY: Humanized COL-1 VH, HuVH
LOCATION: 1.124
OTHER INFORMATION: Humanized heavy chain variable region containing human
OTHER INFORMATION: NEWM VH FRs, murine COL-1 VH CDRs, and Phe-27, Asn-28,
OTHER INFORMATION: Ile-29, Lys-30, Asn-97, and Thr-98
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Pred. No. 4e-07;
1; Mismatches 1; Indels
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                                                                                                                                                                                                                 Score 90; DB 4;
Pred. No. 4e-07;
                                                                                                                                                                                                                                                                 Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME/KEY: Humanized COL-1 VH, HuVHA
                                                                                                                                                                                                                                                                                                                                                                                                                                               US-09-672-609-4; Sequence 4, Application US/09672609; Patent No. 6333405
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 5, Application US/09672609
Patent No. 6333405
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         89.1%;
88.2%;
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                 89.1%;
88.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ORGANISM: Artificial Sequence
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                                                                                                                                                                                                                                        Similarity
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Best Local Similarity
Matches 15; Conserv
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US-09-672-609-5
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US-09-672-609-3
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LENGIH: 124
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NAME/KEY: Humanized COL-1 VH, HuVHAY
LOCATION: 1..124
COTHER INFORMATION: Humanized heavy chain variable region containing human
OTHER INFORMATION: NEWM VH FRs, murine COL-1 VH CDRs, and Ala-24, Phe-27, Asn-28,
COTHER INFORMATION: Ile-29, Lys-30, Tyr-80, Asn-97, and Thr-98
US-09-672-609-7
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LOCATION: 1..124
OTHER INFORMATION: Humanized heavy chain variable region containing human
OTHER INFORMATION: NEWM VH FRs, murine COL-1 VH CDRs, and Ala-24, Phe-27, Asn.
OTHER INFORMATION: 11e-29, Lys-30, Thr-78, Ala-79, Tyr-80, Asn-97, and Thr-98
US-09-672-609-8
APPLICANT: Armour, Kathryn
TITLE OF INVENTION: High Affinity Humanized Anti-CEA Monoclonal Antibodies
FILE REFERENCE:
CURRENT APPLICATION NUMBER: US/09/672,609
CURRENT FILING DATE: 2000-09-28
PRIOR APPLICATION NUMBER: 09/025,403
PRIOR FILING DATE: 1998-02-18
NUMBER OF SEQ ID NOS: 50
SOFTWARE: Microsoft Word 97 SR-2
SEQ ID NO 7
LENGTH: 124
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APPLICANT: Tempest, Philip R.
APPLICANT: Carr, Frank J.
APPLICANT: Harris, William J.
APPLICANT: Armour, Kathryn
TITLE OF INVENTION: High Affinity Humanized Anti-CEA Monoclonal Antibodies
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Pred. No. 4e-07;
1; Mismatches 1; Indels
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CURRENT APPLICATION NUMBER: US/09/672,609
CURRENT FILING DATE: 2000-09-28
PRIOR APPLICATION NUMBER: 09/025,403
PRIOR FILING DATE: 1998-02-18
NUMBER OF SEQ ID NOS: 50
SOFTWARE: Microsoft Word 97·SR-2
LENGTH: 124
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Patent No. 6333405
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; Patent No. 6333405
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88.2%;
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Best Local Similarity 88.2
Matches 15; Conservative
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Best Local Similarity 88.2
Matches 15; Conservative
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US-09-672-609-8
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US-09-672-609-9
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TOTER INFORMATION: Humanized heavy chain variable region containing human OTHER INFORMATION: NEWM VH FRs, murine COL-1 VH CDRs, and Ala-24, Phe-27, Asn-28, OTHER INFORMATION: IIe-29, Lys-30, Thr-78, Asn-97, and Thr-98
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NAME/KEY: Humanized COL-1 VH, HuVHAA
LOCATION: $\frac{1}{2}\ldots\rightarrow{1}{2}\ldots\rightarrow{1}{2}\ldots\rightarrow{1}{2}\ldots\rightarrow{1}{2}\ldots\rightarrow{1}{2}\ldots\rightarrow{1}{2}\ldots\rightarrow{1}{2}\ldots\rightarrow{1}{2}\ldots\rightarrow{1}{2}\ldots\rightarrow{1}{2}\ldots\rightarrow{1}{2}\ldots\rightarrow{1}{2}\ldots\rightarrow{1}{2}\ldots\rightarrow{1}{2}\ldots\rightarrow{1}{2}\ldots\rightarrow{1}{2}\ldots\rightarrow{1}{2}\ldots\rightarrow{1}{2}\ldots\rightarrow{1}{2}\ldots\rightarrow{1}{2}\ldots\rightarrow{1}{2}\ldots\rightarrow{1}{2}\ldots\rightarrow{1}{2}\ldots\rightarrow{1}{2}\ldots\rightarrow{1}{2}\ldots\rightarrow{1}{2}\ldots\rightarrow{1}{2}\ldots\rightarrow{1}{2}\ldots\rightarrow{1}{2}\ldots\rightarrow{1}{2}\ldots\rightarrow{1}{2}\ldots\rightarrow{1}{2}\ldots\rightarrow{1}{2}\ldots\rightarrow{1}{2}\ldots\rightarrow{1}{2}\ldots\rightarrow{1}{2}\ldots\rightarrow{1}{2}\ldots\rightarrow{1}{2}\ldots\rightarrow{1}{2}\ldots\rightarrow{1}{2}\ldots\rightarrow{1}{2}\ldots\rightarrow{1}{2}\ldots\rightarrow{1}{2}\ldots\rightarrow{1}{2}\ldots\rightarrow{1}{2}\ldots\rightarrow{1}{2}\ldots\rightarrow{1}{2}\ldots\rightarrow{1}{2}\ldots\rightarrow{1}{2}\ldots\rightarrow{1}{2}\ldots\rightarrow{1}{2}\ldots\rightarrow{1}{2}\ldots\rightarrow{1}{2}\ldots\rightarrow{1}{2}\ldots\rightarrow{1}{2}\ldots\rightarrow{1}{2}\ldots\rightarrow{1}{2}\ldots\rightarrow{1}{2}\ldots\rightarrow{1}{2}\ldots\rightarrow{1}{2}\ldots\rightarrow{1}{2}\ldots\rightarrow{1}{2}\ldots\rightarrow{1}{2}\ldots\rightarrow{1}{2}\ldots\rightarrow{1}{2}\ldots\rightarrow{1}{2}\ldots\rightarrow{1}{2}\ldots\rightarrow{1}{2}\ldots\rightarrow{1}{2}\ldots\rightarrow{1}{2}\ldots\rightarrow{1}{2}\ldots\rightarrow{1}{2}\ldots\rightarrow{1}{2}\ldots\rightarrow{1}{2}\ldots\rightarrow{1}{2}\ldots\rightarrow{1}{2}\ldots\rightarrow{1}{2}\ldots\rightarrow{1}{2}\ldots\rightarrow{1}{2}\ldots\rightarrow{1}{2}\ldots\rightarrow{1}{2}\ldots\rightarrow{1}{2}\ldots\rightarrow{1}{2}\ldots\rightarrow{1}{2}\ldots\rightarrow{1}{2}\ldots\rightarrow{1}{2}
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Sequence 6, Application US/09672609
Patent No. 633405
GENERAL INFORMATION:
APPLICANT: Frempest, Philip R.
CURRENT PREFERENCE:
CURRENT APPETCATION NUMBER: US/09/672,609
CURRENT PILING DATE: 1908-02-18
FRIOR FILING DATE: 1998-02-18
SPRIOR FILING DATE: 1998-02-18
SOFTWARE: Microsoft Word 97 SR-2
SEQ ID NOS: 50
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88.2%; Pred. No. 4e-07;
tive 1; Mismatches 1; Indels
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Pred. No. 4e-07;
1; Mismatches 1; Indels
                           PRIOR APPLICATION NUMBER: 09/025,403
PRIOR FILINGFDATE: 1998-02-18
NUMBER OF SEQ ID NOS: 50
SOFTWARE: Microsoft Word 97 SR-2
SEQ ID NO 5
LENGTH: 124
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US-09-672-609-7
Sequence 7 Application US/09672609.
Patent No. 633405
GENERAL INFORMATION:
APPLICANT: Anderson, W.H. Kerr
APPLICANT: Tempest, Philip R.
APPLICANT: Carr, Fank J.
APPLICANT: Fank J.
APPLICANT: Harris, William J.
                                                                                                                                                                                                                                                                                                                                          NAME/KEY: Humanized COL-1 VH, HuVHAT
                                                                                                                                                                                                                                  TYPE: PRT ORGANISM: Artificial Sequence
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88.2%;
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Matches 15; Conservative
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nes 15, Conserv
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Matches
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us-09-865-198-2.rai

GENERAL INFORMATION:

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OTHER INFORMATION: Humanized heavy chain variable region expressed from ATCC OTHER INFORMATION: CRL-12208, and containing human NEWM VH FRs, murine COL-1 VH C OTHER INFORMATION: and Phe-27, Asn-28, Ile-29, Lys-30, Ser-76, Thr-78, Ala-79, OTHER INFORMATION: Tyr-80, Asn-97, and Thr-98
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APPLICANT: Harris, William J.
APPLICANT: Armour, Kathryn
TITLE OF INVENTION: High Affinity Humanized Anti-CEA Monoclonal Antibodies
FILE REFERENCE:
                                                                                                                                                                                                                                                                                        High Affinity Humanized Anti-CEA Monoclonal Antibodies
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CCATION: 1..124
COTER INFORMATION: Humanized heavy chain variable region containing human OTHER INFORMATION: NEWM VH FRs, murine COL-1 VH CDRs, and Phe-27, Asn-28, OTHER INFORMATION: Ile-29, Lys-30, Ser-76, Asn-97, and Thr-98
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CURRENT APPLICATION NUMBER: US/09/672,609
CURRENT FILING DATE: 2000-09-28
PRIOR APPLICATION NUMBER: 09/025,403
PRIOR FILING DATE: 1998-02-18
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CURRENT FILING DATE: 2000-09-28
PRIOR APPLICATION NUMBER: 09/025,403
PRIOR FILING DATE: 1998-02-18
NUMBER OF SEQ ID NOS: 50
SOFTWARE: Microsoft Word 97 SR-2
SEQ ID NO 12
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Sequence 12, Application US/09672609
Patent No. 6333405
RENERAL INFORMATION:
APPLICANT: Anderson, W.H. Kerr
APPLICANT: Tempest, Philip R.
                                                                                Sequence 11, Application US/09672609
Patent No. 6333405
                                                                                                                                GENERAL INFORMATION:
APPLICANT: Anderson, W.H. Kerr
APPLICANT: Tempest, Philip R.
APPLICANT: Carr, Frank J.
APPLICANT: Harris, William J.
APPLICANT: Armour, Kathry
TITLE OF INVENTION: High Affinity.
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SOFTWARE: Microsoft Word 97 SR-2
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Best Local Similarity 88.2%;
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US-09-672-609-12
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LENGTH: 124
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ORGANIEM: Artificial Sequence
FEATURE:
NAME/KEY: Humanized COL-1 VH, HuVHASTAY
LOCATION: 1..124
COTHER INFORMATION: Humanized heavy chain variable region containing human
OTHER INFORMATION: NEWM VH FR8, murine CoL-1 VH CDRS, and Ala-24, Phe-27, Asn-28,
OTHER INFORMATION: Thr-98
US-09-672-609-9
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APPLICANT: Anderson, W.H. Kerr
APPLICANT: Tempest, Philip R.
APPLICANT: Carr, Frank J.
APPLICANT: Carr, Frank J.
APPLICANT: Harris, William J.
APPLICANT: Armour, Kathryn
TILLE OF INVENTION: High Affinity Humanized Anti-CEA Monoclonal Antibodies
FILE REFERENCE:
CURRENT APPLICATION NUMBER: US/09/672,609
FUNDR PRIDK PALICATION NUMBER: 09/025,403
PRIOR APPLICATION NUMBER: 09/025,403
PRIOR APPLICATION NUMBER: 09/025,403
PRIOR FILING DATE: 1998-02-18
NUMBER OF SEQ ID NOS: 50
SOFTWARE: Microsoft Word 97 SR-2
SEQ ID NO 9
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APPLICANT: Tempest, Philip R.
APPLICANT: Tempest, Philip R.
APPLICANT: Carr, Frank J.
APPLICANT: Harris, William J.
APPLICANT: Armour, Kathryn
TITLE OF INVENTION: High Affinity Humanized Anti-CEA Monoclonal Antibodies
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88.2%; Pred. No. 4e-07;
tive 1; Mismatches 1; Indels
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Pred. No. 4e-07;
1; Mismatches 1; Indels
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CURRENT FILING DATE: 2000-09-28
PRIOR APPLICATION NUMBER: 09/025,403
PRIOR FILING DATE: 1998-02-18
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Patent No. 6333405
GENERAL INFORMATION:
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SOFTWARE: Microsoft Word 97 SR-2
SEQ ID NO 10
LENGTH: 124
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Best Local Similarity 88.2
Matches 15; Conservative
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Best Local Similarity
Matches 15; Conserv
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Best Local Similarity 88.2%; Pred. No. 4e-07; Matches 15; Conservative 1; Mismatches	OY 1 WIDPENGDSGXAPKFOG 17	Db 50 WIDPENGDTEYAPKFQG 66

Search completed: December 23, 2002, 07:33:12 Job time: 4.06395 secs

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(without alignments)
180.208 Million cell updates/sec
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2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep:*
3: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep:*
4: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep:*
5: /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep:*
6: /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep:*
7: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep:*
7: /cgn2_6/ptodata/2/pubpaa/US09_PUBCOMB.pep:*
8: /cgn2_6/ptodata/2/pubpaa/US09_PUBCOMB.pep:*
10: /cgn2_6/ptodata/2/pubpaa/US09_PUBCOMB.pep:*
11: /cgn2_6/ptodata/2/pubpaa/US09_PUBCOMB.pep:*
11: /cgn2_6/ptodata/2/pubpaa/US09_PUBCOMB.pep:*
11: /cgn2_6/ptodata/2/pubpaa/US09_PUBCOMB.pep:*
13: /cgn2_6/ptodata/2/pubpaa/US00_PUBCOMB.pep:*
13: /cgn2_6/ptodata/2/pubpaa/US00_PUBCOMB.pep:*
14: /cgn2_6/ptodata/2/pubpaa/US00_PUBCOMB.pep:*
GenCore version 5.1.3
Copyright (c) 1993 - 2002 Compugen Ltd.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               106657 segs, 16763532 residues
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Maximum Match 100%
Listing first 45 summaries
                                                                                                                              OM protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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101
1 WIDPENGDSGYAPKFQG 17
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Maximum DB seq length: 200000000
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Sequence:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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	Description		Sequence 2, Appli		Sequence 7, Appli	7	28,	27, 1	22, A				Sequence 29, Appl	-	Sequence 1, Appli	Sequence 3, Appli	Sequence 4, Appli	Sequence 5, Appli	Sequence 6, Appli	Sequence 7, Appli	Sequence 8, Appli
CHANGE	QI		US-09-976-787-2	US-09-865-198-2	US-09-976-787-7	US-09-865-198-7	US-09-976-787-28	US-09-865-198-27	US-09-976-787-22	US-09-865-198-21	US-09-976-787-23	US-09-865-198-22	US-09-976-787-29	US-09-865-198-28	US-09-974-052-1	US-09-974-052-3	US-09-974-052-4	US-09-974-052-5	US-09-974-052-6	US-09-974-052-7	US-09-974-052-8
	DB		10	10	10	10	10	10	10	10	10	10	10	10	6	6	6	6	6	6	6
	Query Match Length DB		17	17	117	117	240	240	17	17	117	117	238	238	124	124	124	124	124	124	124
dР	Query	1111111	100.0	100.0	100.0	100.0	100.0	100.0	93.1	93.1	93.1	93.1	93.1	93.1	89.1	89.1	89.1	89.1	89.1	89.1	89.1
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	Result No.		1	7	3	4		9	7	80	6	10	11	12	13	14	15	16	17	18	19

Sequence 9, Appli Sequence 10, Appl Sequence 11, Appl Sequence 12, Appli Sequence 3, Appli Sequence 5, Appli Sequence 6, Appli Sequence 6, Appli Sequence 7, Appli Sequence 10, Appli Sequence 10, Appli Sequence 11, Appl Sequence 11, Appl Sequence 12, Appl Sequence 12, Appl Sequence 11, Appl Sequence 11, Appl Sequence 12, Appl Sequence 11, Appl
9 US-09-974-052-9 9 US-09-974-052-10 9 US-09-974-052-11 9 US-09-974-051-13 9 US-09-974-051-3 9 US-09-974-051-3 9 US-09-974-051-6 9 US-09-974-051-6 9 US-09-974-051-6 9 US-09-974-051-6 9 US-09-974-051-8 9 US-09-974-051-9 US-09-974-051-10 9 US-09-974-051-11 10 US-09-910-059-31 10 US-09-910-059-31 10 US-09-910-059-11 10 US-09-910-059-11
122
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ALIGNMENTS

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Sequence 2, Application US/09865198
Patent No. US20020103345A1
GENERAL INFORMATION:
APPLICANT: Zhu, Zhenping
TITLE OF INVENTION: Bispecific Immunoglobulin-Like Antigen Binding Proteins and Me
TITLE OF INVENTION: Production
FILE REFERENCE: 11245,47102
CURRENT APPLICATION NUMBER: US/09/865,198
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                                Sequence 2, Application US/09976787; Sequence 2, Application US/09976787; Patent No. US2002006452841
GENERAL INFORMATION:
APPLICANT: Zhu, Zhenping; APPLICANT: Zhu, Zhenping; APPLICANT: Witte, Larry
TITLE OF INVENTION: Antibodies Specific to KDR and Uses Thereof
FILE REFERENCE: 11245/46505; CURRENT APPLICATION NUMBER: US/09/976,787
CURRENT FILING DATE: 2001-10-12
FRIOR APPLICATION NUMBER: US 60/117,726
PRIOR PILING DATE: 1999-01-29
NUMBER OF SEQ ID NOS: 40
SOFTWARE: WordPerfect 8.0 for Windows
SEQ ID NO 2.
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100.0%; Pred. No. 1.5e-09;
ative 0; Mismatches 0;
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Best Local Similarity 100.1
Matches 17; Conservative
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RESULT 1
US-09-976-787-2
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US-09-865-198-2
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RESULT 6
US-09-865-198-27

Sequence 27, Application US/09865198

Patent No. US20020103345A1

GENERAL INFORMATION:

APPLICANT: ZUL, Zhenping

TITLE OF INVENTION: Bispecific Immunoglobulin-Like Antigen Binding Proteins and Me

TITLE OF INVENTION: Production

FILE REFERENCE: 11245/47102

CURRENT APPLICATION NUMBER: US/09/865,198

CURRENT FILING DATE: 2001-05-24

PRIOR APPLICATION NUMBER: US 60/206,749

PRIOR FILING DATE: 2000-05-24

NUMBER OF SEO ID NOS: 34

SOFTWARE: WordPerfect 8.0 for Windows

SEO ID NO 27

SED ID NO 27

MUNICE NO 27
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| Sequence 28, Application US/09976787
| Patent No. US20020064528A1
| CENERAL INFORMATION:
| APPLICANT: Zhu, Zhenping
| APPLICANT: Witte, Larry
| TITLE OF INVENTION: Antibodies Specific to KDR and Uses Thereof
| FILE REFERENCE: 11245/46505
| CURRENT APPLICATION NUMBER: US/09/976,787
| CURRENT FILING DATE: 2001-10-12
| PRIOR PLILING DATE: 2000-01-28
| PRIOR APPLICATION NUMBER: US 60/117,726
| PRIOR APPLICATION NUMBER: US 60/117,726
| PRIOR SECTION NUMBER: US 60/117,726
| NUMBER OF SECTION NOS: 40
| SOFTWARE: WordPerfect 8.0 for Windows
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        Length 117;
                                                Indels
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    Score 101; DB 10;
Pred. No. 1.1e-08;
0; Mismatches 0;
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Best Local Similarity 100.0%; Pred. No. 2.3e-08;
Matches 17; Conservative 0; Mismatches 0;
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      100.0%;
    Ouery Match 100.
Best Local Similarity 100.
Matches 17; Conservative
                                                                                                             50 WIDPENGDSGYAPKFQG 66
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US-09-976-787-28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; ORGANISM: Mouse US-09-865-198-27
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LENGTH: 240
TYPE: PRT
                                                                                                                                                                                                RESULT 5
US-09-976-787-28
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US-09-976-787-22
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Patent No. US30020103345a1
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: Bispecific Immunoglobulin-Like Antigen Binding Proteins and Methor Production
FITLE OF INVENTION: Production
FILE REFERENCE: 11245/47102
CURRENT APPLICATION NUMBER: US/09/865,198
CURRENT FIGING DATE: 2001-05-24
PRIOR APPLICATION NUMBER: US 60/206,749
PRIOR PAPLICATION NUMBER: US 60/206,749
PRIOR FILING DATE: 2000-05-24
NUMBER OF SEQ ID NOS: 34
SOFTWARE: WordPerfect 8.0 for Windows
SEQ ID NO 74:
LENGTH: 147
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Saquence 7, Application US/09976787

Patent No. US2020064528A1

Senetat Incomparation

APPLICANT: Zhu, Larry

TITLE OF INVENTION: Antibodies Specific to KDR and Uses Thereof

FILE REFERENCE: 11245/46505

CURRENT APPLICATION NUMBER: US/09/976,787

CURRENT APPLICATION NUMBER: US 09/493,539

PRIOR APPLICATION NUMBER: US 60/117,726

PRIOR PILING DATE: 2000-01-28

PRIOR FILING DATE: 1099-01-29

NUMBER OF SEQ ID NOS: 40

SOFTWARE: WordPerfect 8.0 for Windows
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100.0%; Pred. No. 1.1e-08;
tive 0; Mismatches 0;
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CURRENT FILING DATE: 2001-05-24
PRIOR APPLICATION NUMBER: US 60/206,749
PRIOR FILING#DATE: 2000-05-24
NUMBER OF SEG ID NOS: 34
SOFTWARE: WordPerfect 8.0 for Windows
SEQ ID NO 2
LENGTH: 17
TYPE: PRT
ORGANISM: Mouse
US-09-865-198-2
                                                                                                                                                                                                                                                                                                                    50 WIDPENGDSGYAPKFOG 66
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Best Local Similarity 100.
Matches 17. Conservative
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Matches 17; Conserv
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US-09-976-787-7
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US-09-865-198-22

Sequence 22, Application US/09865198

Sequence 22, Application US/09865198

Sequence 22, Application US/09865198

Sequence 22, Application US/09865198

Sequence 22, Application US/09/09861

GENERAL INFORMATION:

TITLE OF INVENTION: Bispecific Immunoglobulin-Like Antigen Binding Proteins and Me
TITLE OF INVENTION: Production

TITLE OF INVENTION: Production

CURRENT FILING DATE: 2001-05-24

PRIOR FILING DATE: 2000-05-24

NUMBER OF SEQ ID NOS: 34

SEQ ID NO 22

LENGTH: 117
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Batent No. US20020064528A1

GENERAL INFORMATION:
APPLICANT: Zhu, Zhenping

APPLICANT: Witte, Larry

TITLE OF INVENTION: Antibodies Specific to KDR and Uses Thereof
FILE REFERENCE: 11245/46505

CURRENT APPLICATION NUMBER: US/09/976,787

CURRENT FILING DATE: 2001-10-12

PRIOR APPLICATION NUMBER: US 60/117,726

PRIOR APPLICATION NUMBER: US 60/117,726

PRIOR PELING DATE: 1999-01-29

NUMBER OF SEQ ID NOS: 40

SOFTWARE: WordPerfect 8.0 for Windows

SEQ ID NO 29
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Pred. No. 1.3e-07;
0; Mismatches 1; Indels
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1. 1.3e-07; Indels
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Pred. No.
        PRIOR APPLICATION NUMBER: US 60/117,726 PRIOR FILING DAFE: 1999.01-29 NUMBER OF SEQ ID NOS: 40 SOFTWARE: WordPerfect 8.0 for Windows SOFTWARE: WordPerfect 8.0 for Windows ENG ID NO 23 SEQ ID NO 23 TYPE: PRT
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94.1%;
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94.1%;
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Best Local Similarity 94.1
Matches 16; Conservative
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                                                                                                                                                                                                       Query Match
Best Local Similarity
Matches 16; Conserv
                                                                                                                                              ; ORGANISM: Mouse US-09-976-787-23
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; ORGANISM: Mouse US-09-976-787-29
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Patent No. US20020103345al
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: Bispecific Immunoglobulin-Like Antigen Binding Proteins and Methor TITLE OF INVENTION: Production
FILE REFERENCE: 11245/47102
CURRENT APPLICATION NUMBER: US/09/865,198
CURRENT FILING DATE: 2001-05-24
PRIOR APPLICATION NUMBER: US 60/206,749
PRIOR APPLICATION NUMBER: US 60/206,749
PRIOR FILING DATE: 2000-05-24
NUMBER OF SEQ ID NOS: 34
SSQ ID NO 21
LENGTH: 17
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Sequence 22, Application US/09976787
Patent No. US20020064528a1
GENERAL INFORMATION
SERVERAL INFORMATION
TO SERVERAL INFORMATION
THE PER INVENTION: Antibodies Specific to KDR and Uses Thereof
FILE REFERENCE: 1144546505
CURRENT APPLICATION NUMBER: US/09/976,787
CURRENT APPLICATION NUMBER: US 09/493,539
PRIOR FILING DATE: 2000-01-28
PRIOR FILING DATE: 1909-01-29
PRIOR FILING DATE: 1999-01-29
NUMBER OF SEQ ID NOS: 40
SEQ ID NO 22
LENGTH: 17
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Sequence 23, Application US/09976787
Sequence 23, Application US/09976787
Sequence 23, Application US/09976787
Sequence 23, Application US/09976787
Sequence 23, Application US-08976787
Sequence 23, Application US-08976787
Sequence 23, Application US-0897676, 787
CURRENT APPLICATION NUMBER: US/09/976, 787
CURRENT FILING DATE: 2001-10-12
SPRIOR FILING DATE: 2000-01-28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 17;
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                                                                                                                                                                                                                                                                                                                                                                                                                     Score 94; DB 10;
Pred. No. 1.7e-08;
0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 94; DB 10;
Pred. No. 1.7e-08;
0; Mismatches 1,
                                                                                                                                                                                                                                                                                                                                                                                                                   ch 93.1%;
1 Similarity 94.1%;
16; Conservative
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illarity 94.1%;
Conservative
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Best Local Similarity
Matches 16; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
Matches 16; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: PRT
ORGANISM: Mouse
US-09-865-198-21
                                                                                                                                                                                                                                                                                                                                                            ; ORGANISM: Mouse
US-09-976-787-22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 8
US-09-865-198-21
                                                                                                                                                                                                                                                                                                                                              TYPE: PRT
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Sequence 4, Application US/09974052

Sequence 4, Application US/09974052

Patent No. US20020165387A1

GENERAL INFORMATION:

APPLICANT: Tempest, Philip R.

APPLICANT: Tempest, Philip R.

APPLICANT: Armour, Kathryn

APPLICANT: Armour, Kathryn

TITLE OF INVENTYON: High Affinity Humanized Anti-CEA Monoclonal Antibodies

CURRENT APPLICATION NUMBER: US/09/974,052

CURRENT APPLICATION NUMBER: US/09/974,052

CURRENT APPLICATION NUMBER: US/09/974,052

CURRENT APPLICATION NUMBER: US/09/974,052

PRIOR FILING DATE: 1998-02-18

PRIOR FILING DATE: 1998-02-18

PRIOR FILING DATE: 1997-10-30

PRIOR FILING DATE: 1997-10-31
                                                                                                                                                                                                                                                                              APPLICANT: Tempest, Philip R.
APPLICANT: Tempest, Philip R.
APPLICANT: Tempest, Philip R.
APPLICANT: Tempest, Philip R.
APPLICANT: Haris, William J.
APPLICANT: Armour, Kathryn
TITLE OF INVENTION: High Affinity Humanized Anti-CEA Monoclonal Antibodies
FILE REFERENCE:
CURRENT PAPLICANTON NUMBER: US/09/974,052
CURRENT FILING DATE: 2001-10-09
PRIOR APPLICATION NUMBER: US 09/025,403
PRIOR APPLICATION NUMBER: US 09/025,403
PRIOR APPLICATION NUMBER: US 09/029,694
PRIOR PILING DATE: 1996-10-30
PRIOR FILING DATE: 1996-10-31
NUMBER OF SEQ ID NOS: 50
SOFTWARE: Microsoft Word 97 SR-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME/KEY: Humanized COL-1 VH, HuVH
LOCATION: 1..124
COTHER INFORMATION: Humanized heavy chain variable region containing human OTHER INFORMATION: NEWM VH FRs, murine COL-1 VH CDRs, and Phe-27, Asn-28, COTHER INFORMATION: Ile-29, Lys-30, Asn-97, and Thr-98
US-09-974-052-3
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88.2%; Pred. No. 5.4e-07;
tive 1; Mismatches 1; Indels
                                                                                                                                                                                    Sequence 3, Application US/09974052
Patent No. US20020165387Al
GENERAL INFORMATION:
APPLICANT: Anderson, W.H. Kerr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQ ID NOS: 50
SOFTWARE: Microsoft Word 97 SR-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ORGANISM: Artificial Sequence
                        1 WIDPENGDSGYAPKFQG 17
                                                    50 WIDPENGDTEYAPKFQG 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 WIDPENGDSGYAPKFQG 17
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Best Local Similarity 88.2
Matches 15; Conservative
                                                                                                                                             RESULT 14
US-09-974-052-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQ ID NO 3
LENGTH: 124
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US-09-974-052-4
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US-09-865-198-28
Sequence 28, Application US/09865198
Patent No. US20020103345A1
GENERAL INFORMATION:
APPLICANT: Will Zeneping
TITLE OF INVENTION:
FILE PEPERGENE: 11245/47102
CURRENT PRIGATION NUMBER: US/09/865,198
CURRENT PRIGATION NUMBER: US 60/206,749
PRIOR FILING DATE: 2001-05-24
NUMBER OF SEQ ID NOS: 34
SOFTWARE: WASTORELET 2000-05-24
SEQ ID NOS: 34
SEQ ID NOS: 38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-VU-S-94-UD-Z-1
Sequence 1. Application US/09974052
Patent No. US20020165387A1
GENERAL INFORMATION:
APPLICANT: Anderson, W.H. Kerr
APPLICANT: Tempest, Philip R.
APPLICANT: Tempest, Philip R.
APPLICANT: Frank J.
APPLICANT: Armour, Kathryn
TITLE OF INVENTION: High Affinity Humanized Anti-CEA Monoclonal Antibodies
CURRENT APPLICATION HIGH Affinity Humanized Anti-CEA Monoclonal Antibodies
FILE REFERENCE:
CURRENT APPLICATION NUMBER: US/09/974,052
CURRENT FILING DATE: 1998-02-18
PRIOR FILING DATE: 1998-02-18
PRIOR FILING DATE: 1997-10-30
PRIOR APPLICATION NUMBER: US 60/029,694
PRIOR PRILING DATE: 1996-10-31
NUMBER OF SEQ ID NOS: 50
SOFTWARE: Microsoft Word 97 SR-2
SEQ ID NO 1
LENGTH: 124
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Pred. No. 2.6e-07;
0; Mismatches 1; Indels
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Pred. No. 2.6e-07;
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Pred. No. 5.4e-07;
1; Mismatches 1
                                               0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           93.1%;
94.1%;
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88.2%;
                        Best Local Similarity 94.1%;
Matches 16; Conservative
                                                                                                                       50 WIDPENGDSDYAPKFQG 66
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; LOCATION: 1..124
US-09-974-052-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
Matches 15; Conserva
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Matches 160 Conserv
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; TYPE: PRT
; ORGANISM: Mouse
US-09-865-198-28
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US-09-974-052-1
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GenCore version 5.1.3
Copyright (c) 1993 - 2002 Compugen Ltd.
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OM protein - protein search, using sw model

December 23, 2002, 07:17:57; Search time 3.36047 Seconds Run on:

(without alignments)
486.327 Million cell updates/sec

US-09-865-198-2 101 1 WIDPENGDSGYAPKFQG 17 Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283224 seqs, 96134422 residues Searched:

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

PIR_73:* Database :

pir1:* pir2:* pir3:* pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

		Iq heavy chain V r	q heavy cha	q heavy chain pr	q heavy chain v	q heavy	chain V	Ig heavy chain V r	q heavy	Ig heavy chain V r	ь.	q heavy chain	d heavy	Ig heavy chain V r	g heavy	ь	g heavy	ь	g heavy	g heavy	g heavy	g heavy cha	g heavy cha	ь	g heavy cha	Ig heavy chain V-1	Ig heavy chain V r	Ig heavy chain V r	nti-Sm antibody	Ig heavy chain V-D
	ID	A36025					E37262			S31600	E1HUND	S54912	PH1670	S23623	S34014	826938	S26912	D37262	PH1013	PH1012	S31680	S18551	S36265	S03471	58	354	0	Þ	953	034
	DB	~	7	7	7	7	7	N	7	~	٦	7	7	~	~	7	~	7	~	7	7	7	7	7	7	7	7	7	7	7
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dР	Query Match	89.1	ä	Ξ.	ა	7	66.3	ė.	ů.	ف	66.3	63.4	63.4	63.4	62.4	61.4	61.4	61.4	61.4	61.4	61.4	61.4	61.4	61.4	61.4	61.4	61.4	61.4	61.4	59.4
	Score	06	82	82	80	78	29	67	67	67	67	64	64	64	63	62	62	62	62	62	62	62	62	62	62	62	62	62	62	9
	Result No.		7	m	4	ស	9	7	80	6	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	56	27	28	29

C;Species: Mus musculus (house mouse)
C;Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 21-Jan-2000
C;Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 21-Jan-2000
C;Accession: S23174; S33133
R;Monestier, M.; Fasy, T.M.; Losman, M.J.; Novick, K.E.; Muller, S.
Submitted to the EMBL Data Library, July 1992
A;Description: Structure and binding properties of monoclonal antibodies to core hist
A;Reference number: S25174

A;Cross-references: EMBL:X67622; NID:951854; PIDN:CAA47880.1; PID:9938259 A;Accession: S33133 A;Status: preliminary A;Molecule type: mRNA

A; Residues: 1-118 <MON> A; Accession: S25174 A; Status: preliminary A; Molecule type: mRNA

	chain	Ig heavy chain V r	Ig heavy chain V r	Ig heavy chain V r	chain	chain	Ig heavy chain V r	chain	heavy chain	chair	heavy chair	heavy chair	heavy chair	heavy chair	chair
S49220	S46465	826909	S29544	S26921	S24289	S29594	PH1667	PH1666	S31999	S26911	S03482	144151	A27646	C37262	PH1668
7	7	7	7	7	7	7	7	7	~	7	~	7	~	~	~
221	7.7	86	98	86	116	178	114	118	120	86	115	126	107	66	109
59.4	58.4	58.4	57.4	57.4	57.4	57.4	56.4	56.4	56.4						
				58 57.4										54 53.5	

ALIGNMENTS

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R;Caton, A.J.; Koprowski, H.
Proc. Natl. Acad. Sci. U.S.A. 87, 6450-6454, 1990
A;Title: Influenza virus hemagglutinin-specific antibodies isolated from a combinator
A;Reference number: A36025; MUID:90349634; PMID:1696733
A;Accession: A36025
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
Ig heavy chain V region (PR8-1) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 11-Jan-1991 #sequence_revision 11-Jan-1991 #text_change 23-Jul-1999
C;Accession: A36025, B36025
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                             A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-82 <CAT>
A;Cross-references: GB:M55999; NID:g194955; PIDN:AAA38112.1; PID:g194956
A;Note: PR8-1
                                                                                                                                                                                                                                                                                                                                                                    A;Accession: E36025
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 19-82 <CA2>
A;Cross-references: GB:M57273; NID:g194963; PIDN:AAA38116.1; PID:g194964
A;Note: clone PRS-21
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 90; DB 2; Length 82;
Pred. No. 4.4e-07;
1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 89.1%;
Best Local Similarity 88.2%;
Matches 15; Conservative
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S25174
Ig heavy chain V region - mouse
C; Species: Mus musening '
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 WIDPENGDSGYAPKFQG 17
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C; Species: Homo sapiens (man)
C; Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 23-Jul-1999
C; Accession: S26918
A; Title: The repertoire of human germline V(H) sequences reveals about fifty groups on A; Title: The repertoire of human germline V(H) sequences reveals about fifty groups on A; Reference number: S26885; MUID:93021117; PMID:1404388
A; Reference number: S26885; MUID:93021117; PMID:1404388
A; Residues: TS6918
A; Residues: 1-98 < TOMA
A; Residues: 1-98 < TOMA
A; Residues: 1-98 < TOMA
A; Residues: 1-98 (TOMA)
C; Superfamily: immunoglobulin V region; immunoglobulin homology
C; Keywords: heterotetramer; immunoglobulin
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19 heavy chain V region (6H2) - mouse (fragment)

C;Species: Mus musculus (house mouse)

C;Date: 30-Aug-1991 #sequence_revision 30-Aug-1991 #text_change 09-May-1997

C;Date: 30-Aug-1991 #sequence_revision Notation of the sequence 
                                                                          C.Species: Mas musculus (house mouse)
C.Species: Mas musculus (house mouse)
C.Accession: 552445
Submitted to the EMBL Data Library, November 1994
A.Description: Specific amplification by the polymerase chain reaction of rearranged A.Reference number: S52445
A.Accession: S52445
A.Residues: 1-137 < BER>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;cross-references: EMBL:X82690; NID:g673439; PIDN:CAA58011.1; PID:g673440 C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A:Status: preliminary; not compared with conceptual translation A;Molecule type: mRNA A;Residues: 1-85 <GGS>
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C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Reywords: heterotetramer; immunoglobulin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Introns: 16/1
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;34-115/Domain: immunoglobulin homology <IMM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 137
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Pred. No. 0.0019;
1; Mismatches 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 2;
6e-05;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2; Mismatches
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Pred. No. 6
                                                 - mouse
                                            Ig heavy chain V region precursor
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Local Similarity 75.0%;
les 12; Conservative
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76.5%;
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Best Local Similarity 76.5
Matches 13; Conservative
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Best Local Si
Matches 12;
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C;Species: Mus musculus (house mouse)
C;Species: Mus musculus (house mouse)
C;Species: Mus musculus (house mouse)
C;Date: 18-Feb-1994 #sequence_revision 10-Nov-1995 #text_change 21-Jan-2000
C;Accession: $15672
R;Tempest, P.R; Bremner, P.; Lambert, M.; Taylor, G.; Furze, J.M.; Carr, F.J.; Harris, Bio/Technology, 9, 266-271, 1991
Bio/Technology, 9, 266-271, 1991
A;Title: Reshaping a human monoclonal antibody to inhibit human respiratory syncytial vi A;Reference nümber: $15672; MUID:91337412; PMID:1367835
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R;Kofler, R.; Nonan, D.J.; Strohal, R.; Balderas, R.S.; Moller, N.P.H.; Dixon, F.J.; The Bur. J. Immunol. 17, 91-95, 1987
A;Title: Molecular analysis of the murine lupus-associated anti-self response: involveme A;Reference number: SQ4573; MUID:87133856; PMID:3102255
A;Accession: SQ 576
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ig heavy chain precursor V region (MRL-histone 7H) - mouse (fragment)
C;Species: Musfmusculus (house mouse)
C;Date: 04-Dec 1992 #sequence_revision 04-Dec-1992 #text_change 21-Jan-2000
                                  A,Cross-referenčes: EMBL:X67622; NID:951854; PIDN:CAA47880.1; PID:9938259 C. Superfamilty: Ümmunoglobuln V region; immunoglobulin homology C;Keywords: herefortetramer; immunoglobulin homology <!-- Fixed the continuoglobulin homology <!-- Fixed the continuous homology <!-- Fixed the continuou
                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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A;Molecule type: mRNA
A;Residues: 18-116 <TEM>
A;Residues: 18-116 <TEM>
A;Cross-references: EWBL:X58835; NID:951978; PIDN:CAA41644.1; PID:951979
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Reywords: heterotetramer; immunoglobulin
F;15-98/Domain: immunoglobulin homology <IMM>
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A; Residues: 1-1336 <KOF>
A; Cross-references: EMBL:X14624; NID:952029; PIDN:CAA32777.1; PID:952030
C; Superfamily: £immunoglobulin v region; immunoglobulin homology
C; Keywords: heterotetramer; immunoglobulin
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Pred. No. 2.4e-05;
0; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                 Length 118;
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Pred. No. 1.4e-05;
1; Mismatches 2; Indels
                                                                                                                                                                                                                                              Score 82; DB 2; Length 110
Pred. No. 1.2e-05;
2; Indels
                                                                                                                                                                                                                                                                                                                                                                                     1; Mismatches
                                                                                                                                                                                                                                                                                      81.2%;
82.4%;
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| Similarity 82.48;
| 14; Conservative
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Conservative
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Best Local Similarity 82.4
Matches 14.1 Conservative
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Best Local Similarity
Matches 14; Conserva
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hes 14% Conserv
A; Residues: 1-118 <MO2>
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Matches
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A.Cross-references: GDB:128528; OMIN:147070
A;Map position: 14q32.33-14q32.33
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Superfamily: immunoglobulin V region; pyroglutamic acid
E;1-15/Domain: signal sequence #status predicted <SIG>
F;16-143/Pomain: signal sequence #status predicted <SIG>
F;30-113/Domain: immunoglobulin homology <IMM>
F;30-113/Domain: immunoglobulin homology <IMM>
F;30-113/Domain: immunoglobulin carboxylic acid (Gln) (in mature form) #status experificial site: pyrrolidone carboxylic acid (Gln) (in mature form) **
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R;Kenten, J.H.; Molgaard, H.V.; Houghton, M.; Derbyshire, R.B.; Viney, J.; Bell, L.O. Proc. Natl. Acad. Sci. U.S.A. 79, 6661-6665, 1982
A;Title: Cloning and sequence determination of the gene for the human immunoglobulin A;Reference number: A93933; MUID:83065234; PMID:6815656
                                                                                                                                                                A; Molecule type: mRNA
A; Mesiduces: 1.143 KKEN>
R; Residuces: 1.143 KKEN>
R; Bennich, H.H.; Johansson, S.G.O.; Von Bahr-Lindstrom, H.
in Immediate Hypersensitivity: Modern Concepts and Developments, Bach, M.K., ed., As Reference number: A94418
A; Korntents: annotation; partial sequence
A; Note: this epsilon chain was isolated from a myeloma protein
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C; Species: Homo sapies (man)
C; Date: 24-Feb-1994 #sequence_revision 24-Feb-1994 #text_change 16-Aug-1996
C; Accession: PH1670
B; Hillson, J.L.; Karr, N.S.; Oppliger, I.R.; Mannik, M.; Sasso, E.H.
J. Exp. Med. 178, 331-336, 1993
A; Title: The structural basis of germline-encoded VH3 immunoglobulin binding A; Reference number: PH1642; MUID:93301610; PMID:8315388
A; Accession: PH1670
A; Residues: 1-110 <HIL>A; Resperimental source: B cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    C; Species: Homo sapiens (man) (ring) #text_change 21-Jan-2000 C; Species: Homo sapiens (man) (ring) #text_change 21-Jan-2000 C; Date: 17-Feb-1998 #sequence_revision 26-Feb-1998 #text_change 21-Jan-2000 C; Date: 17-Feb-1998 #sequence_revision 26-Feb-1998 #text_change 21-Jan-2000 C; Date: 17-Feb-1998 #sequence_revision 26-Feb-1998 #text_change 21-Jan-2000 S; Janulinson, M; Walter, G; Cook, X Y.Z.; Winter, G. Stabilinson, S54912 A; Reference number: 554912 A; Reference number: 554912 A; Reference: Feb. S54912 A; Molecule type: DNA A; Molecule type: DNA A; Molecule type: DNA A; Residues: 1-86 CTOM> A; Cross-references: EMBL: 218904; NID:g840779; PIDN:CAA79341.1; PID:g840780 A; Cross-references: EMBL: 218904; NID:g840779; Immunoglobulin homology C; Superfamily: Immunoglobulin homology C; Superfamily: Immunoglobulin homology C; MMA>
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Pred. No. 0.0033;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 64; DB 2; Le
Pred. No. 0.0057;
1; Mismatches 5;
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64.78;
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58.8%;
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Best Local Similarity
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Best Local Similarity
Matches 11; Conser
                                                                                                                                                                                                                                                                                                                                                                                                   A; Gene: GDB: IGHV@
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Matches
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Ig heavy chain V region - human (fragment)
C; Specias: Homo saplens (man)
C; Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 23-Jul-1999
C; Accession: S31596
R; Cuisinier, A.W.; Gauthier, L.; Boubli, L.; Fougereau, M.; Tonnelle, C.
Submitted to the EMBL Data Library, June 1992
A; Recence number: S31585
A; Reference number: S31585
A; Reterence number: S31585
A; Reterence number: S31585
A; Status: preliminary
A; Molecule type: mRNA
A; Residues: 1-132 < Cui>A; Residues: 1-132 < Cui>A; Residues: Li-132 < Cui>A; Cross-references: EMBL: Z14166; NID: 930996; PIDN: CAA78535.1; PID: 930997
C; Superfamily: immunoglobulin V region: immunoglobulin homology
C; Keywords: heterotetramer: immunoglobulin homology < LMM>
F; 34-117/Domain: immunoglobulin homology < LMM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       C; Species: Homo sapiens (main) (itagment)
C; Species: Homo sapiens (main)
C; Species: Homo sapiens (main)
C; Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 23-Jul-1999
C; Accession: S31600
R; Cuisinier, A.M.; Gauthier, L.; Boubli, L.; Fougereau, M.; Tonnelle, C.
R; Cuisinier, A.M.; Gauthier, L.; Boubli, L.; Fougereau, M.; Tonnelle, C.
A; Description: Mechanisms that generate human immunoglobulin diversity operate from the A; Reference number: S31585
A; Reference number: S31585
A; Accession: S31600
A; Status: preliminary
A; Molecule type: mRNA
A; Residues: 1-136 <CUI>
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C;Species: Homo sapiens (man)
C;Date: 31-Mar-1981 #sequence_revision 05-Apr-1983 #text_change 21-Jan-2000
C;Accession: A93933; A02026
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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                                                                              Length 98;
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                                                                           Score 67; DB 2;
Pred. No. 0.0022;
5; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 67; DB 2;
Pred. No. 0.0031;
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Pred. No. 0.0032;
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                  F;15-98/Domain: immunoglobulin homology <IMM>
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58.8%;
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ilarity 58.8%;
Conservative
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larity 58.8%;
Conservative
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WMNPNSGNTGYAQKFQG 85
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Best Local Similarity
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Best Local Similarity
Matches 10; Conserv
                                                                                                      Local Similarity es 10; Conserv
                                                                           Query Match
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1 WIDPENGDSGYAPKFQG 17
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Best Local Similarity
Matches 10; Conserv
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C; Species: Homo sapiens (man)
C; Date: 13-Jan_1995 #sequence_revision 13-Jan-1995 #text_change 23-Jul-1999
C; Accession: S23623
R; Oleo, T.; Luff E.W.; Huang, D.F.; Soto-Gil, R.W.; Deftos, M.; Kozin, F.; Carson, D.A.; J. Exp. Med. 175, 831-842, 1992
A; Title: Genetic analysis of self-associating immunoglobulin G rheumatoid factors from the Reference number: S23623; MUID:92156804; PMID:1740665
A; Reference number: S23623; MUID:92156804; PMID:1740665
A; Residues: preliminary
A; Molecule type: DNA
A; Residues: 1-101 OLE>
A; Cross-references: EMBL:X59702; NID:932010; PIDN:CAA42223.1; PID:932011
C; Superfamily: immunoglobulin V region; immunoglobulin homology
C; Keywords: hereforetramer: immunoglobulin
C; Keywords: hereforetramer: immunoglobulin
F; 34-117/Domain: immunoglobulin homology
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C; Species: Homo sapiens (main)
C; Species: Homo sapiens (main)
C; Date: 02-Dec-1993 #sequence_revision 10-Nov-1995 #text_change 16-Aug-1996
C; Accession: $34014; $30535
R; Marlette, X; Tsapis, A.; Brouet, J.C.
R; Marlette, X; Tsapis, A.; Marlette, Ma
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C;Superfamily: fimmunoglobulin V region; immunoglobulin homology C;Keywords: heterotetramer; immunoglobulin F;7-90/Domain: immunoglobulin homology <IMM>
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C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;15-98/Domain: immunoglobulin homology <IMM>
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                                                                                                                                                  Score 64; DB 2; Length 110
Pred. No. 0.0075;
4; Mismatches 3; Indels
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Pred. No. 0.012;
3; Mismatches
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Ig heavy chain V region (DP-75) - human (fragment)
C;Species: Homo sapiens (man)
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58.8%;
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52.9%;
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58.8%;
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Best Local Similarity 52.9
Matches 9; Conservative
                                                                                                                                                  Query Match Best Local Similarity Matches 10% Conserva
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S23623
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Ritchinson, I.M.; Walter, G.; Marks, J.D.; Llewelyn, M.B.; Winter, G.
J. Mol. Biol. 227, 776-798, 1992
A; Mitle: The repertoire of human germline V(H) sequences reveals about fifty groups o
A; Reference number: $26885; MUID:93021117; PMID:1404388
A; Reference number: $26885; MUID:93021117; PMID:1404388
A; Reference number: acid sequence not shown; translation not shown
A; Molecule type: DNA
A; Residues: 1-98 <TOM>
                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Cross-references: EMBL:214071; NID:g32969; PIDN:CAA78451.1; PID:g32970
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, July 1992
C;Superfamily: immunoglobulin v region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;15-98/Domain: immunoglobulin homology <IMM>
22-Nov-1993 #sequence_revision 17-Nov-1995 #text_change 23-Jul-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 98;
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58.8%; Pred. No. 0.014;
tive 3; Mismatches 4
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Search completed: December 23, 2002, 07:31:31 Job time: 4.36047 secs

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Gaps

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Indels

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December 23, 2002, 07:16:17; Search time 1.68023 Seconds (without alignments) 419.643 Million cell updates/sec
GenCore version 5.1.3
Copyright (c) 1993 - 2002 Compugen Ltd.
                                                                                            OM protein - protein search, using sw model
                                                                                                                                            Run on:
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US-09-865-198-2 101 1 WIDPENGDSGYAPKFQG 17 Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

112892 seqs, 41476328 residues Searched: Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SwissProt_40:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	1	sapien	sapien	sapien	sapien	musculu	musculu	musculu	apil	n ae	culu	apil	n ae .	aln	lla	sia	sia	chia	teri	n ae	sia	culu	culu	sia	sia	sia	sia	sia	sia	sia	pien	gall	pien	ble
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	Description	P01744	P01743	P23083	Q9bw91	P01756	P01757	P06330	P26550	P10388	P06327	P06924	P02861	P46033	048412	P16624	P22882	P23306	006223	P08489	P29697	P01758	P01747	P50927	P50928	P50929	P50930	P50931	P05372	052764	008499	P98157	P98177	011190
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			ents)	Vertebrata; ; Hominidae	Derbyshire	e gene for a myeloma	Strom		ISOLATED			7-I REG	2).		Len 3;	
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AMPE_HUMAN HVOZ_MOUSE ENO_STAAM ENO_STRPY CALB_RAT CALB_RAT IP3S_MOUSE CALB_HUMAN COAL_BOWIN COAL_SHEEP	AL	PRT	ted) sequence up annotation ND precursos	a; Cra s; Cat	15656; Hough	determination of chain expressed	. 0	mode	ILON		Signal.	IG H PYRR	T -> V IH -> H VG -> G MISSING		Score Pred. 4; Mis	
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957 140 434 434 434 482 670 1281 1804 1806 2346		STANDARD;	6	n). ; Cho ; Pri	PubMe ard H	nce d	nsson	sitiv	THIS	D. (6) 19	Gv; 1. region;	147	115 21 54 68 125	14	vat	YAPKFQG : YAPRFQG
11.1 0.04444444444 0.066666666666666666666666666666666666		STA	(Rel. (Rel. (Rel.	ens (Human) ; Metazoa; Eutheria; D=9606;	[1] SEQUENCE FROM N.A. MEDLINE-83065234; Pubmed-6815656; Kenten J.H., Molgaard H.V., Houghton	Bell L.O., Gould H.J.; "Cloning and sequence of immunoglobulin epsilon Proc. Natl Acad Sci	OF 20-147.	(In) Bach M.K. (eds.); Immediate hypersensitivity: Marcel Dekker, New York (197	ANEOUS:	PIR, A02026; EIHUND. HSSP; P01789; IMCP. InterPro; IPR003006; InterPro; IPR003596; Pfam: PF00047; ig: 1.	406; IG lin v r	700 700	41 21 53 67 125	147 147 AA;	66. Similarity 58. O; Conservative	WIDPENGDSGYAPKFQG : : : : WINPNSGGINYAPRFQG
4 .44444444444444444444444444444444444		T 1 HUMAN HVIC_HUMAN	21-JUL-1986 16-OCT-2001 16-OCT-2001 19 heavy cha	Homo sapiens (Hu Eukaryota; Metaz Mammalia; Euther NCBI_TaxID=9606;	NCE FR NE=830	ing an loglobu	[2] SEQUENCE OF Bennich H.H	Bach M liate h	ISCELL	, A02026; E P; P01789; erPro; IPRO erPro; IPRO n: PF00047;	SMART; SM00406; Immunoglobulin V	ES LES		TER	도 근	WIDPEN : : WINPNS
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EMBL; AY026252; AAK07671.1; -. EMBL; BC000542; AAH00542.1; -. Genew; HGNC:8056; NUDT9.
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Best Local Similarity
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MEDLINE-83144028; PubMed-6298778;
Rechavi Garam D., Glazer L., Zakut R., Givol D.;
"Evolutionary aspects of immunoglobulin heavy chain variable region
                                                                                                    21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
15-JUL-1999 (Rel. 03, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
16 heavy chain V-I region HG3 precursor.
Homo saplens (Human).
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID_9906;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE 88296408; PubMed-2841108;
Matsuda F., Lee K.H., Nakai S., Sato T., Kodaira M., Zong S.O.,
Johno H.; Fukuhara S., Honjo T.;
"Dispersed localization of D segments in the human immunoglobulin
heavy-chain locus.";
EMBO J.F7:1047-1051(1988).
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Pred. No. 0.28;
2; Mismatches 5; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Proc. Natl. Acad. Sci. U.S.A. 80:855-859(1983).
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01-NOV-1991 (Rel. 20, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
Homo saplens (Human).
                                                        117 AA.
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56.2%;
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Best Local Samilarity 56.2
Matches 9; Conservative
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70 INPSGGSTSYAQKFQG 85
                                                        STANDARD;
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HV1B_HUMAN
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MEDLINE-21279171; PubMed-11385575;
MEDLINE-21279171; PubMed-11385575;
MEDLINE-21279171; PubMed-11385575;
Schmitz C., Stokes A.J., Zhu Q., Bessman M.J., Penner R.; Kinet J.-P., Scharenberg A.M.;
"ADD-ribose gating of the calcium-permeable LTRPC2 channel revealed by Nudix motif homology.";
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-!- TISSUE SPECIFICITY: Ubiquitous.
-!- SIMILARITY: BELONGS TO THE NUDIX HYDROLASE FAMILY. NUDF SUBFAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        15-JUN-2002 (Rel. 41, Created)
15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
15-JUN-2002 (Rel. 41, Last annotation update)
ADP-ribose pyrophosphatase (EC 3.6.1.13) (ADP-ribose diphosphatase)
(Adenosine diphosphortbose pyrophosphatase) (ADPR-PPase) (ADP-ribose phosphoydrolase) (Nucleoside diphosphate-linked molety X motif 9).
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Submitted (NOV-2000) to the EMBL/GenBank/DDBJ databases.
-!- CATALYTIC ACTIVITY: ADP-ribose + H(2)O = AMP + D-ribose
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             50.5%; Score 51; DB 1; Length 117; 56.2%; Pred. No. 0.28;
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                                                                                                                                                                                      EMBL; X07448; -; NOT_ANNOTATED_CDS
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InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_V.
Pfam; PF00047; ig; 1.
SMART; SM00406; IGV; 1.
Immunoglobulin V region; Signal.
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21-JUL-1986 (Rel. 01, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
16 heavy chain V region J558.
Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Nus.
                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                  SEQUENCE, AND CARBOHYDRATE-LINKAGE SITE ASN-55.
MEDLINE-83075344; PubMed-6816276;
Kehry M.R., Fuhrman J.S., Schilling J.W., Rogers J., Sibley C.H.,
Hood L.E.;
                                                                                                                                                                                                                                                                                                                          'Complete amino acid sequence of a mouse mu chain: homology among
                                                                                           ó
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                BY SIMILARITY, N-LINKED (GLCNAC. . .) (COMPLEX).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               45.5%; Score 46; DB 1; Length 117; 50.0%; Pred. No. 1.7; 51ve 3; Mismatches 5; Indels
                                                                        'Match 49.5%; Score 50; DB 1; Length 350; Local Similarity 46.7%; Pred. No. 1.4; Conservative 4; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                22 96 BY SIMILARITY.
55 55 N-LINKED (GLCNAC. . ) (CC
117 117 AA: 12983 MW: 3CF8ACE4BE447E41 CRC64;
                                            DÓMÁIN 215 237 NUDIX BOX.
SEQUENCE 350 AA; 39125 MW; 2EASB24B88FB3420 CRC64;
                                                                                                                                                                                                21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
12-JUN-2002 (Rel. 41, Last annotation update)
19 heavy chain V region MOPC 104E.
                                                                                                                                                                               117 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       117 AA
                                                                                                                                                                                                                                                                                                                                                                                                                   Pfam; PF00047; 1g; 1.
SMART; SM00406; IGv; 1.
Immunoglobulin V region; Glycoprotein.
 MIM: 60602; ...
Interpro; IPR000086; NUDIX_hydrolase.
Pfam: PF00293; NUDIX; 1.
PROSITE; PS00893; NUDIX; 1.
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nes 8; Conservative
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51 INPNNGGTSYNOKFKG 66
                                                                                                                        STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2 IDPENGDSGYAPKFQG 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STANDARD;
                                                                                                              1 WIDPENGDSGYAPKF 15
                                                                                                                                                                                                                                      Mus musculus (Mouse)
MIM; 606022;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            HV13_MOUSE
ID HV13_MOUSE
AC P01757;
                                                                                                                                                                             HV12_MOUSE
P01756;
                                     Hydrolase.
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SEQUENCE
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Matches
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MEDLINE-80078170; PubMed-6765983; Schilling J., Clevinger B., Davie J.M., Hood L.; Schilling J., Clevinger B., Davie J.M., Hood L.; Amino acid sequence of homogeneous antibodies to dextran and DNA rearrangements in heavy chain V-region gene segments."; Nature 283:35-40(1980).

-!- MISCELLANEOUS: THE SEQUENCES OF 10 HYBRIDOMA PROTEINS THAT ALSO BIND DEXTRAN DIFFER FROM THAT SHOWN AT 1-7 POSITIONS, MANY OF WHICH OCCUR IN THE D AND J SEGMENTS.

-!- MISCELLANEOUS: THIS PROTEIN BINDS DEXTRAN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-JAN-1988 (Rel. 06, Created)
01-JAN-1988 (Rel. 06, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
15-JUL-1999 (Rel. 38, Last annotation update)
Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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                                                                                                                                                                                                                                                                                                                                                                                                  45.5%; Score 46; DB 1; Length 117; 50.0%; Pred. No. 1.7;
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                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 5; Indels
                                                                                                                                                                                                                                                                                                                                                             SEQUENCE 117 AA; 13024 MW; 292E2AF4BE447E41 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   118 AA; 12934 MW; 94F7BEE4C762A018 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 46; DB 1;
Pred. No. 1.8;
3; Mismatches
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J SEGMENT.
BY SIMILARITY.
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                                                                                                                                                                                                                                                                                                                      BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                           3; Mismatches
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                                                                                                                                                                         PIR, A26242; MHMSJ5.
HSSP; P01789; 1MCD.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_V.
Pfam; PF00047; ig; 1.
Immunoglobulin V region.
DISULEID
22 96 B'
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50.0%;
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Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                           8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      |:| || : | ||:|
51 INPNNGGTSYNQKFKG 66
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51 INPNNGGTSYNQKFKG 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2 IDPENGDSGYAPKFQG 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STANDARD;
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SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "Nucleotide sequences of the two high-molecular-weight glutenin genes from the D-genome of a hexaploid bread wheat, Triticum aestivum L. cv
                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Triticum aestivum (Wheat).
Bukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae;
Triticeae, Tritican.
                                                                                                                                                    MEDLINE-91306467; PubMed-1649510; Sabal A., Ogura H.; Sakal A., Hitsumoto T., Kato H., Ogura H.; As subtype of human papillomavirus 5 (HPV-5b) and its subgenomic segment amplified in a carcinoma: nucleotide sequences and genomic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Anderson (0.D.; Submitted (FEB-1997) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRAIN-CY. Cheyenne;
MEDILNE-89098419; PubMed-2563152;
Andersonj O.D., Greene F.C., Yip R.E., Halford N.G., Shewry P.R.,
Malpica-Romero J.M.
                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                                                                                          Score 46; DB 1; Length 245;
Pred. No. 4;
1; Mismatches 4; Indels
                                                                       Viruses; dsDNA viruse type 5b.
Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
Papillomavirus.
NCBI_Taxip=10599;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          P10388; 01-MAR-1989 (Rel. 10, Created) 01-MAR-1989 (Rel. 35, Last sequence update) 15-JUL-1999 (Rel. 38, Last annotation update) 01-Lour-1999 (Rel. 38, Last annotation update) 01-Lour-10-10 Molecular Weight subunit DX5 precursor.
                                                                                                                                                                                                                                                                                                                                           Early protein.
SEQUENCE 245 AA; 25622 MW; E4944F95B3D353B2 CRC64;
                                       01-AUG-1992 (Rel. 23, Created)
01-AUG-1992 (Rel. 23, Last sequence update)
01-AUG-1992 (Rel. 23, Last annotation update)
01-AUG-1992 (Rel. 23, Last annotation update)
Human pap#llomavirus type 5b.
                    245 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Nucleic Acids Res. 17:461-462(1989).
                    PRT;
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                                                                                                                                                                                                                                                                                                                                                                           45.5%;
                                                                                                                                                                                                                                                                                                                     EMBL; D90252; BAA14296.1; -.
PIR; C40480; W4WLB5.
                                                                                                                                                                                                        Virology 183:793-798(1991)
                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                    STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STANDARD;
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                                                                                                                                                                                                                                                                                                                                                                                    Local Similarity
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                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Triticeae; Tritic
                  VE4_HPV5B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GLT5_WHEAT
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                                VISCO-ELASTIC PROPERTY OF WHEAT DOUGH.
-!- SUBUNIT: DISULFIDE-BRIDGE LINKED AGGREGATES.
-!- MISCELLANEOUS: GLUTENINS ARE CODED BY SEVERAL GENES ON EACH OF THE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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                                                                                                                                  GROUP I CHROMOSOMES OF WHEAT.
-!- MISCELLANBOUS: THE MATURE PROTEIN IS CHARACTERIZED BY A LARGE NUMBER OF WELL PRESERVED REPEATS OF THE TWO MOTIFS: GQQPGQ AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mus musculus (Mouse).
Sukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
NCBI_TaxID=10090;
THOUGHT TO BE RESPONSIBLE FOR THE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
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"Developmentally controlled and tissue-specific expression of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 46; DB 1; Length 839;
Pred. No. 15;
1; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Interpro; IPR001419; Glutenin.
Pfam; PF03157; Glutenin.hmw; 1.
PRINTS; PR00210; GLUTENIN.
Seed storage protein; Repeat; Multigene family; Signal.
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01-JAN-1988 (Rel. 06, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ig heavy chain V region VH558 Al/A4 precursor
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Cell 40:271-281(1985).
   PROTEIN OF WHEAT ENDOSPERM.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; X12928; CAA31395.1; -. PIR; S02262; S02262.
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Best Local Similarity 53.8%;
Matches 7; Conservative
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InterPro; IPR003596; Ig_V.
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SMART; SM00406; IGv; 1.
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839 AA;
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                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Zachow K.R., Ostrow R.S., Faras A.J.;
"Nucleotide sequence and genome organization of human papillomavirus
type 5.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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21-JUL-1986 (Rel. 01, Last sequence update)
21-JUL-1994 (Rel. 30, Last annotation update)
Glutenin, high molecular weight subunit PC256 (Fragment).
Triticum aestivum (Wheat).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
                                     IG HEAVY CHAIN V REGION VH558 A1/A4.
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                                                      FRAMEWORK-1.
COMPLEMENTARITY-DETERMINING-1.
                                                                                                               COMPLEMENTARITY - DETERMINING - 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 45; DB 1; Length 245;
Pred. No. 5.7;
1; Mismatches 4; Indels
                                                                                                                                                                                                                        Score 45; DB 1; Length 117;
                                                                                                                                                                                                                                                             6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human papillomavirus type 5.
Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
Papillomavirus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             8F5ECDFB28D87EE0 CRC64;
                                                                                                                                                                                     8B0BC138856DFC9D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (Rel. 33, Last sequence update)
(Rel. 33, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                 245 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               101 AA.
                                                                                                                                                                                                                                         Pred. No. 2.5;
3; Mismatches
                                                                                                                                FRAMEWORK-3.
BY SIMILARITY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                 PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE-87207670; PubMed-3033892;
 Signal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-JAN-1988 (Rel. 06, Created)
                                                                                                                                                                                     12971 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           245 AA; 25758 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  44.68;
                                                                                                                                                                                                                          44.68;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; M17463; AAA46987.1; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Virology 158:251-254(1987).
                                                                                                                                                                                                                                                                                                                         69 WIYPGDGSTKYNEKFKG 85
                                                                                                                                                                                                                                                                                                1 WIDPENGDSGYAPKFQG 17
                                                                                                                                                                                                                                           Local Similarity 47.1 nes 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                 STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STANDARD;
                                                  54
68
68
1117
1115
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            4 PENGDSGYAPKFQ 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Probable E4 protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PIR; E26277; W4WL5.
                                                                                                                                                                                     117 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=10578;
Immunoglobulin V
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Early protein.
SEQUENCE 245
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GLT1_WHEAT
P02861;
                                                                                                                                                                                                                                                                                                                                                                                                                               VE4_HPV05
P06924;
                                                                                                                                                                     NON_TER
SEQUENCE
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                                                                                                                                                DISULFID
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GLT1_WHEAT
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Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 155
                                                                                                                                                                                                                                             Best Loc
Matches
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                                                                                                                                                                                                                                                                                                      -!- FUNCTION: GLUTEMINS ARE THE HIGH MOLECULAR WEIGHT SEED STORAGE PROTEIN OF WHEAT ENDOSPERM. THOUGHT TO BE RESPONSIBLE FOR THE VISCO-ELASTIC PROPERTY OF WHEAT DOUGH.
-!- SUBULT: DISULFIDE-BRIDGE LINKED AGGREGATES.
-!- MISCELLANEOUS: GLUTENINS ARE CODED BY SEVERAL GENES ON EACH OF THE GROUP 1 CHROMOSOMES OF WHEAT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae;
Triticeae; Triticum.
NCBL_TaxID=4565;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Hosted T.J., Rochefort D.A., Benson D.R.;
"Close linkage of genes encoding glutamine synthetases I and II in Frankia alni CpII.";
J. Bacteriol. 175:36/9-3684(1993).
-i- CATALYTIC ACTIVITY: ATP + L-glutamate + NH(3) = ADP + phosphate
                                                                                                                                                 SEQUENCE FROM N.A. Forde B.G., Fry R.P., Kreis M., Shewry P.R., Miflin B.J.; "Identification of barley and wheat cDNA clones related to the high-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ENZYME REGULATION: THE ACTIVITY OF THIS ENZYME IS CONTROLLED BY ADENYLATION. THE FULLY ADENYLATED ENZYME COMPLEX IS INACTIVE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SUBCELLULAR LOCATION: Cytoplasmic.
MISCELLANEOUS: TWO FORMS OF GLUTAMINE SYNTHETASE (GSI AND GSII)
CAN BE FOUND IN THIS NITROGEN FIXING BACTERIA, GSI IS A TYPICAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bacteria; Actinobacteria; Actinobacteria (class); Actinobacteridae;
Actinomycetales; Frankineae; Frankiaceae; Frankia.
NCBI_TaxID=1859;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-NOV-1995 (Rel. 32, Created)
1-NOV-1995 (Rel. 32, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation update)
Glutamine synthetase I (EC 6.3.1.2) (Glutamate--ammonia ligase I)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SUBUNIT: OLIGOMER OF 12 SUBUNITS ARRANGED IN THE FORM OF TWO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              InterPro; IPR001419; Glutenin.
Pfam; Pr03157; Glutenin.hmw; 1.
Seed storage protein; Repeat; Multigene family.
10N, TER 1 1 SEQUENCE 101 AA; 10896 WW; EF6D6ADDDFEED993 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 44; DB 1;
Pred. No. 3.1;
1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         474 AA
                                                                                                                                                                                                                                                  M-r polypeptides of wheat gluten.";
FEBS Lett. 162:360-366(1983).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STANDARD;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
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P46033;
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DB 1; Length 132;

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17KD_RICPR
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 Query Match
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                                                                                                     RESULT 15
17KD_RICPR
                                                                                                                                                                                                                                                                                                                               gene.
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                                                                                                                                                                                                                                                                                                                                                     Gaps
PROKAŘYOTIC GLUTAMINE SYNTHETASE WHEREAS GSII IS SIMILAR TO THE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  George Akw., Hall R.M., Stokes H.W.;
Multidrig resistance in Klebsiella pneumoniae: a novel gene, ramà,
confers à multidrug resistance phenotype in Escherichia coli.";
Microbiology 141:1909-1920(1995).
                                                                                                                                                                                                  Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
                                                                                                                                                                                                                                                                                                                                                     ;
0
                     SIMILÄRITY: BELONGS TO THE GLUTAMINE SYNTHETASE FAMILY.
                                                                                                                                                                                                                                                                                                                           43.6%; Score 44; DB 1; Length 474; 53.8%; Pred. No. 17; tive 3; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   BCB216F27F9C853B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TICLOSTORY 141:1303-1320(1333).
-1- SIMIMARITY: TO M.TUBERCULOSIS RV0906.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Outer membrane protein romA (Fragment).
                                                                                                                                                          IPR001691; GLN_synth.
IPR004809; GlnA.
IPR001637; GlnA_adenyltn.
                                                                                                                                                                                               Pfam, PF00120, gln-synt; 1.
ProDom; PD001057; GlnA_adenyltn; 1.
TIGRFAMS; #TIGR00653; GlnA; 1.
                                                                                                                                       EMBL; L10631; -; NOT_ANNOTATED_CDS:
HSSP; P06201; 1LGR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=96032015; PubMed=7551053;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; U19581; AAA85696.1; -.
                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                          STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                 FIGURGAKPREKG 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Klebsiella pneumoniae.
            EUKARYOTIC ENZYME
                                                                                                                                                                                                                                                                                                                                                                           GYAPKFOG 17
                                                                                                                                                                                                                                                                                                                                     Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxÎD-573;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Outer membrane.
                                                                                                                                                                                                                                                                                                                                                                                                                                                        ROMA_KLEPN
Q48412;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN-EGL8
                                                                                                                                                                          InterPro;
                                                                                                                                                               InterPro;
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SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "Comparative sequence analysis of a genus-common rickettsial antigen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               mitochondria.";
Nature 396:133-140(1998).
-!- SUBCELLULAR LOCATION: Attached to the outer membrane by a lipid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN-Madrid E;
MEDLINE-99039499; PubMed-9823893;
MEDLINE-990739499; PubMed-9823893;
MEDLINE-9007080 S.G.E., Zomorodipour A., Andersson J.O.,
Sicheritz-Ponten T., Alsnark U.C.M., Podowski R.M., Naeslund A.K.,
Eriksson A.-S., Winkler H.H., Kurland C.G.;
"The genome sequence of Rickettsia prowazekii and the origin of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PROSITE; PS00013; PROKAR_LIPOPROTEIN; 1.
Outer membrane; Lipoprotein; Antigen; Signal; Complete proteome.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bacteria; Proteobacteria; alpha subdivision; Rickettsiales;
Rickettsiaceae; Rickettsieae; Rickettsia.
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Pred. No. 7.4;
3; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (PROBABLE)
                                                          Indels
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20 20 N-ACYL DIGLYCERIDE (PROBA
159 AA; 16672 MW; A33D404B65EEB071 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                01-AUG-1991 (Rel. 19, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
                                                          2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Search completed: December 23, 2002, 07:26:02 Job time : 3.68023 secs
42.6%; Score 43;
63.6%; Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; M28482; AAA26378.1; ALT_SEQ.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       17 kDa surface antigen precursor.
OMP OR RP833.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE-89359171; PubMed-2768201;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               . Bacteriol. 171:5199-5201(1989)
                                                                                                                                                                                                                                                                                                                                                      P16624;
01-AUG-1990 (Rel. 15, Created)
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                        Best Local Similarity 63.6
Matches 7; Conservative
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Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                          STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Rickettsia prowazekii.
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102 WRNPDNGNHGY 112
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                                                                                                                    6 NGDSGYAPKFQ 16
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44803
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Q96ga6 homo sapien
Q91185 mus musculu
Q9229 homo sapien
Q9429 homo sapien
Q94195 homo sapien
Q94195 homo sapien
Q8vcv5 mus musculu
Q9402 mus musculu
Q96dQu2 mus musculu
Q95kb3 homo sapien
Q95kb3 homo sapien
Q95ky10 secale cere
Q94112 secale cere
Q94112 secale cere
Q94112 secale cere
Q93wf0 secale cere
Q93wf0 secale cere
Q93wf0 secale cere
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                                         December 23, 2002, 07:17:27; Search time 7.05039 Seconds (without alignments) 496.824 Million cell updates/sec
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                                                                                                                                                                                                                                                                                                                                                                 Description
                                                                                                                                671580
     GenCore version 5.1.3 Copyright (c) 1993 - 2002 Compugen Ltd.
                                                                                                                              Total number of hits satisfying chosen parameters:
                                                                                                                  671580 segs, 206047115 residues
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Maximum Match 100%
Listing first 45 summaries
                               - protein search, using sw model
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Q9UL94
Q8VCV5
Q9UL92
Q9D0U2
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Q96GA6
Q9JL85
Q9Y298
Q8WY24
                                                                                                     Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                 sp_human:*
sp_invertebrate:*
sp_mammal:*
sp_matc:*
sp_mhc:*
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sp_unclassified:*
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1 WIDPENGDSGYAPKFQG 17
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sp_bacteriap:*
sp_archeap:*
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sp_bacteria:*
sp_fungi:*
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                                                                     US-09-865-198-2
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027394 methanobact 0889w6 encephalito 09xx26 pseudomonas 098mio rhizobium 1 092xy6 rhizobium m 08tjq4 methanosarc

ALIGNMENTS

Q98MI0 Q92XY6 Q8TJQ4

08yin7 raistonia s 099la6 mus musculu 08t3b6 mus musculu 091379 mus musculu 0927212 listeria in 0927212 listeria in 027528 caenorhabdi 09xx33 caenorhabdi 09xx33 caenorhabdi 09xx36 mus musculu 093x60 mus musculu 093x70 mus musculu 093x71 caenorhabdi 093x71 mus musculu 094x81 mus musculu 094x81 mus musculu 095x81 caenorhabdi 091x10 mus musculu 096q80 homo sapien 091x10 mus musculu 091x10 mus musculu

099LA6 0807UB3 080B3H6 090LT79 092F12 087AB9 027AB9 091T12 090XF0 090XF0 090XF0 090XF0 090XF0 091TR0 091TR0 091TR0 091TR0 091TR0 091TR0 091TR0 091TR0

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                     099131;
01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Similar to RIKEN CDNA 1810060009 gene.
Similar to RIKEN CDNA 1810060009 gene.
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
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Submitted (FEB-2001) to the EMBL/GenBank/DDBJ databases.
Submitted (FEB-2001) to the EMBL/GenBank/DDBJ databases.
BMEL; BC003878; AAH03878.1; -.
HSSP; P01842; 7FBB.
InterPro; IPR003599; Ig.
InterPro; IPR003500; Ig_like.
InterPro; IPR00306; Ig_MHC.
InterPro; IPR00306; Ig_WHC.
InterPro; IPR00306; Ig_WHC.
InterPro; IPR003596; Ig_V.
RARRT; SM00407; IGc1; 3.
SMART; SM00407; IGc1; 3.
SMART; SM00410; IG_like; 1.
SMART; SM00410; IG_like; 1.
PROSITE; PS00290; IG_MHC; UNKNOWN_1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  74.3%; Score 75; DB 11; Length 468; 75.0%; Pred. No. 0.0013; 1; Indels ive
468 AA
  PRT;
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ses 12; Conserv
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Matches
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1 WIDPENGDSGYAPKFQ 16

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Q94 IL2 Q94 IK9 Q93WF0 Q92ME3

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2 IDPENGDSGYAPKFQG 17
                 43 IDPATGHSKYDPKFQG 58
                                                                                            PRELIMINARY;
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Q9Y298
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Malkiel S. Liao L., Cunningham M.W., Diamond B.;
Malkiel S., Liao L., Cunningham M.W., Diamond B.;
"T-cell-dependent antibody response to the dominant epitope of
streptococcal polysaccharide, N-acetyl-glucosamine, is cross-reactive
with cardiac myosin.";
Infect. Immun. 68:5803-5808(2000).
HSSP; PoiglO: 2FBJ.
InterPro: IPR001306; Ig_MHC.
InterPro: IPR001306; Ig_W.
Ffam: PF00047; Ig. I.
SMART: SW00406; IGV: I.
                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                         01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
Homo saplejns (Human).
Homo saplejns (Human).
Eukaryota, Marmalia; Eutheraa; Chordata; Craniata; Vertebrata; Euteleostomi;
Marmalia; Eutheraa; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus
NCBI_TaxID=10090;
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Pred. No. 0.18;
0; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                        57.4%; Score 58; DB 4; Length 614; 62.5%; Pred. No. 0.93; tive 2; Mismatches 4; Indels
                                                                                                                                                                    SEQUENCE FROM N.A.
TISSUE-B-CELL;
Strausberg, R.;
Submitted (1011-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; BC009851; AAH09851.1; -.
InterPro; IPR000005; HTHArac.
InterPro; IPR003598; Ig_c2.
InterPro; IPR00306; Ig_MHC.
Pfam; PF00047; ig; 5.
SWART; SM00408; IGc2; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
Anti-myosin immunoglobulin heavy chain variable region (Fragment)
                                                                                                                                                                                                                                                                                                                                 Immunoglobulin domain.
SEQUENCE % 614 Aa; 67921 MW; 55EF536E77AA9BBB CRC64;
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                                                                                                                                                                                                                                                                                                    PROSITE; $500041; HTH_ARAC_FAMILY_1; UNKNOWN_1.
PROSITE; $500290; IG_MHC; UNKNOWN_3.
                           614 AA.
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                           PRELIMINARY;
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Best Local Similarity
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SEQUENCE
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                                        Q96GA6;
                          096GA6
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RESULT 2
Q96GA6
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Q9JL85
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Gaps

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SEQUENCE FROM N.A.

Zheng S., Shao X., Cao J., Geng L., Fang Y., Dong Q.;

Zheng S., Shao X., Cao J., Geng L., Fang Y., Dong Q.;

Tdentification and characterization of SNC66, a Ig-like gene which is down-regulated in colorectal cancer.";

Submitted (JUN-2000) to the EMBL/GenBank/DDBJ databases.

EMBL, AF283666, AAL36897.1;

InterPro; IPR003599; Ig.

InterPro; IPR003599; Ig.

InterPro; IPR003006; Ig_MHC.

InterPro; IPR003506; Ig_W.

InterPro; IPR003509; Ig.

SMART; SM00409; IG; 4.
                                                                                                                                                                                                                                                                  MEDLINE-98322155; PubMed-9657749;
MEDLINE-98322155; PubMed-9657749;
A Jacquemin M.G., Vanded Elst L.P.L.;
Mechanism and kinetics of factor VIII inactivation: study with an Igd4 monclonal antibody derived from a hemophilia A patient with inhibitor.":
Igd4 monclonal antibody derived from a hemophilia A patient with inhibitor.":
Blood 92:496-506(1998).
R HSSP; P01772; 2F84.
R HSSP; P01772; 2F84.
R InterPro; IPR003066; Ig_MHC.
R InterPro; IPR003596; Ig_WHC.
R InterPro; IRR003596; Ig_WHC.
R SMART; SM00406; IGv; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                         Homo sapiens (Human).
Sukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      55.9%; Score 56.5; DB 4; Length 150; 55.0%; Pred. No. 0.31; tive 4; Mismatches 2; Indels
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150 150
150 AA; 16031 MW; 563D164AB22802D5 CRC64;
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01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
                                        01-NOV-1999 (TrEMBLrel. 12, Created)
01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
150 AA
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                                                                                                              IgG VH protein precursor (Fragment).
IGG VH.
PRT;
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Best Local Similarity 55.0
Matches 11; Conservative
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53.5%;
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Matches 9; Conservative
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TISSUE=MAMMARY TUMOR;
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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MEDLINE-98277139; PubMed-9614934;
Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
Young D.C.;
"Myosin-reactive autoantibodies in rheumatic carditis and normal
fetus.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "Myosin-reactive autoantibodies in rheumatic carditis and normal
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Young D.C.;
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
Myosin-reactive immunoglobulin heavy chain variable region
                                                                                                                                                                                                                                                                                                                                   01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
Myosin-reactive immunoglobulin heavy chain variable region
                                                                              Length 497;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 55; DB 4; Length 125;
Pred. No. 0.43;
3; Mismatches 5; Indels
                                                                                                                        3; Indels
SMART; SM00406; IGV; 1.
PROSITE; PS00290; IG_MHC; UNKNOWN_1.
SEQUENCE 497 AA; 53665 MW; F24D08DFA5A663E5 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NON_TER 125 125
SEQUENCE 125 AA; 13516 MW; 0D3CD5C232488EAC CRC64;
                                                                              55.4%; Score 56; DB 4; 47.1%; Pred. No. 1.5; ative 6; Mismatches 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; AF035019; AAD56255.1; -... BMSP; PR01801. EMBL; AF035019; AAD56255.1; -... HSSP; P01810; ZFBJ.
HIGEPTO; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_V.
Pfam; PF00047; 19; 1.
NON_TER.
InterPro; IPR0047; 19; 1.
                                                                                                                                                                                                                                                                                                    125 AA.
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                                                                                                                                                                                                                                                                                                      PRT;
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SEQUENCE FROM N.A.
MEDLINE=98277139; Pubmed=9614934;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     54.5%;
                                                            Overy Match
Best Local Similarity 47.1r
Conservative
                                                                                                                                                                                  |::|: |:: | || || || 69 WMNPQTGNTEFAQKFQG 85
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 WIDPENGDSGYAPKFQG 17
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                  PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local Similarity
es 9; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                         (Fragment)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NON_TER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              fetus."
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                                                                                                                                                                                                                                                                                                  09UL95
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Q9UL95
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Gaps
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Strausberg R;
Submitted (DEC-2001) to the EMBL/GenBank/DDBJ databases.
Submitted (DEC-2011) to the EMBL/GenBank/DDBJ databases.
EMBL; BE018455, AAH18455.1; -
InterPro; IPR003599; 1g.-c1.
InterPro; IPR003596; Ig.-wHC.
InterPro; IPR003596; Ig.-v.
Pfam; PF00047; 1g; 4.
SMART; SM00409; IGc]; 3.
SMART; SM00400; IGc]; 3.
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
Myosin-reactive immunoglobulin heavy chain variable region
                                                                                                                                                                                                                                                                                                               Score 54; DB 4; Length 119;
Pred. No. 0.58;
                                                                                                                                                                                                                                                                                                                                                                       5; Indels
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SEQUENCE 481 AA; 52326 MW; 52B44C5826807143 CRC64;
                                                                                                                                                                                                                                                        119 AA; 13205 MW; 13E64F5345F4A16E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-MAR-2002 (TrEMBLrel. 20, Created)
01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
01-UNN-2002 (TrEMBLrel. 21, Last annotation update)
Hypothetical 52.3 kpa protein.
Mus musculus (Mouse).
Clin. Immunol. Immunopathol. 87:184-192(1998).
EMBL; AF035020; AAD56256.1; -.
HSSP; PO1810; ZFBJ.
InterPro: IPR003006; Ig_MHC.
InterPro: IPR00306; Ig_V.
Pfam; PF00047; ig; 1.
SMART; SM00406; IGv; 1.
NON_TER 119 119
SEQUENCE 119 AA; 13205 MW; 13E64F5345F4A16E C
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1 WIDPENGDSGYAPKF 15
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                                                                                                                                  Q96KB3
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                                                                                              RESULT 11
Q96KB3
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X SEQUENCE, FROM N.A.

SEQUENCE, TROBSE66, Dubmed-11217851;

X MEDLINE-21085660, Dubmed-11217851;

X Arakawa T., Hara A., Shibata K., Yoshino M., Itoh M., Ishii Y.,

A Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,

A Atawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,

A Alawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,

A Salto T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,

A Radota M., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,

R A Rebi P., Katudi F., Suzuki R., Tomita M., Wagner L., Washio T.,

A Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,

B Brake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,

B Brake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,

B Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,

Chorse P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,

Nordone P., Ring B., Ringwald M., Rodiguez I., Sakamoto N.,

R Sasaki H., Sato K., Schoenbach C., Seya T., Shipata Y., Storch K.-F.,

R Wynshwejboris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,

A Wynshwejboris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,

A Washing L., Volente R., Wang K.H., Weitz C., Whittaker C., Wilming L.,

A Washing L., Volente R., Wang K.H., Weitz C., Whittaker C., Wilming L.,

A Washing L., Volente R., Wang K.H., Weitz C., Whittaker C., Wilming L.,

A Washing L., Volente R., Wang K.H., Weitz C., Whittaker C., Wilming L.,

A Washing L., Wang K.H., Weitz C., Whittaker C., Wilming L.,

A Washing L., Wang K.H., Weitz C., Whittaker C., Wilming L.,

A Washing L., Wang K.H., Weitz C., Whittaker C., Wilming L.,

A Washing L., Wang K.H., Weitz C., Whittaker C., Wilming L.,

A Wang K.L., Wang K.H., Weitz C., Whittaker C., Wilming L.,

A Wang K.L., Wang K.H., Weitz C., Whittaker C., Willing C.,

A Wang K.L., Wang K.H., Weitz C., Wang K.H., Weitz C., Willing C.,

A Wang K.L., Wang K.H., Weitz C., Wang K.H., Weitz C., Weitz C., Willing C.,

A Wang K.L., Wang K.H., Weitz
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O9D0U2:
O9D0U2:
O9D0U2:
O9D0U2:
O1-JUN-2001 (TEMBLrel. 17, Created)
O1-JUN-2002 (TEMBLrel. 17, Last sequence update)
O1-JUN-2002 (TEMBLrel. 21, Last annotation update)
O1-JUN-2002 (TEMBLrel. 21, Last annotation update)
O1-JUN-2002 (TEMBLrel. 21, Last annotation update)
NUDT9 OR 1190002COTRIK.
MUS MUSCALL (MOUSE).
Eukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Musmanalla: Eutherla; Rodentla; Sciurognathi; Muridae; Murinae; Mus.
                                                                       "Myosin-reactive autoantibodies in rheumatic carditis and normal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Functional annotation of a full-length mouse cDNA collection."; Nature (109:685-690(2001).
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                                       Nu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
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                                                                                                                                                                                                                                                                                                              50.5%; Score 51; DB 4; Length 124; 56.2%; Pred. No. 1.8; tive 2; Mismatches 5; Indels
                                                                                                                                                                                                                                                           124 124
124 AA; 13580 MW; 1BAAACBD96ACD2A2 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          InterProf. IPR000086; NUDIX_hydrolase.
Pfam; PR00293; NUDIX; 1.
SEQUENCE 300 AA; 33550 MW; 5BD71C72E2A4DA50 CRC64;
                                                                                                         Clin. Immunol. Immunopathol. 87:184-192(1998)
EMBL: AF035022; AAD56258.1; -.
HSSP: POM772; 2F84.
InterProf: IPR003006; Ig_MHC.
InterProf: IPR003596; Ig_V.
SEQUENCE∯FROM N.A.
MEDLINE-98277139; PubMed-9614934;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; AK004444; BAB23305.1; -. MGD; MGI: 1921417; Nudt9.
                                                                                                                                                                                                                                                                                                                                 Best Local Similarity 56.2
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                       2 IDPENGDSGYAPKFQG 17
                                                                                                                                                                                                                                                                                                                                                                                                          |:|2 | : |1 |||| 51 INPSGGSTSYAQKFQG 66
                                                                                                                                                                                                Pfam; PF00047; 19; 1.
SMART; SM00406; IGV; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Best Local Similarity
Matches 7; Conserv
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                                                    Young D.C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    [1]
SEQUENCE
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                                                                                        fetus."
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TISSUE-EMBRYO, AND MAINLY HEAD;

A ISOGAI T., Ota T., Hayashi K., Sugiyama T., Otsuki T., Suzuki Y.,

A ISOGAI T., Ota T., Hayashi K., Sugiyama T., Otsuki T., Suzuki Y.,

A Nishikawa T., Nagai K., Sugano S., Shiratori A., Sudo H., Sugawara M.,

A Wagatsuma M., Hosoiri T., Kaku Y., Kodaira H., Rondo H., Sugawara M.,

A Ratanabe S., Kinnia K., Nurakawa K., Ono Y., Takiguchi S.,

A Watanabe S., Kinnia K., Nurakawa K., Ono Y., Takiguchi S.,

A Watanabe S., Kinnia K., Nakamura Y., Nagahari K., Masuho Y.,

A Ninomiya K., Iwayanagi T.,

"NEDO human cDNA sequencing project.";

"NEDO human cDNA sequencing project.";

Submitted (MAY-2001) to the BML/GenBank/DDBJ databases.

EMBL; AK027295, BAB55021.1; - MBL/GenBank/DDBJ databases.

R EMBL; AK027395, BAB55021.1; - MBL/GenBank/DDBJ CRC64;

SEQUENCE 350 AA; 39042 MW; &BBELA3IECCFB343D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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EMBL: BC005951; AAH05951.1; -.
HSSP; POIT99; IMCP.
InterPro; IPR003599; Ig.
InterPro; IPR003599; Ig.
InterPro; IPR003599; Ig.
InterPro; IPR003006; Ig.Ike.
InterPro; IPR003006; Ig.AHC.
InterPro; IPR003596; Ig.V.
Fram; PR0047; Ig. 4.
SWART; SW00407; IG.1; 2.
SWART; SW00406; IG.4.
SWART; SW00406; IG.1ke; 1.
PROSITE; PS00290; IG.AHC; UNKNOWN_1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 50; DB 4; Length 350; Pred. No. 8.9; 4; Mismatches 4; Indels
                                                                                                                                                                                                                                       01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DEC-2002 (TrEMBLrel. 20, Last annotation update)
CDNA FL14389 fis, clone HEMBA1002876.
HOMO sapiens (Human)
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01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
Hypothetical 54.2 kDa protein.
                                                                                                                                                                                350 AA
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                                                                                                                                                                                PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 46.7.
7; Conservative
                                                                                                                                                                                PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           | ||: :|||
110 WADPQISESNFSPKF 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRELIMINARY;
| | ||: :| ::|||
60 WADPQISESNFSPKF 74
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 WIDPENGDSGYAPKF 15
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Triticeae; Secale.
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                                                                    Score 50; DB 4; Length 500;
Pred. No. 14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 encoded by Glu-1R gene of Secale cereale.";
Submitted (MAY-2001) to the EMBL/GenBank/DDBJ databases.
Hypothetical protein.
SEQUENCE 500 AA; 54154 MW; 0A9BF43F2A3CC6D9 CRC64;
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80179 MW; 89B4D795A3DC91BB CRC64;
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01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
High molecular weight glutenin subunit x precursor.
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                                                                    Query Match
Best Local Similarity 47.1%;
Matches 8; Conservative
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69 WISPSSDNTRFAKKFQG 85
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de Bustos A., Jouve N.;
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STRAIN=CV. PETKUS;
de Bustos A., Jouve N.;
"Characterization and analysis of new subunits-like wheat HMW-glutenin encoded by Glu-1R gene of Secale cereale.";
Submitted (MAY-2001) to the EMBL/GenBank/DDBJ databases.
"Characterization and analysis of new subunits-like wheat HMW-glutenin encoded by Glu-1R gene of Secale cereale."; Submitted (MAY-2001) to the EMBL/GenBank/DDBJ databases.
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de Bustos A., Rubio P., Jouve N.;

de Bustos A., Rubio P., Jouve N.;

de Bustos A., Rubio P., Jouve N.;

"Characterization of two gene subunits on the 1R chromosome of rye as orthologs of each of the Glu-1 genes of hexaploid wheat.";

Submitted (MAY-2001) to the EMBL/GenBank/DDBJ databases.

EMBL; AJ314768; CAC46679.1; -.

EMBL; AJ31478; CAC46679.1; -.

InterPro; IPR001419; Glutenin.

Pfam; PF03157; Glutenin_hmw; 1.
                                                                                                                               STRAIN-CV. SMITH:

de Bustos A., Rubio P., Jouve N.;

de Bustos A., Rubio P., Jouve N.;

"Characterization of two gene submits on the 1R chromosome of rye as orthologs of each of the Glu-1 genes of hexaploid wheat.";

Submitted (MAY-2001) to the EMBL/GenBank/DDBJ databases.

EMBL, A314/19; CAC46080.1;

InterPro; IPR001419; Glutenin.

PF03157; Glutenin_hmw; 1.
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01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
High molecular weight glutenin subunit x precursor.
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Immunoglobulin; antibody; complementary determing region; CDR; VBGF; vascular endothalial growth factor; KDR, kinase insert domain containing receptor; multivalent; monovalent; humanised antibody; chimeric antibody; tumour; diabody; triabody; glioblastoma multiforme; hemangloblastoma AIDS; central nervous system neopplasms; AIDS associated Karposi's sarcoma; acquired immune deficiency syndrome; AIDS; human.
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Thermotoga maritim

28-JAN-2000; 2000WO-US02180

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03-AUG-2000

Complementary dete Humanised antibody VEGF antagonist an chain comple

Description

SUMMARIES

Heavy chain com Variable heavy

AAE13139 AAB82705 AAU74408 AAY97235

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26437

AAY97231

DB

Query Match Length

Score

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Result

Homo sapiens.

Synthetic.

99US-0117726 99US-0240736

29-JAN-1999; 29-JAN-1999; (IMCL-) IMCLONE SYSTEMS INC

Humanised antibody VEGF antagonist an Antigen-binding pr Antigen-binding pr Chimeric plCll hea

AAE13143 AAB82709 AAU74412 AAU74417 AAE13145

Zhu Z, Witte L;

Herbicidally active Raccoonpox virus B

Listeria monocytog Drosophila melanog

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Disclosure; Page 37; 42pp; English
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                                                                                                                 New immunoglobulin molecules are described that bind kinase insert domain-containing receptor (KDR) with a comparable affinity to human vascular endothelial growth factor (VEGF). The antibodies neutralise KDR activation. The immunoglobulin may be a multivalent single chain antibody, a monovalent single chain antibody, a diabody, a chimarised antibody, a diabody, a triabody, a humanised antibody or a chimarised antibody.

The immunoglobulin molecules bind specifically to an extracellular domain of the KDR receptor with the same affinity as VEGF. Overexpression of VEGF has been implicated in a number of human tumour cell lines including glioblastoma multiforme, chemangloblastoma, central nervous system neoplasms and AIDS associated Karposi's sarcoma. The antibodies therefore have capplications in treating these conditions. This sequence encodes a furnamental party of the complementary determining region of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Vascular endothelial growth factor receptor; VEGFR; antagonist; tumour; cytostatic; heavy chain hypervariable region; VH; myelocytic leukaemia; lymphocytic; erythrocytic; monocytic; multiple myeloma; lymphoid cell; Hodgkin's disease; complementarity determining region-3; CDR-3; mouse,
                                              Novel immunoglobulin molecules binding kinase insert domain-containing receptor with the same affinity as vascular endothelial growth factor,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Humanised antibody murine heavy chain hypervariable region (VH) CDR3.
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                                                                                              Claim 3; Page 50; 55pp; English.
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                                                                      used to reduce tumour growth
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The invention relates to a method for inhibiting the growth of non-solid tumour cells that are stimulated by a ligand of vascular endothelial growth factor receptor (VEGFR) in mammals particularly humans. The method involves treating the mammals with humanised vEGFR monoclonal antibodies (antagonists) Humanised monoclonal antibody comprises humanised mouse variable region joined to human constant region, where the humanised mouse variable region contains mouse complementarity determining region (CDR) grafted into human variable region. The method is useful for treating leukaemias such as acute or chronic myelocytic leukaemia, acute or chronic lymphocytic leukaemia, erythrocytic or monocytic leukaemia, multiple myelomas and lymphoid cells, particularly those related to nono Hodgkin's and Hodgkin's disease. The present sequence is humanised antibody murine heavy chain hypervariable region (VH) CDR-3 used in the exemplification of the invention.
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100.0%; Pred. No. 7.8e+05;
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Claim 8; Page 14; 68pp; English.
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31-MAR-2000; 2000US-0539692.
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The present sequence is that of complementarity determining region 3 of the heavy chain variable region (see also AAB82701) of IMC-1C11, a mouse-human chimeric antibody that has vascular endothelial growth factor (VEGF) antagonist activity. The antibody, or a fragment of it, can be used as an anti-angiogenic molecule, corpether with a chemotherapeutic acid, for the treatment of an angiogenic dependent condition in a mammal, especially a human. The invention relates generally to a method of treating or controlling an angiogenic dependent condition by administering an anti-angiogenic molecule and a chemotherapeutic agent. The anti-angiogenic molecule inhibits or blocks the action of a vascular endothelium survival factor such as VEGF or its receptor, and is especially IMC-1C11. Conditions that can be treated include a neoplasm, a collagen-vascular disease or an autoimmune disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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                                                                                                                                                                                                                                                                                            carcinoma, prostate carcinoma, colon carcinoma, prostate carcinoma, ovarian carcinoma, neuroblastoma, central nervous system tumour, neuroblastoma, glioblastoma multiforme or melanoma (all claimed).
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                                                                                                                                                                                                                                                                            especially a solid tumour, including breast carcinoma, lung
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cantigen-binding site located to the N terminus of immunoglobulin (Ig)

light chain constant domain (CL domain), and P2 has an antigen-binding

site located to the N terminus of the CH1 domain. (I) is useful for:

can contralising the activation of a vascular endothelial growth factor

(VEGF) receptor; reducing tumour growth; inhibiting angiogenesis;

cc reducing endothelial cell proliferation; inhibiting VEGF induced

migration of human leukaemia cells; blocking interaction of a protein and

its ligand; promoting interactions between immune calls and target cells;

cand in vivo and in vitro for investigative, diagnostic or treatment

cmethods. The design of (I) provides for efficient production so that

cand in vivo and in vitro for investigative, diagnostic or treatment

combistantially all of the antigen-binding proteins produced are assembled

in the desired configuration. (I) is bivalent and bispecific, homogeneous

and in tetrament for mr. The heavy chain constant domains which constitute

the Fc region (e.g., CH2 and CH3 for an IgG molecule) of a natural

cantibody and which provide other antibody functions can be present. There

considerative sequence represents the heavy chain variable domain

complementarity determining region (H3 (CDRH3) incorporated into an

complementarity determining region in the method of the invention.
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N-PSDB; AAA53767.
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens.
Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         29-JAN-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                              Sequence
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Claim 4; Page 50-51; 55pp; English.

New bispecific immunoglobulin-like antigen-binding protein for reducing tumour growth and for inhibiting angiogenesis, comprises a complex of two polypeptides and two second polypeptides

WPI; 2002-106189/14.

N-PSDB; AAS20279.

Claim 55; Page 56; 64pp; English.

The invention describes an antigen-binding protein (I) comprising a complex of two polypeptides (P1) and two second polypeptides (P2) which are stably associated in an immunoglobulin like complex. P1 has an

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variable region joined to human constant region, where the humanised
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Vascular endothelial growth factor receptor; VEGFR; antagonist; tumour; cytostatic; heavy chain; myelocytic leukaemia; lymphocytic; erythrocytic; multiple myeloma; lymphoid cell; Hodgkin's disease; mouse; human; chimeric.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Inhibiting growth of non-solid tumor cells useful to treat bone marrow tumors souch as leukemias or multiple myeloma comprises treatment with an antagonist of a vascular endothelial growth factor receptor -
                   New immunoglobulin molecules are described that bind kinase insert domain-confaining receptor (KDR) with a comparable affinity to human vascular endchelial growth factor (VEGF). The antibodies neutralise KDR activation. The immunoglobulin may be a multivalent single
                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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                                                                                      triabody, a humanised antibody or a chimerised antibody, a diabody, a monovalent single chain antibody, a diabody, a monovalent single chain antibody, a diabody, a humanised antibody or a chimerised antibody, a humanised antibody or a chimerised antibody, a cartacellular domain of the KDR receptor with the same affinity and VEGF. Overgexpression of VEGF has been implicated in a number of human tumour cell lines including glioblastoma multiforme, hemangioblastoma, central nervous system neoplasms and AIDS associated Karposi's sarcoma. The antibodies therefore have applications in treating these conditions. This sequence encodes preferred these variance concodes and the complementary determining region of the
                                                                                                                                                                                                                                                                                                                                                                                            ó
                                                                                                                                                                                                                                                                                                                                                         21; Length 117;
                                                                                                                                                                                                                                                                                                                                      antibody heavy chain fragment.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAE131431standard; Protein; 117 AA.
                                                                                                                                                                                                                                                                                immunoglobulins of the invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (IMCL-) IMCLONE SYSTEMS INC. (CORR-) CORNELL RES FOUND INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       30-MAR-2001; 2001WO-US10504.
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                                                                                                                                                                                                                                                                                                                                                                                            Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 2001-662942/76.
                                                                                                                                                                                                                                                                                                                                                     Rafii S;
                                                                                                                                                                                                                                                                                                                 Sequence 117 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                99 YYGDYEGY 106
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mouse variable region contains mouse complementarity determining region (CDR) grafted into human variable region. The method is useful for treating leukaemias such as acute or chronic myelocytic leukaemia, acute or chronic lymphocytic leukaemia, erythrocytic or monocytic leukaemia, multiple myelomas and lymphoid cells, particularly those related to non-Hodgkin's and Hodgkin's disease. The present sequence is humanised antibody heavy chain frgament used in the exemplification of the
                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  IMC-1C11; chimeric antibody; mouse; human; antagonist; VEGF; vascular endothelial growth factor; angiogenesis; antiangiogenic; antitumour; neoplasm; collagen-vascular disease; autoimmune disease; tumour; breast carcinoma; lung carcinoma; prostate carcinoma; colon carcinoma; ovarian carcinoma; neuroblastoma; ovarian carcinoma; therapy; heavy chain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ø
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Treating or controlling an anglogenic dependent condition (e.g. neoplasm, collagen-vascular or autoimmune disease) in mammal by administering a combination of an antianglogenic molecule and a chemocherapeutic agent.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       VEGF antagonist antibody IMC-1C11 heavy chain variable region.
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                                                                                                                                                                                  100.0%; Score 51; DB 22; Length 117; 100.0%; Pred. No. 0.53; ive 0; Mismatches 0; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                      AAB82709 standard; Protein; 117 AA.
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/label= CDR-H1
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/label= CDR-H2
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/label= CDR-H3
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31-MAR-2000; 2000US-0539692.
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                                                                                                                                                                                  Query Match 100.
Best Local Similarity 100.
Matches 8; Conservative
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- Homo sapiens.
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N-PSDB; AAH26405.
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                                                                                                                     invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Chimeric
Chimeric
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                                                                                                                                                                                                                                                                                                                                                                                                     AAB82709;
                                                                                                                                                      Sequence
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Region
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                                                                                                                                                                                 The present sequence is that of the heavy chain variable region of inc-1c11, a mouse-human chimeric antibody that has vascular endothelial growth factor (VEGF) antagonist activity. The antibody, or a fragment of it, can be used as a nati-angiogenic molecule, cogether with a chemotherapeutic acid, for the treatment of an angiogenic dependent condition in a mammal, especially a human. The invention relates generally to a method of treating or controlling an angiogenic dependent condition by administering an ini-angiogenic molecule and a chemotherapeutic agent, to produce a regression or arrest of the condition while minimalsing or preventing significant toxicity of the chemotherapeutic agent.

The anti-angiogenic molecule inhibits or blocks the action of a vascular endothelium survival factor such as VEGF or its receptor, and is especially INC-1C11. Conditions that can be treated include a neoplasm, a collagen-vascular disease or an autoimmune disease, carcinoma, prostate carcinoma, colon carcinoma, lung carcinoma, prostate carcinoma, colon carcinoma, prostate carcinoma, colon carcinoma, prostate carcinoma, cultiforme or melanoma (all claimed).
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                                                                                                                                                                                                           The invention describes an antigen-binding protein (I) comprising
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                                                                     Disclosure; Page 38; 42pp; English.
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                                                               Claim 57; Page 57; 64pp; English.
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Best Local Similarity 100.

Matches 8; Conservative
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                                                                                                                                                    migration of human leukaemia cells; blocking interaction of a protein and its ligand; promoting interactions between immune cells and target cells; and in vivo and in vitoo for investigative, diagnostic or treatment methods. The design of (I) provides for efficient production so that substantially all of the antigen-binding proteins produced are assembled in the designed configuration. (I) is bivatent and bispecific, homogeneous and in tetrameric form. The heavy chain constant domains which constitute the Fc region (e.g., CH2 and CH3 for an IgG molecule) of a natural antibody and which provide other antibody functions can be present. There is no requirement for processing in vitro to obtain the complete product. This sequence represents a heavy chain variable domain (VH) incorporated into Fv, an engineezed protein containing a heavy chain variable domain and a light chain variable domain in one polypeptide chain, described in the method of the invention.
complex of two polypeptides (P1) and two second polypeptides (P2) which are stably associated in an immunoglobulin like complex. P1 has an antigen-binding site located to the N terminus of immunoglobulin (Ig) light chain constant domain (CL domain), and P2 has an antigen-binding site located to the N terminus of the CH1 domain. (I) is useful for: neutralising the activation of a vascular endothelial growth factor (VEGF) receptor; reducing tumour growth; inhibiting angiogenesis; reducing endothelial cell proliferation; inhibiting VEGF induced
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New bispecific immunoglobulin-like antigen-binding protein for reducing tumour growth and for inhibiting angiogenesis, comprises a complex of two polypeptides and two second polypeptides
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Antigen-binding protein; antibody heavy chain variable domain;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               100.0%; Score 51; DB 23; Length 117; 100.0%; Pred. No. 0.53; 1. Indels () Mismatches () Indels ()
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Antigen-binding protein heavy chain variable domain (VH) #2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 61; Page 60; 64pp; English.
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N-PSDB; AAS20288.
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                            117 AA;
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The invention describes an antigen-binding protein (I) comprising

us-09-865-198-3.rag

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complex of two polypeptides (P1) and two second polypeptides (P2) which are stably associated in an immunoglobulin like complex. Pl has an antiably associated in an immunoglobulin like complex. Pl has an entiably associated to the N terminus of immunoglobulin (Ig) [19] thain constant domain (CL domain), and P2 has an antigen-binding site located to the N terminus of the CH1 domain. (I) is useful for: neutralising the activation of a vascular endothelial growth factor (VEGF) receptor; reducing tumour growth; inhibiting angiogenesis; reducing endothelial cell proliferation; inhibiting vEGF induced [CC] migration of human leukaemia cells; blocking interaction of a protein and its ligand; promoting interactions between immune cells and target cells; and in vivo and in vitro for investigative, diagnostic or treatment can in vivo and in vitro for investigative, diagnostic or treatment complementally all of the antigen-binding proteins produced are assembled in the desired configuration. (I) is bivalent and bispecific, homogeneous custom in tetrameric form. The heavy chain constant domains which constitute antibody and which provide other antibody functions can be present. There is no requirement for processing in vitro to obtain the complete product. This sequence represents a heavy chain variable domain (VH) incorporated into the method of the invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note= "Residue 'O' is present at this location in the sequence shown in fig-11 of the specification"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             100.0%; score 51; DB 23; Length 117; 100.0%; Pred. No. 0.53; 0; Indels 0
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20..136
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/label= CDR_H1
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Chimeric - Unidentified.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         99 YYGDYEGY 106
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The invention relates to a method for inhibiting the growth of non-solid tumour cells that are stimulated by a ligand of vascular endothelial crown receptor (VEGFR) in mammals particularly humans. The method involves treating the mammals with humanised VEGFR monoclonal antibodies involves treating the mammals with humanised vEGFR monoclonal antibodies cartable region folmed to human constant region, where the humanised mouse complementarity determining region core variable region contains mouse complementarity determining region (CDR) grafted into human variable region. The method is useful for treating leukaemias such as acute or chronic myelocytic leukaemia, acute or chronic lymphocytic leukaemia, erythrocytic or monocytic leukaemia, cor chronic lymphocytic leukaemia, erythrocytic or monocytic leukaemia, con-Hodgkin's and Hodgkin's disease. The present sequence is chimeric picli heavy chain fragment which is used for the construction of chimeric picli igg expression vector. Chimeric picli heavy chain contains cloned decreated the contains cloned decreated the contains contains cloned decreated the contains cloned decreated the
                                                                                                                                                                                                                                                                                                                                            Inhibiting growth of non-solid tumor cells useful to treat bone marrow tumors such as leukemias or multiple myeloma comprises treatment with an antagonist of a vascular endothelial growth factor receptor -
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/label= Mature_protein
45..54
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/label= Signal_peptide
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                                                                                                                                (IMCL-) IMCLONE SYSTEMS INC. (CORR ) CORNELL RES FOUND INC.
                                                                              31-MAR-2000; 2000US-0540770.
                         30-MAR-2001; 2001WO-US10504
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    Homo sapiens.

                                                                                                                                                                                                                                                                   WPI; 2001-662942/76.
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ovarian carcinoma, neuroblastoma, central nervous system tumour, neuroblastoma, glioblastoma multiforme or melanoma (all claimed)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  or controlling an angiogenic dependent condition (e.g. collagen-vascular or autoimmune disease) in mammal by ring a combination of an antianglogenic molecule and a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      .;
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                                                                            /note= "complementarity determining region 2"
118..125
/label= CDR-H3
                      "complementarity determining region 1"
                                                                                                                                                                  /note= "complementarity determining region 3"
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Pred. No. 0.63;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Disclosure; Fig 1; 42pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 100.0%; S. Best Local Similarity 100.0%; P. Matches 8; Conservative 0;
                                                               /label= CDR-H2
/label= CDR-H1
                                                                                                                                                                                                                                                                                                                  29-JAN-2001; 2001WO-US02839
                                                                                                                                                                                                                                                                                                                                                             28-JAN-2000; 2000US-0178791.
                                                                                                                                                                                                                                                                                                                                                                                                                                                             (IMCL-) IMCLONE SYSTEMS INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         26-MAR-2002 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  administering a combina
chemotherapeutic agent
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 2001-514531/56.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 136 AA;
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                                                                                                                                                                                                               WO200154723-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Treating or
                                                                                                                                                                                                                                                                  02-AUG-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 neoplasm,
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AAU74420
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The invention describes an antigen-binding protein (I) comprising a complex of two polypeptides (P1) and two second polypeptides (P2) which are stably associated in an immunoglobulin like complex. Pl has an antigen-binding site located to the N terminus of immunoglobulin (Ig) light chain constant domain (CL domain), and P2 has an antigen-binding site located to the N terminus of the CHI domain. (I) is useful for: neutralising the activation of a vascular endothelial growth factor (VEGF) receptor; reducing tumour growth; inhibiting angiogenesis; ceducing endothelial cell profileration; inhibiting useful indication of human leukaemia cells; blocking interaction of a protein and its ligand; promoting interactions between immune cells and target cells; and in vivo and in viro for investigative, diagnostic or treatment methods. The design of (I) provides for efficient production so that substantially all of the antigen-binding proteins produced are assembled in the desired configuration. (I) is bivalent and bispecific, homogeneous and in tetrameric form. The heavy chain constant domains which constitute the Fc region (e.g., CH2 and CH3 for an IgG molecule) of a natural cantibody and which provide other antibody functions can be present. There
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            is no requirement for processing in vitro to obtain the complete product. This is the amino acid sequence of a single chain variable fragment
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New bispecific immunoglobulin-like antigen-binding protein for reducing tunnour growth and for inhibiting angiogenesis, comprises a complex of two polypeptides and two second polypeptides  . \\
      Antigen-binding protein; single chain variable fragment; svFv; antigen; cytostatic; angiogenesis inhibitor; tumour; leukaemia; antibody; vascular endothelial growth factor receptor; VEGF; cell proliferation inhibitor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (scFv), an engineered protein containing a variable light and variable heavy domain on one polypeptide, described in the method of the
                                                                                                                                                                                                                                                                                        /label= Linker
/note= "15 amino acid linker joins the VH and VL
regions of the single chain variable fragment
protein. Encoded by AAS20285"
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                                                                                                                                                                                                                                                                                                                                                                                                          /note= "Light chain variable domain. Specifically claimed in claim 61"
                                                                                                                                                                                                                                /note= "Heavy chain variable domain. Specifically claimed in claim 61"
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                                                                                                                                                                         Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 63; Page 62-63; 64pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          24-MAY-2000; 2000US-206749P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (IMCL-) IMCLONE SYSTEMS INC.
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                                                                                                                                                                                                                /label= VH
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                                                                                                                Mus sp.
Synthetic.
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25-JAN-1996
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                                                                                      nvention.
                                                                                                                                                                                                                                                                                                                                                                                                                           Synthetic.
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                                                                                                            Sequence
                                                                                                                                                                                                                                  RESULT 14
                                                                                                                                                                                                                                           AAR92576
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (VEGF) receptor; reducing tumour growth; inhibiting anglogenesis; reducing endothelial cell proliferation; inhibiting VEGF induced migration of human leukaemia cells; blocking interaction of a protein and its ligand; promoting interactions between immune cells and target cells; and in vitro for investigative, diagnostic or treatment methods; The design of (1) provides for efficient production so that substantially all of the antigen-binding proteins produced are assembled
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The invention describes an antigen-binding protein (I) comprising a complex of two polypeptides (P1) and two second polypeptides (P2) which are stably associated in an immunoglobulin like complex. P1 has an antigen-binding site located to the N terminus of immunoglobulin (Ig) light chain constant domain (CL domain), and P2 has an antigen-binding site located to the N terminus of the CH1 domain. (I) is useful for: neutralising the activation of a vascular endothelial growth factor
                                                                                                                                                                    Antigen-binding protein; single chain variable fragment; scFv; antigen; cytostatig; angiogenesis inhibitor; tumour; leukaemia; antibody; vascular endothelial growth factor receptor; VEGF; cell proliferation inhibitor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New bispecific immunoglobulin-like antigen-binding protein for reducing tumour growth and for inhibiting angiogenesis, comprises a complex of two polypeptides and two second polypeptides.
                                                                                                                                                    Antigen-binding protein, single chain variable fragment version #1
                                                                                                                                                                                                                                                                                                                                                                          133..240
/label- VL
/note- "Light chain variable domain. Specifically
claimed in claim 57"
                                                                                                                                                                                                                                                                                                  /note= "Heavy chain variable domain. Specifically claimed in claim 57"
                                                                                                                                                                                                                                                                                                                                  /label= Linker
/note= "15 amino acid linker joins the VH and VL
regions of the single chain variable
fragment protein. Encoded by AAS20285"
                                                                                                                                                                                                                                                                  Location/Qualifiers
1..117
                                                                                    AAU74419 standard; Protein; 240 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 63; Page 62; 64pp; English.
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                   99 YYGDYEGY 106
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         1 YYGDYEGY
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                                                                                                                                                                                                                                  Mus sp.
                                                                                                          AAU74419;
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in the desired configuration. (I) is bivalent and bispecific, homogeneous and in tetrameric form. The heavy chain constant domains which constitute the Fc region (e.g., CH2 and CH3 for an IgG molecule) of a natural antibody and which provide other antibody functions can be present. There is no requirement for processing in vitro to obtain the complete product. This is the amino acid sequence of a single chain variable fragment (scFV), an engineered protein containing a variable light and variable heavy domain on one polypeptide, described in the method of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           VLA-4; inhibitor; binding peptide; leucocyte adhesion; CD49d/CD29; CDR; alpha4betal integrin; VCAM-1; endothelial cell; antibody; meningitis; complementarity determining region; inflammatory brain disorder; therapy; multiple sclerosis; encephalitis; Alzheimmer's disease; atherosclerosis; ALDS dementia; diabetes; inflammatory bowel disease; tumour metaetases; rheumatoid arthritis; transplant rejection; myocardial ischaemia; asthma.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAR92563-R92594 represents VLA-4 binding peptides derived from the FGN region of VCAM-1. VLA-4 is also known as alpha4betal integrin and CD494CVCD3. VLA-4 binds to the non-matrix molecule VCAM-1, which is expressed by endothelial and other cells. These sequences mimic a short consensus sequence in the FGN region of VCAM-1. These sequences inhibit the adhesion of leucocytes mediated by VLA-4. It is useful for treating inflammatory brain disorders (especially multiple sclerosis), meningitis, encephalitis, asthma, Alzheimer's disease, atherosclerosis, AIDS dementia, diabetes, inflammatory bowel disease, rheumatoid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           peptide(s) that bind VLA-4, inhibit leucocyte adhesion - usefu. for treatment of inflammatory disease, e.g. multiple sclerosis
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                                                                                                                                                                                                                                                                                                                                                                                                                                       100.0%; Score 51; DB 23; Length 240; 100.0%; Pred. No. 1.1;
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Best Local Similarity 100.
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                                                                                                                                                                                                                                                                                                                                                                    240 AA;
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Modified-site
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arthritis, transplant rejection, tumour metastases and myocardial ischaemia. These sequences can also be labelled, and can then be used for in vivo or in vitro diagnosis, such as monitoring inflammatory responses, isolating leucocytes, in assays for inhibitors of VLA-4/VCAM-1 interactions and imaging sites of inflammation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            This amino acid sequence codes for the N-terminal end of the control fusion protein. It was obtd. from the DNA and makes up the putative binding domain of the control fusion protein. The fusion proteins, termed Totally Synthetic Affinity Reagents (TSARS) are useful for in vitro and in vivo applications that make use of binding regions of antibodies. DNA binding proteins, adhesive proteins, etc. e.g. in the field of biomedicine, bioregulation and control. Also in the prodn. of vaccines, (immunogens) in separations and purifications, and in diagnostics. The method is quick, simple, efficient and relatively inexpensive. A great diversity of binding characteristics can be obtd. There is no need for detailed knowledge of the function of portions of the binding sequence or the amino acids that are involved in ligand binding in order to produce the TSARS. See also AAR13722.
                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Prodn. of hetero-functional binding fusion proteins - used for in vitro and in vivo applications, e.g. diagnosis and vaccine prodn.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Heterofunctional; totally synthetic affinity reagents; TSAR
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                                                                                                                                         Score 39; DB 17; Length 11; Pred. No. 3.7; 1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                           Control fusion protein putative binding site.
                                                                                                                                                                                                                                                                                                                                    AAR13721 standard; Protein; 120 AA.
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                                                                                                                                         Match 76.5%;
Local Similarity 75.0%;
les 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   91WO-US01013
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      90US-0480420
                                                                                                                                                                                                                                                                                                                                                                                                          (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 75.0
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (FOWL/) FOWLKES D M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 1991-267139/36.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Fowlkes D, Kay BK;
                                                                                                         11 AA;
                                                                                                                                                                                                                                |||:| ||
3 YYGNYGGY 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           N-PSDB; AAQ13360
                                                                                                                                                                                                              1 YYGDYEGY 8
                                                                                                                                                                                                                                                                                                                                                                                                          06-NOV-1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 22-AUG-1991.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   14-FEB-1991;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      15-FEB-1990;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WO9112328-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Synthetic.
                                                                                                          Sequence
                                                                                                                                                                                                                                                                                                                                                                        AAR13721;
                                                                                                                                           Query Match
                                                                                                                                                           Best Loca
Matches
                                                                                                                                                                                                                                                                                                   RESULT 15
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Search completed: December 23, 2002, 07:25:04 Job time: 5.29457 secs

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Gaps

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Sequence 1, Sequence 2, Sequence 2, Sequence 2, Sequence 2, Sequence 6, Sequence 6, Sequence 1, Sequence 2, Sequence 7, Sequence 1, Sequence 6, Sequence 7, Sequence 6, Sequence 7, Sequence 6, Sequence 7, Sequence 7, Sequence 7, Sequence 6, Sequence 7, Sequence 6, Sequence 7, Sequen
                                                                                                                                                                                                                                                                                               Seguence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           OTHER INFORMATION: Description of Artificial Sequence: Peptide OTHER INFORMATION: derived from VCAM-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 39; DB 3; Length 11; Pred. No. 1.7;
                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 43, Application US/08467580B
Fatent No. 6001809
GENERAL INFORMATION:
APPLICANT: Thorselve, Eugene D
APPLICANT: Thorselve, Theodore A
APPLICANT: Pleiss, Michael A
TITLE OF INVENTION: Inhibitors of Leukocyte Adhesion
FILE REFERENCE: 123-US-CIP1
CURRENT APPLICATION NUMBER: US/08/467,580B
CURRENT FILING DATE: 1995-06-06
EARLIER APPLICATION NUMBER: 08/273,055
EARLIER APPLICATION NUMBER: 08/273,055
SEQIID NOS: 163
SOFTWARE: PatentIN Ver. 2.0
SEQ ID NO 43
LENGTH: 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 43, Application PC/TUS9508516
GENERAL INFORMATION:
APPLICANT: ATHENA NEUROSCIENCES, INC.
TITLE OF INVENTION: INHIBITORS OF LEUROCYTE ADHESION
NUMBER OF SEQUENCES: 157
CORRESPONDENCE ADDRESS:
ADDRESSEE: ATHENA NEUROSCIENCES, INC.
STREET: 800 Gateway Blvd.
CITY: South San Francisco
STATE: CA
US-08-600-656-1
US-08-600-656-2
US-09-170-670-1
US-09-170-670-2
US-09-170-670-8
US-09-170-670-8
US-09-170-670-8
US-09-193-068-1
US-09-193-068-2
US-09-193-068-2
US-09-193-068-2
US-09-193-068-2
US-09-183-412-1
US-09-183-412-2
US-09-183-412-2
US-09-183-412-2
US-09-183-412-6
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US-09-183-412-6
US-09-183-412-6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; LOCATION: (1)
; OTHER INFORMATION: ACETYLATION
US-08-467-580-43
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: PRT ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   76.5%;
75.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 76.5
Best Local Similarity 75.0
Matches 6; Conservative
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LOCATION: (1)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     YYGDYEGY 8
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   FEATURE:
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Sequence 1, Appli
Sequence 12, Appli
Sequence 2, Appli
Sequence 6, Appli
Sequence 61, Appli
Sequence 42, Appli
Sequence 42, Appli
Sequence 8, Appli
Sequence 14, Appli
Sequence 14, Appli
Sequence 14, Appli
Sequence 14, Appli
Sequence 16, Appli
Sequence 2, Appli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Seguence 43, Appl
                                                                                                                  December 23, 2002, 07:20:23 ; Search time 1.44186 Seconds (without alignments) 163.250 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 43, P
Sequence 35, P
Sequence 61, P
Sequence 25, P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Description
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /cgn2_6/ptodata/1/iaa/5A_COMB.pep:*
/cgn2_6/ptodata/1/iaa/5B_COMB.pep:*
/cgn2_6/ptodata/1/iaa/6A_COMB.pep:*
/cgn2_6/ptodata/1/iaa/6B_COMB.pep:*
/cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
/cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
              GenCore version 5.1.3
Copyright (c) 1993 - 2002 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-08-888-366-12
US-09-136-315-2
US-09-134-001C-3350
US-09-134-001C-3350
US-08-467-580-42
PCT-US95-08516-42
US-08-25-477B-8
PCT-US95-08516-42
US-09-25-765-13
US-09-055-765-14
US-09-055-765-14
US-09-055-765-14
US-09-055-765-14
US-09-05-765-14
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US-09-113-750A-35
US-09-134-078-61
US-09-134-078-25
US-08-313-200-1
PCT US93-03837-1
5268270-2
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US-08-861-837-1
US-08-861-837-2
US-08-600-908A-12
US-08-683-838A-12
                                                                                                                                                                                                                                                                                                                                          Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-08-467-580-43
                                                                                                                                                                                                                                                                                                            262574 seqs, 29422922 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SUMMARIES
                                                                                                                                                                                                                                                                                                                                                                                                                             Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                    OM protein - protein search, using sw model
                                                                                                                                                                                                                                                        BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Issued_Patents_AA:*
                                                                                                                                                                                                                                                                                                                                                                          Minimum DB seq length: 0
Maximum DB seq length: 2000000000
                                                                                                                                                                               US-09-865-198-3
51
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Match Length
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Perfect score:
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                                                                                                                                         Length 525;
                                                                                                                                         Score 36; DB 4; Length 525
Pred. No. 2.1e+02;
0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDIUM TYPE: Diskette
COMPUTER: Diskette
COMPUTER: Diskette
OPERATING SYSTEM: Windows95
SOFTWARE: FastSEO for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/134,078
FILING DATE: 13-AUG-1998
CLASSIFCATION ATA:
APPLICATION NUMBER: 08/949,026
FILING DATE: 10-OCT-1997
APPLICATION NUMBER: 60/056,916
FILING DATE: 10-OCT-1997
APPLICATION NUMBER: 60/056,916
FILING DATE: 06-DEC-1996
ATTORNEY-AGENT INFORMATION:
NAME: HAILE, LISA A.
REGISTRATION NUMBER: 38,347
REFERENCE/DOCKET NUMBER: 09010/024002
TELECOMMUNICATION INFORMATION:
TELECHMUNICATION INFORMATION:
TELECHMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                            Sequence 61, Application US/09134078
Patent No. 6368844
GENERAL INFORMATION:
APPLICANT: Bylina, Edward J.
TITLE OF INVENTION: GLYCOSIDASE ENZYMES
NUMBER OF SEQUENCES: 72
CORRESPONDENCE ADDRESS:
ADDRESSEE: Gray Cary Ware & Freidenrich LLP
STREET: 4365 Executive Drive, Suite 1600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; Sequence 25, Application US/09134078 ; Patent No. 6368844
                               STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-09-113-750A-35
                                                                                                                                         70.6%;
75.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        663 amino acids
                                                                                                                                         Query Match
Best Local Similarity 75.0°
Matches 6; Conservative
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Best Local Similarity 62...
5. Conservative
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 663 amino ació
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TOPOLOGY: linear
MOLECULE TYPE: protein
FRAGMENT TYPE: internal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
             TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                San Diego
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          || ||:|:
361 YYPDYDGF 368
                                                                                                                                                                                                                                                        71 YSGDYENY 78
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                                                                                                                                                                                                                               1 YYGDYEGY 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 YYGDYEGY 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ZIP: 92121
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US-09-134-078-25
                                                                                                                                                                                                                                                                                                                                          RESULT 4
US-09-134-078-61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CITY:
STATE:
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COUNTRY: USA

21P: 94080
COMPUTER READABLE FORM:
MEDIUW TYPE: FIDPPY disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: PATENT: PC-DOS/MS-DOS
SOFTWARE: PATENT: PC-DOS/MS-DOS
SOFTWARE: PATENT: PC-DOS/MS-DOS
SOFTWARE: PATENT: DO-JUL-1995
CURRENT APPLICATION DATA:
PRIOR APPLICATION UNBER: PCT/US95/08516
FILING DATE: 11-JUL-1995
FILING DATE: 11-JUL-1994
ATTORNEY/AGENT INFORMATION:
NAME: MOOI, LESLIE A.
REFERENCE/PCKET NUMBER: 002010-008
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION FOR SEQ ID NO: 43:
SEQUENCE (EHRACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: David E. Junker and Mark D. Cochran TITLE OF INVENTION: Recombinant Raccoonpox virus NUMBER OF SEQUENCES: 58
CORRESPONDENCE ADDRESS: ADDRESSE: John P. White STREET: 1185 Avenue of the Americas CITY: New York STATE: New York COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPENATURE: THO PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/113,750A
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-09-113-750Å-35

; Sequence 35% Application US/09113750A

; Patent No. 294176

; GENERAL INFORMATION:

APPLICANT: David E. Junker and Mai
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: White, John P.
REGISTATION NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 5574.
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212)262-0400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELER: 4.2553
INFORMATION FOR SEQ ID NO: 35:
SEQUENCE CHARACTERISTICS:
FENGTH: 525 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      11 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (212)664-0525
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; STRANDEDNESS: Single
; TOPOLOGY: linear
PCT-US95-08516-43
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Flobov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        umino acid
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Matches & Conserva
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3 YYGMYGGY 10
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/note= "TPO epitopic region within
fusion protein: MBP-TPO (AA 376-631)"
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TPO(1-455) or N-terminal half of TPO'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note= "TPO epitopic region within fusion protein: MBP-TPO (AA 1-400)'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note= "TPO C-terminus containing binding region"
                                                                                                                                                                                                                                                                                                                                                              HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGENET TYPE: N-terminal
ORIGINAL SOURCE:
ORGANISM: Homo sapiens
DEVELOPMENTAL STAGE: Mature
TISSUE TYPE: Thyroid gland(from people with Grave's
TISSUE TYPE: disease)
IMMEDIATE SOURCE:
CLONE: phTPO-2.8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME/KEY: Peptide
LOCATION: Join(1..3, 456..631)
OCHER INFORMATION: /note= "TPO region within fusion
OTHER INFORMATION: plasmid: TPO(delta4-455)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note= "TPO epitopic or binding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note= "C-terminal truncation:
TPO(1-120)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note= "C-terminal truncation:
TPO(1-631)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          join(455..532, 590..933)
MATION: /note= "alternatively spliced
MATION: C-terminus of TPO"
                                                                                                RESERVATION NOMBER: 34,202
REFERENCE/DOCKET NUMBER: 2034
TELECOMMUNICATION INFORMATION:
TELEFAM: (415) 494-0792
TELERA: 706141
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENTH: 933 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
                                     ATTORNEY AGENT INFORMATION:
NAME: Konski, Antoinette F.
REGISTRATION NUMBER: 34,202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME/KEY: Region
LOCATION: 266..281
OTHER INFORMATION: /note= "
OTHER INFORMATION: region"
  08-NOV-1994
N: 435
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NAME/KEY: Region
LOCATION: 455.933
OTHER INFORMATION: /
OTHER INFORMATION: beature:
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LOCATION: 1..400
OTHER INFORMATION:
OTHER INFORMATION:
FEATURE:
NAME/KEY: Peptide
LOCATION: 1..455
OTHER INFORMATION:
OTHER INFORMATION:
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LOCATION: 1..631
OTHER INFORMATION:
OTHER INFORMATION:
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OTHER INFORMATION:
OTHER INFORMATION:
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OTHER INFORMATION:
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    FILING DATE: 08 CLASSIFICATION:
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Fatent No. 5999153
GENERAL INFORMATION
GENERAL INFORMATION:
APPLICANT: Baker, James R.
APPLICANT: Koenig, Ronald J.
TITLE OF INVENTION: THYROID PEROXIDASE EPITOPIC REGIONS
TITLE OF SEQUENCES: 13
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORRISON & FOERSTER
STREET: 755 Page Mill Road
CITY: Palo Alto
STATE: GA
COUNTRY: USA
COUNTRY: USA
COUNTRY: USA
COUNTRY HANDABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 680;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 36; DB 4; Length 680
Pred. No. 2.7e+02;
2; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/313,200
               APPLICANT: BYINA, Edward J.

TITLE OF INVENTION: GLYCOSIDASE ENZYMES
NUMBER OF SEQUENCES: 72
CORRESPONDENCE ADDRESS:
ADDRESSEE: Gray Cary Ware & Freidenrich LLP
STREET: 4365 Executive Drive, Suite 1600
CITY: San Diego
STATE: CA
COUNTRY: USA
                                                                                                                                                                                                                           COMPUTER READBLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows95
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/134,078
FILING DATE: 13-AUG-1998
CLASSIFICATION NATA:
APPLICATION NUMBER: 08/949,026
FILING APPLICATION NUMBER: 08/949,026
FILING DATE: 10-OCT-1997
APPLICATION NUMBER: 60/056,916
FILING DATE: 06-DEC-1996
ATTORNEY,AGENT THOORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME: Halle, Lisa A.
REGISTRATION NUMBER: 38,347
REFERENCE/DOCKET NUMBER: 09010/024002
TELECOMMUNICATION INFORMATION:
TELEPHONE: 858/677-1465
INFORMATION FOR SEQ ID NO: 25:
SEQUENCE CHARACTERISTICS:
LENGTH: 680 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 70.6%;
Best Local Similarity 62.5%;
Matches 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MOLECULE TYPE: protein
; FRAGMENT TYPE: internal
US-09-134-078-25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: amino acid
TOPOLOGY: linear
GENERAL INFORMATION:
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378 YYPDYDGF 385
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EATURE:

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Sequence 1, Application PC/TUS9303837
GENERAL INFORMATION:
APPLICANT: Baker, Jr., James R.
APPLICANT: Roenig, Ronald J.
TITLE OF INVENTION: Thyroid Peroxidase Epitopic Regions
NUMBER OF SEQUENCEs: 2
CORRESPONDENCE ADDRESS:
ADDRESSEB: Harness, Dickey & Pierce
STREET: P.O. Box 828
CITY: Bloomfield Hills
STATE: MI
COUNTRY: USA
2IP 48303 J.
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note= "TPO region within maltose binding fusion protein"
                                                                                                                             /note= "Tpo region within fusion
protein"
                                      /note= "TPO binding or epitopic region"
                                                                                                                                                                                                                                                                                                                                                                                                                           /note= "TPO binding or epitopic region"
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COMPUTER: IBM PC compatible
OPPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/03837
FILING DATE: 19930422
CLASSIFICATION:
ATTORNEY/ACEDIN:
                                                                                                                                                                                                                                                                                                                               /note= "TPO binding or epitopic region"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note= "TPO binding or epitopic
                                                                                                                                                                                                                                        /note= "TPO region containing
divergent sequences"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 36; DB 2; Le
Pred. No. 3.7e+02;
0; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ATTORNEY/AGENT INFORMATION:
NAME: Lewak, Anna M.
REGISTRATION NUMBER: 23006
REFERENCE/DOCKET NUMBER: 2115-00658PPA
TELECOMUNICATION INFORMATION:
TELEPHONE: (313) 641-1600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 75.0%;
Matches 6; Conservative (
                                                                                               NAME/KEY: Region
LOCATION: 596..611
OTHER INFORMATION: /
OTHER INFORMATION: p
FEATURE:
NAME/KEY: Region
LOCATION: 602..615
OTHER INFORMATION: /
OTHER INFORMATION: /
FEATURE:
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LOCATION: 611..615
OTHER INFORMATION: //
CTHER INFORMATION: r/
FEATURE:
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LOCATION: 631.933
OTHER INFORMATION: /
OTHER INFORMATION: r
FEATURE:
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LOCATION: 632..933
OTHER INFORMATION: /
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LOCATION: 633..768
OTHER INFORMATION:
                          LOCATION: 592..613
OTHER INFORMATION:
OTHER INFORMATION:
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PCT-US93-03837-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note= "TPO binding region of maltose binding region fusion construct"
NAME/KEY: Region
LOCATION: 456.631
OTHER INFORMATION: /note= "TPO binding or epitopic OTHER INFORMATION: region"
NAME/KEY: Region
NAME/KEY: 456.633
COTHER INFORMATION: /note= "TPO binding or epitopic OTHER INFORMATION: region"
NAME/KEY: Region
LOCATION: 456.933
OTHER INFORMATION: region"
LOCATION: 456.933
OTHER INFORMATION: region"
LOCATION: 456.933
OTHER INFORMATION: region"
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LOCATION: 590..611
OTHER INFORMATION: /note= "TPO region within maltose
OTHER INFORMATION: binding fusion protein"
                                                                                                                                                                                                                                                                                                                                      /note- "TPO region within maltose binding fusion protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note= "TPO binding region within plasmid pMalTPO"
                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME/KEY: Region
LOCATION: 517..637.
COTHER WINDORMATION: /note= "TPO binding or epitopic
OTHER FINFORMATION: region"
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LOCATION: 590..615
OTHER! INFORMATION: /note= "TPO binding or epitopic
OTHER INFORMATION: region"
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LOCATION: 590..675
COTHER INFORMATION: /note= "TPO binding or epitopic
OTHER INFORMATION: region"
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                                                                                                                                                                                                                                                                                                                                                                                                                                     /note= "non-reactive fragment"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note= "recombinant TPO
                                                                                                                                                                                                                                                                                               NAME/KEŽ: Region
LOCATION: 456.933
OTHER INFORMATION: OTHER INFORMATION: FEATURE: ERATURE: Region
LOCATION: 457.517
OTHER INFORMATION: OTHER
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LOCATION: 457.933
OTHER INFORMATION: /
OTHER INFORMATION: p
FEATURE:
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LOCATION: 465..933
OTHER INFORMATION: /
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LOCATION: 517..633
OTHER TINFORMATION: /
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LOCATION: 513..633
OTHER (INFORMATION:
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LOCATION: 573..633
OTHER INFORMATION:
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Gaps

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Length 933; Indels us-09-865-198-3.rai

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APPLICANT: Wagner, Fred W.

TITLE OF INVENTION: Mercury Binding Polypeptides and Nucleotides Coding Therefo
NUMBER OF SEQUENCES: 39

CORRESPONDENCE ADDRESS:

ADDRESSEE: Merchant & Gould

STREET: 90 South 7th Street, 3100 No. 5972656west Ctr.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-09-136-315-2

Sequence 2, Application US/09136315B

Sequence 2, Application US/09136315B

Sequence 2, Application US/09136315B

Sequence 2, Application US/09136315B

Sequence 2, Application US/0816B

GENERAL INFORMATION:

APPLICANT: CO, MAN SUNG

APPLICANT: CO, MAN SUNG

TITLE OF INVENTION: FACTOR MONOCLONAL ANTIBODY

FILE REFERENCE: 0010-0933-0

CURRENT APPLICATION NUMBER: US/09/136,315B

CURRENT FILING DATE: 1998-08-19

NUMBER OF SEQ ID NOS: 8

SOFUMARE: Patentin Ver. 2.0

SEQ ID NO 2

LENGTH: 139
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                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/888,366
FILING DATE: 03-JUL-1997
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 34; DB 2;
Pred. No. 1e+02;
2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/187,407
FILING DATE: 27-JAN-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/990,542
FILING DATE: 14-DEC-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/493,299
FILING DATE: 14-MAR-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/324,392
FILING DATE: 14-MAR-1989
ATTONNEY/AGENT INFORMATION:
NAME: CARLET, CHARLES G.
REGISTRATION NUMBER: 35,093
REFERENCE/DOCKT NUMBER: 8648.39USC1
TELECOMUNICATION INFORMATION:
TELECOMUNICATION INFORMATION:
TELECOMUNICATION INFORMATION:
TELECOMUNICATION INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         66.7%;
ilarity 62.5%;
Conservative
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ORGANISM: Mus musculus
                                                                                                                                                                                                                CITY: Minneapolis
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Best Local Similarity
Matches 5; Conserv
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96 YYGNYEWF 103
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                                                                                                                                                                                                                                                                                  COUNTRY: US
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;Patent No. 5268270
Thomas F.;Halter, Roman;Pohlner, Johnnnes
TITLE OF INVENTION: PROCESS FOR PRODUCING PROTEINS USING GRAM
NUMBER OF SEQUENCES: 6
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/171,872
FILING DATE: 01-JUL-1987
                                                                                                                                                                                                                                                                                                                                                                                                                                                                IMMEDIATE SOURCE:
CLONE: phrpo-2.8
PUBLICATION INFORMATION:
AUTHORS: Kimura, S.
AUTHORS: Wasyama, T.
AUTHORS: Umeki, K.
AUTHORS: Umeki, K.
AUTHORS: Ohtaki, S.
AUTHORS: Hirai, K.
TITLE: Human thyroid peroxidase: Complete cDNA and TITLE: protein sequence, chromosome mapping, and TITLE: identification of two alternately spliced mRNAs JOHNANDER.
AUTHORS: A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         68.6%; Score 35; DB 6; Length 1507; 62.5%; Pred. No. 8.4e+02;
tive 1; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             70.6%; Score 36; DB 5; Length 933; 75.0%; Pred. No. 3.7e+02; ive 0; Mismatches 2; Indels
                                                                                                                                                                TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
FRAGMENT TYPE: N terminal
ORIGINAL SOURCE:
ORGANISM: Homo sapiens
DEVELOPMENTAL STAGE: Mature
TISSUE TYPE: Thyroid gland (from people with Grave's
TISSUE TYPE: disease)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RELEVANT RESIDUES IN SEQ ID NO: 1: FROM 1 TO 3048
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10S-08-888-366-12
Sequence 12, Application US/08888366
Patent No. 5972656
TELEFAX: (313) 641-0270
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 933 amino acids
TYPE: AMINO ACID
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APPLICANT: Lopez, Osvaldo
APPLICANT: Wylie, Dwane E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 70.6 Best Local Similarity 75.0 Matches 6; Conservative
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DATE: 1987
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Best Local Similarity
Matches 5; Conserv
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JOURNAL:
VOLUME: 8
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Gaps
                                 Sequence 61, Application US/07857224B

Sequence 61, Application US/07857224B

Patent No. 5958784

GENERAL INFORMATION:
TITLE OF INVENTION: Predicting Folded Structures of Proteins
TITLE OF INVENTION: Predicting Folded Structures of Proteins
NUMBER OF ENQUENCES: 114

CORRESPONDENCE ADDRESS:
STREET: Hadlaubstrasse 151

CITY: Larich
STRIET: none
COUNTRY: Switzerland
IP: (note: this is an international post code) CH-8092

COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch diskette, 1.4 Mb storage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 261;
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Fatent No. 6001809
GENERAL INFORMATION:
APPLICANT: Thorsett, Eugene D
APPLICANT: Yednock, Theodore A
TITLE OF INVENTION: Inhibitors of Leukocyte Adhesion
FILE REFERENCE: 123-US-CIPI
CURRENT APPLICATION NUMBER: US/08/467,580B
CURRENT FILING DATE: 1995-06-06
EARLIER APPLICATION NUMBER: 08/273,055
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 33.5; DB 2;
Pred. No. 2.6e+02;
0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                  COMPUTER: Apple MacIntosh
OPERATING SYSTEM: MacIntosh 7.0
SOFTWARE: Microsoft Word
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/857,224B
FILING DATE: 03/25/92
CLASSIFICATION: 436
PRIOR APPLICATION INFORMATION:
TELECHMUNICATION INFORMATION:
TELECHMUNICATION INFORMATION:
TELEFEAX: (International) 41 1 532 2830
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AUTHORS: Hanks, S. K.
AUTHORS: Quinn, A. M.
AUTHORS: Hunter, T.
TITLE: The protein kinase family
JOURNAL: Science
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ORGANISM: Caenorhabditis elegan
ERATURE: Protein kinase; Table 8
PUBLICATION INFORMATION:
AUTHORS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      61:
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Best Local Similarity 87.5%;
Matches 7; Conservative
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DESCRIPTION: protein
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  RESULT 13
US-07-857-224B-61
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Patent No. 6380370

GENERAL INCORDATION:

APPLICANT: Lynn Doucette-Stamm et al
APPLICANT: Lynn Doucette-Stamm et al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS
TITLE OF INVENTION: DEPLOEMIDIS FOR DIAGNOSTICS AND THERAPEUTICS

FILE REPRÉMENC: GT-C07

CURRENT FILING DATE: 1998-08-13

PRIOR FILING DATE: 1997-11-08

PRIOR FILING DATE: 1997-11-08

PRIOR FILING DATE: 1997-10-14

RIOR FILING DATE: 1997-10-14

RIOR FILING DATE: 1997-10-14

SEQ ID NO 3330

LENGTH: 660
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US-09-136-1315-6
Sequence 6, Application US/09136315B
Sequence 6, Application US/09136315B
Sequence 6, Application US/09136315B
Setent No. 6228360
GENERAL INFORMATION:
APPLICANT: WASOUEZ, MAXIMILLIANO
TITLE OF INVENTION: FACTOR MONOCLONAL ANTIBODY
TITLE OF INVENTION: FACTOR MONOCLONAL ANTIBODY
FILE REPERENCE: 0010-0933-0
CURRENT APPLICATION NUMBER: US/09/136,315B
CURRENT FILENCE DATE: 1998-08-19
NUMBER OF SEQ ID NOS: 8
SOTWARE: Patentin Ver. 2.0
SEQ ID NO 6
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                                             Length 139;
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Pred. No. 1.2e+02;
1; Mismatches 2; Indels
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                                                                                     2; Indels
                                          Score 34; DB 4; I
Pred. No. 1.2e+02;
1; Mismatches 2;
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US-09-134-001C-3350
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TYPE: PRT M
ORGANISM: Artificial Sequence
                                          66.7%;
62.5%;
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Best Local Similarity 62.5%;
Matches 5; Conservative
                                          Query Match
Best Local Similarity 62.5
Matches 5% Conservative
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Matches 5; Conservative
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US-09-136-315-2
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                                            TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Peptide
FEATURE:
FEATURE:
NAME/KEY: MOD_RES
LOCATION: (1)
COTHER INFORMATION: ACETYLATION
US-08-467-580-42
                                                                                                                                                                                                                                         Query Match

64.7%; Score 33; DB 3; Length 11;
Best Local Similarity 62.5%; Pred. No. 14;
Matches 5; Conservative 1; Mismatches 2; Indels
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                                                                                                                                                                      2; Indels
EARLIER FILING DATE: 1994-07-11
NUMBER OF SEQ ID NOS: 163
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 42
LENGTH: 11
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Best Local Similarity 62.59
...+rhes 5; Conservative
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STRANDEDNESS: single
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PCT-US95-08516-42
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Search completed: December 23, 2002, 07:33:13 Job time: 2.44186 secs

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Sequence 3, Appli
Sequence 7, Appli
Sequence 23, Appli
Sequence 27, Appli
Sequence 28, Appli
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Sequence 27, Appli
Sequence 11, Appli
Sequence 11, Appli
Sequence 11, Appli
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Sequence 25, Appli
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Sequence 2696, Appli
Sequence 2696, Appli
Sequence 12133, Appli
Sequence 12133, Appli
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180.208 Million cell updates/sec
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /cgn2_6/ptodata/2/pubpaa/USOB_NEW_PUB.pep:*
/cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep:*
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GenCore version 5.1.3
Copyright (c) 1993 - 2002 Compugen Ltd.
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US-09-815-242-5896
US-09-815-242-12135
US-09-815-242-13013
US-09-815-242-13013
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US-09-865-198-3
US-09-976-787-2
US-09-976-787-23
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US-09-865-198-28
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Maximum Match 100%
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                                                                                                                                                                                                                                                                                                                            Sequence:
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                                                                                                                                                            Run on:
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20 34 66.7 677 10 US-09-815-242-10663 Sequence 10663, A Sequence 13, Appl 24 33 64.7 389 12 US-09-918-543-13 Sequence 13, Appl 25 33 64.7 389 12 US-09-918-543-8 Sequence 13, Appl 26 4.7 392 10 US-09-918-843-8 Sequence 13, Appl 27 9 US-09-918-945-822-8 Sequence 14, Appl 28 4.7 402 10 US-09-143-127-10 Sequence 14, Appl 29 US-09-918-543-4 Sequence 14, Appl 29 US-09-918-543-4 Sequence 14, Appl 30 44.7 485 9 US-09-918-543-4 Sequence 14, Appl 31 33 64.7 485 9 US-09-918-543-1 Sequence 1, Appl 31 33 64.7 485 9 US-09-918-543-1 Sequence 1, Appl 31 33 64.7 485 9 US-09-918-543-1 Sequence 1, Appl 31 33 64.7 485 10 US-09-918-64-1 Sequence 1, Appl 31 33 64.7 485 10 US-09-769-864-1 Sequence 1, Appl 31 34 485 10 US-09-769-864-1 Sequence 1, Appl 31 64.7 485 10 US-09-769-864-1 Sequence 1, Appl 31 64.7 485 10 US-09-769-864-1 Sequence 2, Appl 31 64.7 485 10 US-09-769-864-1 Sequence 2, Appl 31 64.7 485 10 US-09-984-36-2 Sequence 2, Appl 31 64.7 485 10 US-09-984-36-2 Sequence 2, Appl 31 64.7 485 10 US-09-984-36-2 Sequence 1, Appl 31 64.7 485 10 US-09-984-36-2 Sequence 2, Appl 31 64.7 485 10 US-09-984-36-2 Sequence 2, Appl 31 64.7 485 10 US-09-984-36-2 Sequence 2, Appl 31 64.7 485 10 US-09-984-36-1 Sequence 2, Appl 31 64.7 485 10 US-09-984-36-1 Sequence 1, Appl 31 64.7 485 10 US-09-984-36-1 Sequence 1, Appl 41 33 64.7 485 10 US-09-984-36-1 Sequence 1, Appl 41 33 64.7 485 10 US-09-984-36-1 Sequence 1, Appl 41 33 64.7 485 10 US-09-984-36-1 Sequence 2, Appl 44 33 64.7 485 10 US-09-984-36-1 Sequence 1, Appl 44 33 64.7 485 10 US-09-984-36-1 Sequence 2, Appl 44 33 64.7 485 10 US-09-984-36-1 Sequence 1, Appl 44 33 64.7 485 10 US-09-984-36-1 Sequence 2, Appl 54.7 485 10 US-09-984-36-1 Sequence 1, Appl 54.7 485 10 US-09-984-36-1 Sequence 2, Appl 54.7 485 10 US-09-984-36-1 Sequence 3, Appl 54.7 485 10
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ALIGNMENTS

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Sequence 3, Application US/0985198
Patent No. US20021013345A1
GENERAL INFORMATION:
APPLICANT: Zhu, Zhenping
TITLE OF INVENTION: Bispecific Immunoglobulin-Like Antigen Binding Proteins and Me
FILE REPERENCE: 11245/47102
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                                 Sequence 3, Application US/09976787

Sequence 3, Application US/09976787

Patent No. US20020064528A1

GENERAL INFORMATION:

APPLICANT: Zhu, Zhenping

APPLICANT: Witte, Larry

TUTLE OF INVENTION: Antibodies Specific to KDR and Uses Thereof

FILE REFERENCE: 11245,46505

CURRENT APPLICATION NUMBER: US/09/976,787

CURRENT FILING DATE: 2001-10-12

PRIOR APPLICATION NUMBER: US 60/493,539

PRIOR PLING DATE: 1999-01-28

PRIOR PLING DATE: 1999-01-29

NUMBER OF SED ID NOS: 40

SOFTWARE: WordPerfect 8:0 for Windows
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100.0%; Pred. No. 8.9e+04;
ive 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                       ; ORGANISM: Mus musculus US-09-976-787-3
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Best Local Similarity
Matches 8; Conserv
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US-09-976-787-3
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US-09-865-198-3
                                                                                                                                                                                                                                                                                                                                                          SEQ ID NO 3
LENGTH: 8
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Sequence 22, Application US/09865198
Patent No. US20020103345al
GENERAL INFORMATION:
APPLICANT: Zhu, Zhenping
TITLE OF INVENTION: Bispecific Immunoglobulin-Like Antigen Binding Proteins and Me:
TITLE OF INVENTION: Production
TITLE OF INVENTION: Production
CURRENT APPLICATION NUMBER: US/09/865,198
CURRENT FILING DATE: 2001-05-24
PRIOR APPLICATION NUMBER: US 60/206,749
PRIOR FILING DATE: 2000-05-24
NUMBER OF SEQ ID NOS: 34
NUMBER OF SEQ ID NOS: 34
NUMBER OF SEQ ID NOS: 34
                                                                                                                                                                                                                                                                                                                           APPLICANT: Zhu, Zhenping
TITLE OF INVENTION: Bispecific Immunoglobulin-Like Antigen Binding Proteins and Me
TITLE OF INVENTION: Production
FILE REFERENCE: 11245/47102
CURRENT APPLICATION NUMBER: US/09/865,198
CURRENT APPLICATION NUMBER: US 60/206,749
PRIOR APPLICATION NUMBER: US 60/206,749
PRIOR FILING DATE: 2000-05-24
NUMBER OF SEQ ID NOS: 34
SOFTWARE: WordPerfect 8.0 for Windows
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100.0%; Score 51; DB 10; Length 117;
Best Local Similarity 100.0%; Pred. No. 0.083;
Matches 8; Conservative 0; Mismatches 0; Indels 0
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                                         Score 51; DB 10; Length 117;
Pred. No. 0.083;
                                                                                  Indels
                                                                               0; Mismatches
                                                                                                                                                                                                                                                      US-09-865-198-7; Sequence 7, Application US/09865198; Patent No. US-20020103345Al; GENERAL INFORMATION:
                                         Query Match 100.0%;
Best Local Similarity 100.0%;
Matches 8; Conservative 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; SEQ ID NO 22
; LENGTH: 117
; TYPE: PRT
; ORGANISM: MOUSE
US-09-865-198-22
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US-09-865-198-22
    US-09-976-787-23
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US-09-976-787-29
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Patent No. US20020064528A1

GENERAL INFORMATION

APPLICANT: July Inenping

APPLICANT: July Inenping

APPLICANT: July Inenping

TITLE OF INVENTION Antibodies Specific to KDR and Uses Thereof

FILE REPERBOR: 11245/46505

CURRENT APPLICATION NUMBER: US/09/976,787

CURRENT FIRMS DATE: 2001-110-12

PRIOR PILING DATE: 2000-01-28

PRIOR PILING DATE: 1999-01-29

NUMBER OF SEQ ID NOS: 40

SOFTWARE: WORTHERED NOS: 40

SOFTWARE: WORTHERED NOS: 40

LENGTH: 117
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Sequence 23, Application US/08976787

Sequence 23, Application US/08976787

GENERAL INFORMATION:

APPLICANT 2nu, Zhenping

APPLICANT 2nu, Zhenping

APPLICANT 2nu, Zhenping

TITLE OF INVENTION: Antibodies Specific to KDR and Uses Thereof

FILE REFERENCE: 11245,46505

CURRENT APPLICATION NUMBER: US/09/976,787

CURRENT FILING DATE: 2001-10-12

PRIOR PILING DATE: 2000-01-28

PRIOR PILING DATE: 1999-01-29

NUMBER OFFISEO ID NOS: 40

SOFTWARE: WordPerfect 8.0 for Windows

SET IN NOTE 1177
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                                                                                                                                                                                                                                    Length 8;
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100.0%; Pred. No. 8.9e+04;
                                                                                                                                                                                                                                                                              0; Mismatches
CURRENT FILING DATE: 2001-05-24
PRIOR PPLICATION NUMBER: US 60/206,749
PRIOR FILINGEDATE: 2000-05-24
NUMBER OF SEG ID NOS: 34
SEG ID NOS: 34
SEG ID NOS: 34
LENGTH: 8
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Best Local Similarity 100.
Matches 8% Conservative
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Best Local Similarity
Matches 8% Conserv
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99 YYGDYEGY 106
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ORGANISM: Mouse
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US-09-976-787-7
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GENERAL INFORMATION:
APPLICANT: Zhu, Zhenping
TITLE OF INVENTION: Bispecific Immunoglobulin-Like Antigen Binding Proteins and Me
TITLE OF INVENTION: Bispecific Immunoglobulin-Like Antigen Binding Proteins and Me
TITLE OF INVENTION: Bispecific Immunoglobulin-Like Antigen Binding Proteins and Me
TITLE OF INVENTION: Production
FILE REFERENCE: 11245/47102
CURRENT APPLICATION NUMBER: US 60/206,749
PRIOR APPLICATION NUMBER: US 60/206,749
PRIOR FILING DATE: 2000-05-24
NUMBER OF SEO ID NOS: 34
SOFTWARE: WordPerfect 8.0 for Windows
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Pred. No. 0.16;
Mismatches 0; Indels
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                                                                                                                                                                                                                              0.16;
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100.0%; Pred. No. v.....
0; Mismatches
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Sequence 11, Application US/09821687

PATENT NO. US20020106724A1

SERENAL INFORMATION:
APPLICANT: MIXORAIDA, KATSUHIKO

TITLE OF INVENTION: RNA-BINDING PROTEIN

FILE REFERENCE: 081356/0162

CURRENT APPLICATION NUMBER: US/09/821,687

CURRENT FILING DATE: 2001-07-03

PRIOR APPLICATION NUMBER: JP 2000-299812

PRIOR FILING DATE: 2000-09-29
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    PRIOR APPLICATION NUMBER: US 60/117,726
PRIOR FILING DATE: 1999-01-29
NUMBER OF SEQ ID NOS: 40
SCFTWARE: WordPerfect 8.0 for Windows
SEQ ID NO 28
LENGTH: 240
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US-00-865-198-27
Sequence 27, Application US/09865198
Patent No. US20020103345A1
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Best Local Similarity luv...
8; Conservative
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Best Local Similarity 100.
Matches 8; Conservative
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                                                                                                                                 ; TYPE: PRT
; ORGANISM: Mouse
US-09-976-787-28
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US-09-865-198-27
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LENGTH: 240
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LENGTH: 335
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APPLICANT: Zhu, Zhenping
TITLE OF INVENTION: Bispecific Immunoglobulin-Like Antigen Binding Proteins and Methor TITLE OF INVENTION: Bispecific Immunoglobulin-Like Antigen Binding Proteins and Methor TITLE OF INVENTION: Production
FILE REFERENCE: 11245/47102
CURRENT APPLICATION WUMBER: US/09/865,198
CURRENT FILING DATE: 2001-05-24
PRIOR FILING DATE: 2000-05-24
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; Sequence 29, Application US/09976787; Patent No. US20020064528A1; GENERAL INFORMATION; AD120020064528A1; APPLICANT: Zhu, Zhenping; APPLICANT: Zhu, Zhenping; TITLE OF INVENTION: Antibodies Specific to KDR and Uses Thereof; FILE REPERBNCE: 11245,46505 CURRENT APPLICATION NUMBER: US/09/976,787; CURRENT FILING DATE: 2001-10-12; PRIOR APPLICATION NUMBER: US 60/117,726; PRIOR PILING DATE: 1999-01-29; NUMBER OF SEQ ID NOS: 40: SOCTHARE: WordPerfect 8:0 for Windows; SEQ ID NO 29
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Batent No. US20020064528A1

GENERAL INFORMATION:
APPLICANT: Zhu, Zhenping
APPLICANT: Witte, Larry
TITLE OF INVENTION: Antibodies Specific to KDR and Uses Thereof
FILE REFERENCE: 11245/46505
CURRENT APPLICATION UNMER: US/09/976,787

CURRENT FILING DATE: 2001-10-12
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SOFWARE: WordPerfect 8.0 for Windows
SEQ ID NO 28
LENGTH: 238
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Patent No. US20020103345A1
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Best Local Similarity 100.
Matches 8; Conservative
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                                                                                                                                                                                                                                                                                                                                                              ; TYPE: PRT
; ORGANISM: Mouse
US-09-976-787-29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; ORGANISM: Mouse US-09-865-198-28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 8
US-09-865-198-28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-09-976-787-28
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Matches
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Gaps
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                                                                                                                                                                                                                                                                                                                              Length 663;
                                                                                                                                                                                                                                                                                                                                                                          1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Bylina, Edward J.
TITLE OF INVENTION: GLYCOSIDASE ENZYMES
NUMBER OF SEQUENCES: 72
CORRESPONDENES:
ADDRESSEE: Gray Cary Ware & Freidenrich LLP
STREET: 4365 Executive Drive, Suite 1600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER: IBM Compatible
COMPUTER: IBM Compatible
OPERATING SYSTEM; Windows 95
SOFTWARE: Fast5EQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/121,032
FILING DATE: 09-Apr-2002
CLASSIFICATION: <unknown>
             REGISTRATION NUMBER: 38,347
REFERENCE/DOCKET NUMBER: 09010/024002
                                                                                                                                                                                                                                                                                                                                Score 36; DB 9;
Pred. No. 89;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REFERENCE/DOCKET NUMBER: 09010/024002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/134,078
FILING DATE: 13-AUG-1998
APPLICATION NUMBER: 08/949,026
FILING DATE: 10-OCT-1997
APPLICATION NUMBER: 60/056,916
FILING DATE: 06-DEC-1996
                                                                                                                                                                                                                                                                                                                                                                          2; Mismatches
                                                                                                                                                                                  TOPOLOGY: linear
HOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 61:
US-10-121-032-61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY: linear

MOLECULE TYPE: protein

FRACMENT TYPE: Internal

SEQUENCE DESCRIPTION: SEQ ID NO: 25:
US-10-121-032-25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME: Haile, Lisa A.
REGISTRATION NUMBER: 38,347
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELECOMMUNICATION INFORMATION:
TELEPHONE: 858/677-1456
                                                    TELECOMMUNICATION INFORMATION:
TELEPHONE: 858/677-1456
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 25, Application US/10121032 Patent No. US20020155550A1 GENERAL INFORMATION:
                                                                                                                  INFORMATION FOR SEQ ID NO: 61:
SEQUENCE CHARACTERISTICS:
LENGTH: 663 amino acids
TYPE: amino acid
                                                                        TELEPHONE: 858/677-1456
TELEFAX: 858/677-1465
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LENGTH: 680 amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEFAX: 858/677-1465
                                                                                                                                                                                                                                                                                                                                70.68;
62.58;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   INFORMATION FOR SEQ ID NO: 25
SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ZIP: 92121
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                Query Match 70.69
Best Local Similarity 62.59
Matches 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CITY: San Diego
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                            || ||:|:
361 YYPDYDGF 368
                                                                                                                                                                                                                                                                                                                                                                                                                    1 YYGDYEGY 8
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US-10-121-032-25
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; OTHER INFORMATION: Description of Unknown Organism: hnRNPR US-09-821-687;10
                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-10-121-032-61
Sequence 61 Application US/10121032
SEQUENCES: 72
CORRESOUNDENCE ADDRESS:
SEQUENCES: 4365 Executive Drive, Suite 1600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        **COMPUTER: IBM Compatible COPERATING SYSTEM: Windows95 COPERATING SYSTEM: Windows95 COPERENT SOFTWARENT SPELICATION DATA: APPLICATION NUMBER: US/10/121,032
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 37; DB 10;
Pred. No. 60;
        75.0%; Pred. No. 34;
tive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: US/09/134,078
FILING DATE: 13-AUG-1998
APPLICATION NUMBER: 08/949,026
FILING DATE: 10-OCT-1997
APPLICATION NUMBER: 60/056,916
FILING DATE: 06-DEC-1996
                                                                                                                                                                                                                                                          GENERAL INCOMENTION:
APPLICANT: MIKOSHIBA, KATSUHIKO
APPLICANT: MIKOSHIBA, KATSUHIKO
FILEANT: MIKOSHIBA, KATSUHIKO
FILE REPERENCE: 081356/0162
CURRENT APPLICATION NUMBER: US/09/821,687
CURRENT APPLICATION NUMBER: US/09/821,687
CURRENT APPLICATION NUMBER: JP 2000-299812
PRIOR APPLICATION NUMBER: JP 2000-299812
PRIOR FILING DATE: 2000-09-29
SOFTWARE: Pâtentin Ver: 2.1
SEQ ID NO 101
LENGTH: 633
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE: 09-Apr-2002 CLASSIFICATION: <un>
                                                                                                                                                                                                                           Sequence 10, Application US/09821687
Patent No. US20020106724A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ZIP: 92121
JTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ATTORNEY/AGENT INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        72.5%;
75.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: PRT ORGANISM: Unknown Organism
Best Local Similarity 75.0
Matches 67 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match<sup>‡;</sup> 72.5
Best Local Ŝimilarity 75.0
Matches Ĝ; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CITY: San Diego
STATE: CA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COUNTRY: USA
                                                                                                  11 [] 11
470 YYDDYYGY 477
                                                                        1 YYGDYEGY 8
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                          0; Gaps
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                                                                                                                                                                        RESULT 15
US-09-925-299-990
; Sequence 990, Application US/09925299
; Patent No. US20020055627A1
; GENERAL INFORMATION:
; APPLICART: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
; FILE REFERENCE: PA102
; CURRENT APPLICATION NUMBER: US/09/925,299
; CURRENT FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: PCT/US00/05883
; PRIOR PILING DATE: 2000-03-08
; PRIOR FILING DATE: 1999-03-12
; NUMBER: OF EXD ID NOS: 1556
; SOFTWARE: PatentIN Ver. 2.0
; SEQ ID NO 990
; LENGTH: 214
; TYPE: PRT
; ORGANISM: HOMO Sapiens
US-09-925-299-990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ouery Match

68.6%; Score 35; DB 10; Length 214;
Best Local Similarity 62.5%; Pred. No. 46;
Matches 5; Conservative 1; Mismatches 2; Indels
                          1; Indels
Best Local Similarity 62.5%; Pred. No. 92;
Matches 5; Conservative 2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Search completed: December 23, 2002, 07:58:18 Job time: 0.744186 secs
                                                                                            || ||:|:
378 YYPDYDGF 385
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ||| | |:
105 YYGHYHGF 112
                                                                  1 YYGDYEGY 8
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Mon Dec 23 04:53:16 2002
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GenCore version 5.1.3 Copyright (c) 1993 - 2002 Compugen Ltd.

OM protein - protein search, using sw model

Run on:

December 23, 2002, 07:17:57 ; Search time 1.5814 Seconds (without alignments) 486.327 Million cell updates/sec

US-09-865-198-3 51 Title: Perfect score:

1 YYGDYEGY 8 Sequence: BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

Searched:

283224 Total number of hits satisfying chosen parameters:

283224 segs, 96134422 residues

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

PIR_73:* Database

pirl:* pir2:* pir3:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

SUMMAKIES	Description	hypothetical prote	MPA43 protein -		hypothetical pro	f22b7.4 prote				hypothetical	Ig heavy chai									Ig heavy chai	II	ro	ro	Ø						
WOS.	ID	D81272	S63222	SYTWMT	T18444	844634	B70402	E83656	C90538	T19805	S13688	A69012	S38115	B81910	E81105	T26053	T02673	A48832	T19536	PH1366	A54256	AE1218	AH1571	A95071	T49265	G90518	F69631	T03473	D72278	
	DB				7							٦	7	7	7	7	7									7	7	7	7	
	Length				1650	63	595	099	3216	8	110	154	271	542	542	564	633	730	1657	15	120	191	191	252	441	565	587	929	699	
æ	Query Match	80.4	œ	œ	œ	ė.	4.		4.	'n	ď		ς.	ς.		ď.	ď	72.5	ď.	o.	ö	o.		ö	。			。	ö	
	Score	41	40	40	40	39	38	38	38	37	37	37	37	37	37	37	37	37	37	36	36	36	36	36	36	36	36	36	36	
	Result No.	-	7	m	4	S	9	7	80	σ	10	11	12	13	14	12	16	17	18	19	20	21	.22	23	24	25	56	27	28	•

receptor protein k	probable receptor-	iodide peroxidase	iodide peroxidase	iodide peroxidase	hypothetical prote	Ig heavy chain (38	Ig heavy chain pre	dTDP-sugar epimera	hypothetical prote	unknown protein en	hypothetical prote	ubiquinol-cytochro	probable transamin	probable transamin	homeotic protein 1
T51545	A84518	JN0550	S07047	OPHUIT	G82387	S16280	S03844	AB1210	н91066	н85910	869529	T14243	A75128	D71003	161573
8	~	, ,	-1	Н	N	~	~	7	7	7	~	7	~	~	Н
851	868	914	914	933	113	126	145	186	188	201	376	386	398	401	402
9	و	9	9	و	9	و	و	9	9	9	9	9	9	9	9
70.6	70.	70.	70.	70.	68.	68.	68.	68.	68.	68.	68.	68.	68.	68.	68.
36	36	36				35		35	35	35	32	35	35	35	35
30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

ALIGNMENTS

: O E U U U U X C Z K K K K	RESULT 1 D81272 hypothetical protein Cj1295 [imported] - Campylobacter jejuni (strain NCTC 11168) C;Species: Campylobacter jejuni C;Species: Campylobacter jejuni C;Species: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 03-Jun-2002 C;Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 03-Jun-2002 C;Accession: D81272 R;Parkhill, J; Wren, B.W.; Mungall, K.; Ketley, J.M.; Churcher, C.; Basham, D.; Chill R;Parkhill, M.; Rajandream, M.A.; Rutherford, K.M.; VanVliet, A.; Whitehead, S.; Bar Nature 403, 665-668, 2000 A;Pitle: The genome sequence of the food-borne pathogen Campylobacter jejuni reveals A;Reference number: A81250; MUID:20150912; PMID:10688204
ααααυαυ	A; Motecute type: UNA A; Motecute type: UNA A; Residues: 1-435 < CPAR> A; Cross-references: GB:AL139078; GB:AL111168; NID:g6968723; PIDN:CAB73722.1; PID:g696 A; Experimental source: serotype O2, strain NCTC 11168 C; Genetics: A; Gene: Cj1295 C; Superfamily: Campylobacter jejuni hypothetical protein Cj1295
	Query Match Best Local Similarity 85.7%; Pred. No. 14; Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
O O	Qy 2 YGDYEGY 8 : Db 325 YGDYDGY 331
~ W Z Z C C C C C C C C C C C C C C C C C	RESULT 2 S63222 MPA43 protein - yeast (Saccharomyces cerevisiae) MyA15 protein - yeast (Saccharomyces cerevisiae) MyA16 protein - yeast (Saccharomyces cerevisiae) MyA16 protein N0875; protein NNL249c C;Species: Saccharomyces cerevisiae C;Sacharomyces cerevisiae C;Accesion: S63222 A;Reference number: S63220 A;Reference number: S6322 A;Reference number: S6322 A;Reference number: S6322 A;Reference number: S61594 A;Reference number: S61594 A;Recession: Recession: Recessio

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f22b7.4 protein - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 09-Sep-1997
C;Accession: S44634
R;Anderson, K.
                                                                                                                                                                                                                submitted to the EMBL Data Library, March 1993
A;Description: Sequence of the C. elegans cosmid F22B7.
A;Reference number: S44628
A;Reference: S44634
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-63 <AND>
Coss. references: EMBL:L12018; NID:g156298; PID:g156305
C;Genetics:
A;Introns: 21/2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 76.55
Best Local Similarity 75.0°
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity 85.7
Matches 6; Conservative
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A;Molecule type: DNA
A;Residues: 1-660 <STO>
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56 YYGGYNGY 63
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                                                    RESULT 5
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                                                                                                                                                                                                                                                                                                                                                                          ### PILON THE TRANS A LIGASE (EC 6.1.1.10) - Thermus aquaticus

N.Alternate names: methionyl-tRNA synthetase
C; Species: Thermus aquaticus
C; Date: 30-Uun_1992 #sequence_revision 30-Jun-1992 #text_change 03-Jun-2002
C; Accession: A_0517
R; Nureakl, O.; Muramatsu, T.; Suzuki, K.; Kohda, D.; Matsuzawa, H.; Ohta, T.; Miyazawa, J. Biol. Cham 266, 3268-3277, 1991
A; Title: Methionyl-tRNA synthetase gene from an extreme thermophile, Thermus thermophilu esis.
A; Reference number: A39517; MUD:91131636; PMID:1993699
A; Accession: A_39517
A; Molecule type: DNA
A; Residues: 1,506 Auny
A; Residues: Methionine-tRNA ligase
C; Reywords: aminoacyl-tRNA synthetase; ATP; homodimer; ligase; protein biosynthesis
F; 13, 19, 50, 300/Active site: Tyr, His, Asp, Lys #status predicted
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                                                                                                                                                                         Gaps
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Pred. No. 29;
1; Mismatches 0; Indels
                                                                                                                       2; Length 542;
                                                                                                                                                                      0; Indels
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Pred. No. 78;
1; Mismatches
                                                                                                                       Score 40; DB
Pred. No. 25;
1; Mismatches
C;Genetics: 1
A;Gene: SGD:MPA43
A;Cross-references: SGD:S0005193; MIPS:YNL249c
A;Map position; 14L
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 85.7%;
Matches 6; Conservative 1
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75.0%;
                                                                                                                    Query Match & 78.4%;
Best Local Similarity 85.7%;
Matches 6% Conservative
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Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Map position: 3
A; Introns: 1597/3; 1625/3
A; Note: C0385c
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                                                                                                                                                                                                                                                                                                                                          RESULT 3
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A;Status: preliminary; nucleic acid sequence not shown; translation not shown A;Molecule type: DNA A;Molecule type: DNA A;Residues: 1-555 <AQF>
A;Residues: 1-555 <AQF>
A;Cross-references: GB:AE000727; NID:92983623; PIDN:AAC07204.1; PID:92983636; GB:AE00 A;Experimental source: strain VF5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        methionyl-tRNA synthetase metS [imported] - Bacillus halodurans (strain C-125)
C;Species: Bacillus halodurans
C;Species: Dace-2000 #sequence_revision 01-Dec-2000 #text_change 15-Jun-2001
C;Accession: E83656
R;Takami, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Masui, N.; Fuji, F.; H
Nucleic Acids Res. 28, 4317-4331, 2000
A;Title: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans a A;Reference number: A83650; MUID:20512582; PMID:11058132
                                                                                                                                                                                                                                                                                                                                                                                                                             C:Accession: B70402
R;Deckert, G.; Warren, P.V.; Gaasterland, T.; Young, W.G.; Lenox, A.L.; Graham, D.E.;
V.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Nature 392, 353-358, 1998
A;Title: The complete genome of the hyperthermophilic bacterium Aquifex aeolicus.
A;Reference number: A70300; MUID:98196666; PMID:9537320
A;Accession: B70402
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                                                                                                                                                                                                                                                                                                                                    hypothetical protein aq_1185 - Aquifex aeolicus
C;Species: Aquifex aeolicus
C;Date: 08-May_1998 #sequence_revision 08-May-1998 #text_change 04-Mar-2000
                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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Length 63;
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                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Gene: aq_1185
C;Superfamily: Aquifex aeolicus hypothetical protein aq_1185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 2;
62;
Score 39; DB 2;
Pred. No. 4.3;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       74.5%; Score 38; DB
85.7%; Pred. No. 62;
Live 0; Mismatches
76.5%;
75.0%;
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3

Page

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Ig heavy chain V region - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 18-Feb-1994 #sequence_revision 10-Nov-1995 #text_change 30-May-1997
C;Accession: S1368
R;Pennell, C.A.; Mercolino, T.J.; Grdina, T.A.; Arnold, L.W.; Haughton, G.; Clarke, S Eur. J. Immunol. 19, 1289-1295, 1989
A;Title: Biased immunoglobulin variable region gene expression by Ly-1 B cells due to A;Reference number: S13688
A;Molecule type: MID:8938557; PMID:2503389
A;Molecule type: mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 72.5%;
Best Local Similarity 71.4%;
Matches 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Residues: 1-110 <PEN>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 YY--GDYEGY 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 YYGDYEG 7
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                                  S13688
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                                                                                                                                                                                                                                                                                                                                                                                                                                     hypothetical protein MYPU_2110 [imported] - Mycoplasma pulmonis (strain UAB CTIP)
C;Species: Mycoplasma pulmonis
C;Accession: C90538
R;Chambaud, I.; Heilig, R.; Ferris, S.; Barbe, V.; Samson, D.; Gallsson, F.; Moszer, I.;
Rvichambaud, I.; Heilig, R.; Ferris, S.; Barbe, V.; Samson, D.; Gallsson, F.; Moszer, I.;
Rvichambaud, I.; Heilig, R.; Ferris, S.; Barbe, V.; Samson, D.; Gallsson, F.; Moszer, I.;
Rvichambaud, I.; Heilig, R.; Ferris, S.; Barbe, V.; Samson, D.; Gallsson, F.; Moszer, I.;
Rvicheit Complete genome sequence of the murine respiratory pathogen Mycoplasma pulm A;Reference number: A99512; MUID:21267165; PMID:11353084
A;Gatesin preliminary
A;Molecule type: DNA
A;Residues: I-3216 cKUR>
A;Cross-references: GB:AL445566; PID:g14089624; PIDN:CAC13384.1; GSPDB:GN00153
A;Cross-references: strain UAB CTIP
C;Genetics:
A;Gene: MYPU_21100
A;Cross-references: GB:AP001507; GB:BA000004; NID:g10172612; PIDN:BAB03772.1; GSPDB:GN0d A;Experimental source: strain C-125 C;Genetics: A;Genet: metS C;Superfamily: methionine-tRNA ligase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Apportetical protein C37A5.8 - Caenorhabditis elegans
C.Species: C.Species: Caenorhabditis elegans
C.Species: C.Species: Caenorhabditis
A.Reference number: Z19180
A.Stetus: preliminary; translated from GB/EMBL/DDBJ
A.Stetus: preliminary; translated from GB/EMBL/DDBJ
A.Stetus: preliminary;
A.Molecule type: DNA
A.Molecule type: DNA
A.Residues: 1-89 cWLD
A.Sterimental source: CIONE C37A5.8
A.Sterimental source: clone C37A5
C.Genetics:
A.Gene: CESP:C37A5.8
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Pred. No. 3.4e+02;
1; Mismatches 1; Indels
                                                                                                                                                              Length 660
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                                                                                                                                                              DB 2;
69;
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Pred. No. 14;
0; Mismatches
                                                                                                                                                              Score 38; DB
Pred. No. 69;
1; Mismatches
                                                                                                                                                         h 74.5%;
Similarity 75.0%;
6; Conservative
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Best Local Similarity 75.0%;
Matches 6; Conservative
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75.0%;
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Best Local Similarity 75.0
Matches 6; Conservative
                                                                                                                                                         Query Match
Best Local Similarity
Matches 6; Conserv
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| Db | 1978 YYVDYEGF 1985
                                                                                                                                                                                                                                                                                            121 YLGDYEGW 128
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61 YYGGYGGY 68
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Map position: 1
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C; Accession: A69012
R; Smith, D. R.; Doucette-Stamm, L.A.; Deloughery, C.; Lee, H.; Dubois, J.; Aldredge, T. Qiu, D.; Spadafora, R.; Vicaire, R.; Wang, Y.; Wierzbowski, J.; Gibson, R.; Jiwani, K.; S.; Church, G. M.; Daniels, C.J.; Mao, J.; Rice, P.; Noelling, J.; Reeve, J.N. J. Bacteriol. 179, 7135-7155, 1997
A; Title: Complete genome sequence of Methanobacterium thermoautotrophicum Delta H: fu A; Reference number: A69000; MUID:98037514; PMID:9371463
A; Scession: A69012
A; Status: preliminary; nucleic acid sequence not shown; translation not shown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Molecule type: DNA
A; Residues: 1-154 <MTH>
A; Cross-references: GB: AE000879; GB: AE000666; NID: 92622175; PIDN: AABB5580.1; PID: 9262
A; Experimental source: strain Delta H
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Molecule type: DNA
A;Reafdues: 1-271 <URN.
A;Cross-references: EMBL:228268; NID:9486490; PID:9486491; GSPDB:GN00011; MIPS:YKR043
A;Experimental source: strain S288C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           conserved hypothetical protein MTH1091 - Methanobacterium thermoautotrophicum (strain
                                                                                                                                                                                                                                               1;
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S38115
hypothetical protein YKR043c - yeast (Saccharomyces cerevisiae)
hypothetical protein YKR043c - yeast (Saccharomyces cerevisiae)
C;Species: Saccharomyces cerevisiae
C;Date: 03-May-1994 #sequence_revision 03-May-1994 #text_change 19-Apr-2002
C;Accession: S38115
B;Urrestarazu, L.A.; Jaunlaux, J.C.
B;Urrestarazu, L.A.; Jaunlaux, J.C.
B;Reference number: S38097
A;Reference number: S38097
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           C;Species: Methanobacterium thermoautotrophicum
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 21-Jul-2000
                                                                                                                                                                                                                                                   Gaps
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A;Cross-references: EMBL:X53341
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;10-33/Domain: immunoglobulin homology <IMM>
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A;Gene: MTH1091
A;Start codon: GTG
C;Superfamily: conserved hypothetical protein MJ0375
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 1;
                                                                                                                                                                        72.5%; Score 37; DB 2; 70.0%; Pred. No. 17; tive 1; Mismatches
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Pred. No. 24;
2; Mismatches
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A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-564 <WILD.
A;Coss-references: EMBL:249969; PIDN:CAA90270.1; GSPDB:GN00020; CESP:W01C9.2
A;Experimental source: clone W01C9
                                                                                                                            hypothetical protein W01C9.2 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
C;Accession: T26053
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Map position: 2
A;Introns: 30/1; 64/1; 100/3; 124/3; 229/3; 272/3; 536/2
                                                                                                                                                                                                                                        R;Sims, M. submitted to the EMBL Data Library, June 1995 Nateference number: 220143 A;Accession: T26053
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85.7%;
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Best Local Similarity
'-hag 6; Conserva
528 YLGDYESY 535
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A;Gene: CESP:W01C9.2
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                                                                                                                                                                                                                                                                                                                                                                                                              Accession: Relice ATP-binding protein NWB1240 [imported] - Neisseria meningitidis (strain C) Species: Neisseria meningitidis
C; Species: Species: Neisseria meningitidis serogroup B. Jan. 2001
R; Tettelin, HR; Saunders, N.J.; Heidelberg, J.; Jeffries, A.C.; Nelson, K.E.; Eisen, J.P.
Hickey, E.K.; Haft, D.H.; Salzberg, S.L.; White, O.; Fletschmann, R.D.; Dougherty, B.A.;
ri, H.; Qin, H.; Vamathevan, J.; Gill, J.; Scarlato, V.; Masignani, V.; Pizza, M.
Science 287, 1809-1815, 2000
A; Authors: Gråndi, G.; Sun, L.; Smith, H.O.; Fraser, C.M.; Moxon, E.R.; Rappuoli, R.; Ve
A; Title: Complete genome sequence of Neisseria meningitidis serogroup B strain MC58.
A; Reference number: A81000; MUID: 20175755; PMID: 10710307
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Cross-references: GB:ALL62755; GB:AL157959; NID:g7379742; PIDN:CAB84649.1; PID:g738006
A;Experimental source: serogroup A, strain 22491
C;Genetimental source: serogroup A, strain 22491
A;Genet: NNA1409
C;Superfamily; unassigned ATP-binding cassette proteins; ATP-binding cassette homology
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A;Molecule type: DNA
A;Residues: 1:542 <TEP
A;Cross-refegences: GB:AE002472; GB:AE002098; NID:g7226475; PIDN:AAF41621.1; PID:g722641
A;Experimental source: serogroup B, strain MC58
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C;Superfamily: unassigned ATP-binding cassette'proteins; ATP-binding cassette homology
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       A;Gene: MIPS:YKR043c
A;Cross-referencices: SGD:S0001751
A;Map position; 11R
C;Superfamily: !phosphoglycerate mutase; phosphoglycerate mutase homology
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                                                                                                                                   72.5%; Score 37; DB 2; Length 271; 100.0%; Pred. No. 42; 1.tve 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    72.5%; Score 37; DB 2; Length 542; 75.0%; Pred. No. 85; ive 0; Mismatches 2; Indels
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Matches 6; Conserv
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Matches (6; Conserv
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102 YGDYEG 107
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Gaps ö

Length 564; 1; Indels

Score 37; DB 2; Pred. No. 88; 0; Mismatches

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GenCore version 5.1.3
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OM protein - protein search, using sw model

December 23, 2002, 07:16:17; Search time 0.790698 Seconds (without alignments) 419.643 Million cell updates/sec Run on:

US-09-865-198-3 51

BLOSUM62 Gapop 10.0 , Gapext 0.5 1 YYGDYEGY 8 Title: Perfect score: Sequence: Scoring table:

112892 seqs, 41476328 residues Searched:

112892 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SwissProt_40:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description		xenop	P53583 saccharomyc			Q28793 potorous tr		_	P52889 brachydanio	homo	рошо	-	P54422 bacillus su	068040 rhodobacter	P35419 mus musculu	P14650 rattus norv		paste		P50459 mus musculu	Q90476 brachydanio	P09806 kluyveromyc	P54331 bacillus su	P05453 saccharomyc	Q05884 streptomyce		Q9y719 schizosacch	P53257 saccharomyc		86	\sim	065	P94972 mycobacteri
SUMMARIES	ΩI			_				YK23		LHX				_												_					SYM			UVRA_MYCTU
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O9gzz4 mus musculu P06226 bacterlopha	P03949 caenorhabdi P36623 schizosacch		P58460 sulfolobus Q9uxe7 sulfolobus			Q48485 klebsiella
MY15_MOUSE GP33_BPSP1	ABL1_CAEEL PMGY_SCHPO	LICD_HAEIN	EGSA_SULTO EGSA_SULSO	HIS8_PARDE	SAT_PYRAB	GLF1_KLEPN
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3511 101	211	265	350 351	367	379	384
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ALIGNMENTS

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                                                                                                                                                                                                                                                                                                                                                                                                             P37137; Care Control C
                                                                                                                                                                                                  Gaps
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MEDLINE-95377545; PubMed-7649385;
Toyama R., Curtiss P.E., Otani H., Kimura M., Dawid I.B., Taira M.;
"The LIMMclass homeobox gene lim5: implied role in CNS patterning in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE OF 188-225 FROM N.A.
MEDLINE—92192449; PubMed=1347750;
Taira M., Jamrich M., Good P.J., Dawid I.B.;
Taira M., Jamrich M., Good P.J., Dawid I.B.;
"The LIM; domain-containing homeo box gene Xiim-1 is expressed specifically in the organizer region of Xenopus gastrula embryos.";
Genes Dev. 6:356-366(1992).
-I- FUNCTION: PROBABLY INVOLVED IN THE PATTERNING OF THE NERVOUS SYSTEM, IN PARTICULAR IN THE EARLY SPECIFICATION OF THE DIENCEPHALON.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -i- SUBĞELLULAR LOCATION: Nuclear (Probable).
-i- SIMÇLARITY: CONTAINS 1 HOMEOBOX DOMAIN.
-i- SIMÇLARITY: CONTAINS 2 LIM DOMAINS. THE LIM DOMAIN BINDS 2 ZINC
                                                                                                                                                                                             ö
Homeobox; DNA-binding; Nuclear protein; Repeat; LIM domain; Metal-binding; Zinc; Transcription regulation.

DOMAIN 3 61 LIM 1.

DOMAIN 62 125 LIM 2.

DNA_BIND 180 239 HOMEOBOX.

SEQUENCE 402 AA; 44405 MW; E880138AlA3FGA2A CRC64;
                                                                                                                                                 Query Match (* 80.4%; Score 41; DB 1; Length 402; Best Local Sümilarity 85.7%; Pred. No. 10; Matches 6% Conservative 1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                         402 AA.
                                                                                                                                                                                                                                                                                                                                                                                         PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FRANSFAC; T04209; -.
InterPro; IPR001356; Homeobox.
InterPro; IPR001781; LIM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PD000010; Homeobox; 1 PD000094; LIM; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Dev. Biol. 170:583-593(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; L42546; AAA99464 1; -.
EMBL; Z11587; CAA77672.1; -.
HSSP; P06601; 1FJL.
TRANSFAC; T04209; -.
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Pfam; PF00412; LIM; 2.
                                                                                                                                                                                                                                                                                                                                                                                       STANDARD;
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                                                                                                                                                                                                                                                                             278 YYGDYQG 284
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                                                                                                                                                                                                                                     1 YYGDYEG 7
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P37137;
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SMART;
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Submitted (DEC-1995) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "Sequence analysis of the 33 kb long region between ORC5 and SUll from the left arm of chromosome XIV from Saccharomyces cerevisiae."; Yeast 13:849-860(1997).
PROSITE; PS50023; LIM_DOMAIN_2; 2.
PROSITE; PS00027; HOMEOBOX_1; 1.
PROSITE; PS50071; HOMEOBOX_2; 1.
HOMEOBOX; DNA-binding; Nuclear protein; Developmental protein;
Repeat; LIM domain; Metal-binding; Zinc; Transcription regulation.
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MPA43 protein.
MPA43 OR YNLA49C OR NO875.
Saccharomyces cerevisiae (Baker's yeast).
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes; Saccharomycetales; Saccharomycetales;
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830AA8D4E95365AD CRC64;
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Pred. No. 20;
1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                  Score 41; DB 1; Length 402;
Pred. No. 10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
STRAIN-S288c / FY1679;
MEDLINE-97377992; PubMed-9234673;
Sen Gupta M., Gueldener U., Beinhauer J.D., Fiedler T.A.,
                                                                                                                                                                                                                                                                                                                                          0; Indels
                                                                                                                                                                              62 125 LIM 2.
, 180 239 HOMEOBOX.
402 AA; 44959 MW; AS852B94747E09F9 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-0CT-1996 (Rel. 34, Created)
01-0CT-1996 (Rel. 34, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              542 AA
                                                                                                                                                                                                                                                                                                                                       1; Mismatches
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                                                                                                                                                                                                                                                                                    80.4%;
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EMBL; Z71525; CAA65495.1; --
EMBL; X94214; CAA63905.1; --
SGD; S0005193; MPA43.
CONFLICT 46 53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 85.7%;
Matches 6; Conservative 1
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                                                                                                                                                                                                                                                                                                                                          6; Conservative
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                                                                                                                                                                                                                                                                                                                  Sest Local Similarity
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278 YYGDYQG 284
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360 FYGDYEG 366
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P53583;
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Gaps

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Indels

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red. No. 22; Mismatches

Pred.

Conservative

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Best Local Similarity
Matches 6; Conserv
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PROSITE; PS00178; AA_TRNA_LICASE_I; FALSE_NEG.
Aminoacyl-tRNA synthetase; Protein biosynthesis; Ligase; ATP-binding;
                                                                                                                                                                                                                         Nureki O., Muramatsu T., Suzuki K., Kohda D., Matsuzawa H.,
Ohta T., Miyazawa T., Yokoyama S.;
"Methionyl-tRNA synthetase gene from an extreme thermophile, Thermus
thermophilus HBB. Molecular cloning, primary-structure analysis,
expression in Escherichia coli, and site-directed mutagenesis.";
J. Biol. Chem. 266:3268-3277(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SUBCELLULAR LOCATION: Cytoplasmic.
SIMILARITY: BELONGS TO CLASS-I AMINOACYL-TRNA SYNTHETASE FAMILY.
STRONG, TO CYSTEINYL-TRNA SYNTHETASE.
                                                                                                                                                                                                                                                                                                                                                                      Sugiura I., Nureki O., Ugaji-Yoshikawa Y., Kuwabara S., Shimada A., Tateno M., Lorber B., Giege R., Moras D., Yokoyama S., Konno M.;
"The 2.0-a crystal structure of Thermus thermophilus methionyl-tRNA synthetase reveals two RNA-binding modules.";
Structure 8:197-208(2000).
-!- FUNCTION: IT IS PROBABLY ESSENTIAL FOR CELL SURVIVAL, BEING REQUIRED NOT ONLY FOR ELONGATION OF PROTEIN SYNTHESIS BUT ALSO FOR THE INITIATION OF ALL MRNA TRANSLATION THROUGH INITIATOR
                        01-NOV-1991 (Rel. 20, Created)
01-NOV-1991 (Rel. 20, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Methionyl-tRNA synthetase (EC 6.1.1.10) (Methionine--tRNA ligase)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -1- CATALYTIC ACTIVITY: ATP + L-methionine + tRNA(Met) = AMP diphosphate + L-methionyl-tRNA(Met).
-1- SUBUNIT: HOMODIMER.
                                                                                                                            Bacteria; Thermus/Deinococcus group; Deinococci; Thermales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "KMSKS" REGION.
ATP (BY SIMILARITY).
TRNA BINDING.
053982C62558B72A CRC64;
616 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "HIGH" REGION.
                                                                                                                                                                                                                                                                                                                              X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            InterPro; IPR004495; MetG_Cterm.
InterPro; IPR004495; MetG_Cterm.
InterPro; IPR001412; tRNA-synt_I.
InterPro; IPR002304; tRNA-synt_met.
InterPro; IPR002547; tRNA_bind.
Pfam; PF00133; tRNA-synt_1; 1.
Pfam; PF01508; tRNA_bind; 1.
                                                                                                                                                                                                                                                                                                                                           STRAIN-HB8 / ATCC 27634;
MEDLINE-20139706; PubMed-10673435;
                                                                                                                                                                                 SEQUENCE FROM N.A.
STRAIN-HBB / ATCC 27634;
MEDLINE-91131636; PubMed-1993699;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRINTS; PR01041; TRNASYNTHMET.
TIGREAMS; TIGR00398; metG; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   70638 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; M64273; AAA27510.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           tRNA-binding; 3D-structure.
 STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PDB; 1A8H; 04-MAY-99.
                                                                                                               Thermus thermophilus.
                                                                                                                                           Thermaceae; Thermus.
NCBI_TaxID=274;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   300
524
616 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SYTWMT
                                                                                                 METG OR METS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PIR; A39517;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      BINDING
                                                                                    (MetRS)
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DB 1; Length 616;

78.4%; Score 40;

Query Match

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN-BRISTOL N2;
MEDLINE-94150718; PubMed-7906398;
MISON R., Alnderson K., Baynes C., Berks M.,
Mison R., Alnscough R., Anderson K., Copper J., Cooper J., Confield J., Burton J., Connell M., Copsey T., Cooper J., Coulson A.,
Craxton M., Dear S., Du Z., Durbin R., Favello A., Fraser A.,
Fulton L., Gardner A., Green P., Hawkins T., Hillier L., Jer M.,
Johnston L., Jones M., Kershaw J., Kirsten J., Laisster N.,
Latreille P., Lightning J., Lloyd C., Mortimore B., O'Callaghan M.,
Parsons J., Percy C., Rifken L., Roopera A., Saunders D., Shownkeen R.,
Sins M., Smaldon N., Smith A., Sonnhammer E., Staden R.,
Sulston J., Thierry-Weg J., Thomas K., Vaudin M., Vaughan K.,
Waterston R., Watson A., Weinstock L., Wilkinson-Sproat J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
Rhabditidae; Peloderinae; Caenorhabditis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 '2.2 Mb of contiguous nucleotide sequence from chromosome III of C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Potorous tridactylus (Potoroo).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 39; DB 1; Length 63; Pred. No. 3.8; 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2F7579C4907024B0 CRC64;
                                                                                                                                                                                                                                      01-FEB-1994 (Rel. 28, Created)
01-FEB-1994 (Rel. 28, Last sequence update)
01-SUN-2002 (Rel. 41, Last annotation update)
Hypothetical protein F2287.4 in chromosome III.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Created)
Last sequence update)
Last annotation update)
                                                                                                                                                                                       63 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         489 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           76.5%;
75.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 protein.
63 AA; 6803 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; L12018; AAA65461.1;
WormPep; F22B7.4; CE00157.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STANDARD;
                                                                                                                                                                                       STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Nature 368:32-38(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      OCLN_POTTR STANDARD Q28793; 15-DEC-1998 (Rel. 37, C. 15-DEC-1998 (Rel. 37, Li. 30-MAY-2000 (Rel. 39, Li.
                                                                                                                                                                                                                                                                                                                                                                      Caenorhabditis elegans.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ||| | ||| 56 YYGGYNGY 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=6239;
                                                    118 YYGEYEG 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 YYGDYEGY 8
1 YYGDYEG 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Hypothetical
                                                                                                                                                                                    YLW4_CAEEL
P34407;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Wohldman P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Occludin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                elegans
                                                                                                                                  RESULT 5
YLW4_CAEEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 6
OCLN_POTTR
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Urrestarazu L.A., Jauniaux J.-C.;
Submitted (MAR.1994) to the EMBL/GenBank/DDBJ databases.
    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    igase)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                08TNY5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ASSY_METAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 8
    NAME OF STREET O
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             δŏ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the Buropean Bloinformatics Institute. There are no restrictions on its use by mon-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or sendin email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                       Ando-Akatguka Y., Saitou M., Hirase T., Kishi M., Sakakibara A., Itoh M., Yonemura S., Furuse M., Tsukita S.;
"Interspecies diversity of the occludin sequence: cDNA cloning of human, mouse, dog, and rat-kangaroo homologues.";
J. Cell Biol. 133:43-47(1996).
-i- FUNCTION: MAY PLAY A ROLE IN THE FORMATION AND REGULATION OF THE TIGHTENINCTION (TJ) PARACELLULAR PERMEABILITY BARRIER. INTERACTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                       -!- DOMATM: THE C-TERMINAL IS CYTOPLASMIC AND IS IMPORTANT FOR INTERACTION WITH 20-1. NECESSARY FOR THE TIGHT JUNCTION LOCATION. INVOLVED IN THE REGULATION OF THE PERWEABILITY BARRIER FUNCTION OF THE TIGHT JUNCTION (BY SIMILARITY).
-!- PTM: PHOSPHORYLATED (BY SIMILARITY).
-!- SIMILARITY: BELONGS TO THE ELL / OCCLUDIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Saccharomyces cerevisiae (Baker's yeast).
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Saccharomyces.
NCBL Taxlb=4932;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-JUN-1994 (Rel. 29, Created)
01-JUN-1994 (Rel. 29, Last sequence update)
01-JUN-1994 (Rel. 29, Last annotation update)
Hypothetical 31.0 kDa protein in GAPI-NAPI intergenic region.
                                                                                                                                                                                                                                                                                            -!- SUBCELLULAR LOCATION: Integral membrane protein.
-!- TISSUE SPECIFICITY: LOCALIZED AT TIGHT JUNCTIONS OF BOTH
EPITHELIAL AND ENDOTHELIAL CELLS.
Mammalia; Metatheria; Diprotodontia; Macropodidae; Potorous.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Tight jünction; Transmembrane; Coiled coil; Phosphorylation.

DOMAIN 51 74 POTENTIAL.

TRANSMEM 52 74 POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       76.5%; Score 39; DB 1; Length 489; 75.0%; Pred. No. 26;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EXTRACELLULAR (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EXTRACELLULAR (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COILED COIL (POTENTIAL).
4F0CA45A41094860 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CYTOPLASMIC (POTENTIAL).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    271 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pred. No. 26;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYR/GLY-RICH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               POTENTIAL.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRT;
                                                                                                   MEDLINE-96181088; Pubmed-8601611;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               InterProf. IPR002958; Occludin. Pfam; PF02168; Occludin; 1. PRINTS; PR01258; OCCLUDIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          434 CK
54075 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; U49183; AAC48565.1; -.
InterProj; IPR002958; Occludi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       112
137
147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       173
223
245
76
407
489 AA;
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tes 6; Conserv
                                                            EROM N.A.
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                       NCBI_TaxID=9310;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 YYGDYEGY 8
                                                                                  TISSUE=Kidney;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    YK23_YEAST
P36136;
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TRANSMEM
DOMAIN
                                                                                                                                                                                                                                                                           WITH
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DOMAIN
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DOMAIN
DOMAIN
                                                                 SEQUENCE
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Matches
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RESIDENCE FROM N.A.

SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

SERAIN-218 / ATCC 35395 / DSM 2834;

RA Salagan J.E., Nusbaum C., Roy A., Endrizzi M.G., Macdonald P.,

RA Galagan J.E., Nusbaum C., Roy A., Endrizzi M.G., Macdonald P.,

RA Allen N., Naylor J., Stange-Thomann N., DeArellano K., Johnson R.,

Linton L., McEwan P., McKernan K., Talamas J., Tirrell A., Ye W.,

RA Limton L., McEwan P., McKernan K., Talamas J., Tirrell A., Ye W.,

RA Limer A., Barber R.D., Caraham D.E., Grahame D.A., Guss A.M.,

RA Hedderich R., Ingram-Smith C., Kuettner H.C., Krzycki J.A.,

RA Springer T.A., Umayam L.A., White O., White R.H., de Macario E.C.,

RA Springer T.A., Umayam L.A., White O., White R.H., de Macario E.C.,

RA Pritchett M., Sowers K.R., Swanson R.V., Zinder S.H., Lander E.,

Metcalf W.W., Birren B.;

RT The genome of Methanosarcina acetivorans reveals extensive metabolic
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entities requires a license agreement (See http://www.isb-sib.ch/announce/
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    this SWISS-PROT entry is copyright. It is produced through a collaboration
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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-!- SUBUNIT: Homotetramer (By similarity).
-!- SIMILARITY: BELONGS TO THE ARGININOSUCCINATE SYNTHASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Argininosuccinate synthase (EC 6.3.4.5) (Citrulline--aspartate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            and physiological diversity.";
Genome Res. 12:532-542(2002).
-!- CATALYTIC ACTIVITY: ATP + L-citrulline + L-aspartate - AMP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 271;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Archaea; Euryarchaeota; Methanococci; Methanosarcinales;
Methanosarcinaceae; Methanosarcina.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        .l protein.
271 AA; 31022 MW; FF934DE2F5145C40 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      72.5%; Score 37; DB 1;
100.0%; Pred. No. 32;
ive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    394 AA
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                                                                                                                                                                                                                                                                                                                                          PIR; S38115; S38115.
SGD; S0001751; YKR043C.
InterPro; IPR001345; PG/BPCM_mutase.
Pfam, PF00300; PGAM; 1.
Hypothetical protein.
SEQUENCE 271 AA; 31022 MW; FF934I
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15-JUN-2002 (Rel. 41, Last seq
15-JUN-2002 (Rel. 41, Last anno
                                                                                                                                                                                                                                                                                                       EMBL; Z28268; CAA82119.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Methanosarcina acetivorans.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ouery Match
Best Local Similarity
Matches 6; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=2214;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           102 YGDYEG 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ARGG OR MA2142.
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Gaps

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Indels

Mismatches

Score 37; DB 1; Length 399; Pred. No. 45;

C0D7BB1B86D032DA CRC64;

HOMEOBOX

44513 MW; 72.5%; Sc 71.4%; Pi

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5; Conservative
   180 2
399 AA;
                                                                    Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ellington
   DNA_BIND
SEQUENCE
                                                    Query Match
                                                                                                                                                                                                                             SOX8_HUMAN
                                                                                        Matches
                                                                                                                                                                                                               RESULT 10
   FT
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                                                                                                                                                         QQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@lsb-sib.ch).
                                                                                                                                                                           ö
                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Toyama R., Curtiss P.E., Otani H., Kimura M., Dawid I.B., Taira M.; "The LIM class homeobox gene lim5: implied role in CNS patterning in Xannone and patrafish "."
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Brachydanio rerio (Zebrafish) (Danio rerio).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
Cyprinidae; Danio.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -1- SUBCELLULAR LOCATION: Nuclear (Probable).
-1- SIMILARITY: CONTAINS 1 HOMEOBOX DOMAIN.
-1- SIMILARITY: CONTAINS 2 LIM DOMAINS. THE LIM DOMAIN BINDS 2 ZINC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PROSITE; PS00478; LIM_DOMAIN_1; 2.
PROSITE; PS00027: LIM_DOMAIN_2; 2.
PROSITE; PS00027: HOMEGOAZ,1; 1.
PROSITE; PS50071; HOMEGOAZ,2; 1.
HOMEGODX; DNA-binding; Nuclear protein; Developmental protein;
HOMEGO X, DNA-binding; LIM domain; Metal-binding; Zinc; Transcription regulation.
DOMAIN 62 125 LIM 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Xenopus and zebrafish.";
Dev. Biol. 170:583-593(1995).
-!- FUNCTION: PROBABLY INVOLVED IN THE PATTERNING OF THE NERVOUS SYSTEM, IN PARTICULAR IN THE EARLY SPECIFICATION OF THE
                                                                                                                                                                           6;
                            EMBL; AE010900; AAM05540.1; -.
PROSITE; PS00564; ARGININOSUCCIN_SYN_1; 1.
PROSITE; PS00565; ARGININOSUCCIN_SYN_2; 1.
ARGININOSUCCIN_SYN_2; 1.
ARGININOSIS; Ligase; ATP-binding; Complete proteome.
SEQUENCE 394 AA; 43994 MW; 2B995B9C138E7EF1 CRC64;
                                                                                                                                         72.5%; Score 37; DB 1; Length 394; 100.0%; Pred. No. 45;
                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                   01-ocr-1996 (Rel. 34, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
LIM/homeobox protein Lhx5 (Homeobox protein LIM-5).
LHX5 OR LIM5.
                                                                                                                                                                           ő
                                                                                                                                                     100.0%; Pred. No. 45;
ive 0; Mismatches
or send an email to license@isb-sib.ch).
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STN; ZDB-GENE-980526-484; lim5.
InterPro; IPR001356; Homeobox.
InterPro; IPR001781; LIM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pfam; PF00046; homeobox; 1.
Pfam; PF00412; LIM; 2.
ProDom; PD000010; Homeobox; 1.
ProDom; PD000094; LIM; 2.
                                                                                                                                                                                                                                                                                                                                                                   01-OCT-1996 (Rel. 34, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; L42547; AAA99465.1; -.
                                                                                                                                                         Best Local Similarity 100.
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                 STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SMART; SM00389; HOX; 1. SMART; SM00132; LIM; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DIENCEPHALON.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=7955;
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81 GDYEGY 86
                                                                                                                                                                                                          3 GDYEGY 8
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P52889;
                                                                                                                                         Query Match
                                                                                                                                                                                                                                                                                                                LHX5_BRARE
                                                                                                                                                                                                                                                                                              RESULT 9
 SO RE BRESCO
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "Sequence, structure and pathology of the fully annotated terminal Mb of the short arm of human chromosome 16."; Hum. Mol. Genet. 10:339-352(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Cheng Y.-C., Badge R.M., Armour J.A.L., Scotting P.J.; "SOX8: a newly identified human gene expressed in paediatric brain tumours and a candidate for the mental retardation phenotype in
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Daniels R.J., Peden J.F., Lloyd C., Horsley S.W., Clark K.,
Tufarelli C., Kearney L., Buckle V.J., Doggett N.A., Flint J.,
Higgs D.R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Submitted (JAN-2000) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Submitted (FEB-2000) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                             Last sequence update)
Last annotation update)
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EMBL; 299757; CAB75612.1; ALT_INIT.
EMBL; AF164104; AAF37424.1; -.
HSSP; P48436; 1SX9.
Genew; HGNC:11203; SOX8.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
MEDLINE=21096910; PubMed=11157797;
                                                                                                                                                                                                                       SOX8_HUMAN STANDARD; F P57073; Q9NZW2; 16-0CT-2001 (Rel. 40, Created) 16-0CT-2001 (Rel. 40, Last sequil 16-0CT-2001 (Rel. 40, Last annotation)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; AF226675; AAF35886.1; -.
                                                                                                                                                                                                                                                                                                                                                                                              Transcription factor SOX-8.
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                                  111:1:1
278 YYGEYOG 284
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1 YYGDYEG 7
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REPEAT
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                                                                          Matches
                                                                                                                                                      RESULT 12
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RNA-BINDING (RRM) 1.
RNA-BINDING (RRM) 2.
RNA-BINDING (RRM) 3.
RNA-BINDING (RRM) 3.
RNA-BINDING (RGC-BOX).
3 x 11 AA APPROXIMATE REPEATS OF D-D-Y-Y-Y-G-Y-D-Y-H-D-Y.
1 (APPROXIMATE).
                                                                                                                                                                                                                                                                                                                                                                                                                                 Nucleic Acids Res. 26:439-445(1998).
-I-FUNGTION: COMPONENT OF RIBONUCLEOSOMES, WHICH ARE COMPLEXES OF AT LEAST 20 OTHER DIFFERENT HETEROGENIOUS NUCLEAR RIBONUCLEOPROTEINS (HNRNP). HNRNP PLAY AN IMPORTANT ROLE IN PROCESSING OF PRECURSOR MRNÀ IN THE NUCLEUS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AINCEAN PERONO STAIN, - SMART, SMOOD SO, RRM; 3.

PROSITE; PS50102; RRM; 3.

PROSITE; PS50102; RRM; 3.

PROSITE; PS50030; RRM-1; 2.

NUCLear protein; Repeat.

1 153 ASP/GLU-RICH (ACIDIC).

118 NUCLEAR LOCALIZATION SIGNAL (POTENTIAL).

- TANDING (RRM) 1.
                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
MEDILINE-98083170; PubMed-9421497;
MEDILINE-98083170; PubMed-9421497;
MEDILINE-98083170; Promed E.K.L., Mathison D.A., Portman D., Dreyfuss G.,
Steiner G., Tan E.M.;
"Modecular definition of heterogeneous nuclear ribonucleoprotein R
(hnRNP R) using autoimmune antibody: immunological relationship with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SUBCELLUIAR LOCATION: Nuclear; nucleoplasm.
SIMALARITY: CONTAINS 3 RNA RECOGNITION MOTIFS (RRM).
                                                                                                                                                                                                                                                                                                  Homo sapiens (Human).
Makaryotë; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammaliaf; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBL_raxipo=9606;
                                                                                                                     ö
                                                                                            72.5%; Score 37; DB 1; Length 446; 75.0%; Pred. No. 50; 1.ve 0; Mismatches 2; Indels
                                               Transcription regulation; DNA-binding; Nuclear protein.
DNA_BIND 102 170 HMG BOX.
                                                           DNA_BIND 102 170 HMG BOX.
SEQUENCE 446 AA: 47314 MW; AE453359051A6DB3 CRC64;
                                                                                                                                                                                                                                           16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Heterogemeen nuclear ribonucleoprotein R (hnRNP R).
                                                                                                                                                                                                                       633 AA.
                                                                                                                                                                                                                       PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; AF000364; AAC39540.1; -.
HSSP; P09651; 1HA1.
HSCP; HROKC:5047; HNRPR.
INTERPF; IPR000504; RNA_rec_mot.
Pfam; PF00076; rrm; 3.
MIM; 605923; -.
ThterPro; #FR000910; HMG_12_box.
              InterPro; IPR000910; HMG_12
Pfam; PF00505; HMG_box; 1.
SMART; SMQ0398; HMG; 1.
                                                                                                                    Conservative
                                                                                                                                                                                                                       STANDARD;
                                                                                                       Best Local Similarity
Matches 67 Conserv
                                                                                                                                                              391 YYGAYPGY 398
                                                                                                                                         1 YYGDYEGY 8
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                                                                                                                                                                                                                    ROR_HUMAN
043390;
                                                                                               Query Match
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ROR_HUMAN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            REMOVED IN MATURE FORM (POTENTIAL). GPI-ANCHOR (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3 X 4 AA TANDEM REPEATS OF P-S-T-T.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CELL SURFACE GLYCOPROTEIN GP138A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; D12883; BAA02287.1; -.
PIR; A48832; A48832.
D1ctyDb; DD03014; fusA.
InterPro: IPR002909; IPT_TIG.
Pfam; PF01833; TIG; 1.
Glycoprotein; Signal; Multigene family; GPI-anchor; Repeat.
                                                                       Length 633;
                                                                                                             Indels
3 (APPROXIMATE).
GLN/ASN-RICH DOMAIN.
9 088341F6465ED46F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                           Dictyostelium discoideum (Slime mold).
Eukaryota, Mycetozoa, Dictyosteliida, Dictyostelium.
NCBL_TaxID-44689;
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(GLCNAC.
(GLCNAC.
(GLCNAC.
(GLCNAC.
                                                                       Score 37; DB 1;
Pred. No. 70;
                                                                                                                                                                                                                                                                                                          01-FEB-1994 (Rel. 28, Created)
01-FEB-1994 (Rel. 28, Last sequence update)
01-OCT-1994 (Rel. 30, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                    Cell surface glycoprotein GP138A precursor
                                                                                                             Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A., AND SEQUENCE OF 21-32
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                                   70943 MW;
                                                                       72.5%;
75.0%;
                                                                                                             Conservative
                                     633 AA;
                                                                                    Local Similarity
Les 6; Conserv
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RA Azevedo V., Bertero M.G., Bessieres P., Bolotin A., Borchert S.,

RA Borriss R., Boursier L., Brans A., Braun M., Brighell S.C., Bron S.,

RA Brouillet S., Bruschi C.V., Caldwell B., Capuano V., Carter N.M.,

RA Brouillet S., Brischi C.V., Cannerton I.F., Cummings N.J., Daniel R.A.,

RA Broillet S., Deviner K.M., Dusterhoft A., Erlich S.D., Emmerson P.T.,

RA Brian K.D., Errington J., Febret C., Ferrari E., Foulger D.,

RA Fritz C., Fujita M., Fujita Y., Fuma S., Galizzi A., Galleron N.,

RA Guiseppi G., Guy B.J., Haga K., Haiech J., Harwood C.R., Henaut A.,

RA Hilbert H., Holsappel S., Hosono S., Hullo M.F., Itaya M., Jones L.,

RA Kobayashi Y., Koetter P., Koningstein G., Krogh S., Kumano M.,

RA Kunita K., Lapidus A., Lardinois S., Lauber J., Lazarevic V.,

RA Medina N., Mellado R.P., Mizuno M., Moestl D., Nakai S., Noback M.,

RA Medina N., Mellado R.P., Mizuno M., Moestl D., Nakai S., Noback M.,

RA Persecan E., Pujic P., Purnelle B., Rapoport G., Rey M., Sadaie Y.,

RA Rieger M., Rivolta C., Rocha E., Roche B., Rose M., Sadaie Y.,

RA Sextguchi A., Tacconi E., Taragi T., Taramaru K.,

RA Sextguchi A., Tacconi E., Taragi T., Taragansu K.,

RA Sorokin A., Tacconi E., Taragi T., Taragansu K.,

RA Sorokin A., Tamakoshi A., Taraka T., Terpstra P., Tognoni A.,

RA Viari A., Wambutt R., Wedler E., Wedler H., Weitzenegger T.,

RA Winters P., Wipat A., Yamamoto H., Yamane K., Yasunoto K., Yata K.,

RA Viari A., Wambutt R., Zumstein E., Yoshikawa H., Danchin A.;
                                                                                                                                                                 ö
                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN=168 / JH642;
MEDLINE=96312380; PubMed-8763966;
Xu K., Strauch M.A.;
"Identification, sequence, and expression of the gene encoding gamma-glutamyltranspeptidase in Bacillus subtilis.";
J. Bacteriol. 178:4319-4322(1996).
                                                         (POTENTIAL).
                                              (POTENTIAL).
                                  (POTENTIAL)
                                                                                (POTENTIAL)
                                                                                           (POTENTIAL)
                                                                                                         (POTENTIAL)
                                                                                                                                                                 ö
                                                                                                                                          DB 1; Length 730;
                                                                                                                                                                 2; Indels
                                                                                                                                                                                                                                                                                                                                                                   Firmicutes; Bacillales; Bacillaceae; Bacillus.
                                                                                                                   C2BDB82BC24CD133 CRC64;
                                                                                                                                                                                                                                                                                           01-077-1996 (Rel. 34, Created)
01-0CT-1996 (Rel. 34, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Gamma-glutamyltranspeptidase precursor (EC 2.3.2.2)
                                                                                             (GLCNAC. . .)
                                                         (GLCNAC. . .)
                                               (GLCNAC.
                                                                                (GLCNAC.
                                  (GLCNAC.
                        GLCNAC
                                                                                                                                                                 0; Mismatches
                                                                                                                                          Score 37;
Pred. No.
N-LINKED
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N-LINKED
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N-LINKED
N-LINKED
N-LINKED
N-LINKED
                                                                                          N-LINKED
N-LINKED
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                                                                                                                   80960 MW;
                                                                                                                                         72.5%;
75.0%;
                                                                                                                                                                 6; Conservative
                                                                                                                                                                                                                                                                       STANDARD;
                                                                   614
620
621
630
730 AA;
                                                                                                                                      Query Match
Best Local Similarity
Matches 6; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                       Bacillus subtilis.
                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A
                                                                                                                                                                                                    NCBI_TaxID=1423;
                                                                                                                                                                                      1 YYGDYEGY 8
                                                                                                                                                                                                                                                                      GGT_BACSU
P54422;
                                                                                                                                                                                                                                                                                                                                                                      Bacteria;
                                             CARBOHYD
                                                                    CARBOHYD
                                                                                CARBOHYD
                                                                                           CARBOHYD
                                                                                                        CARBOHYD
                                                                                                                   SEQUENCE
                       CARBOHYD
                                  CARBOHYD
                                                         CARBOHYD
                                                                                                                                                                                                                                                 RESULT 13
                                                                                                                                                                                                                                                           GGT_BACSU
5111111118
8111111118
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between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This SWISS-PROT entry is copyright. It is produced through a collaboration
                                                                                                                                                                    Ogawa Y., Hosoyama H., Hamano M., Motai H.;

"Purification and properties of gamma-glutamyltranspeptidase from Parification and properties of gamma-glutamyltranspeptidase from Bacillus subtilis (natto).";

Agric. Biol. Chem. 55:2971-2977(1991).

-!- CATALYTIC ACTIVITY: (5-L-glutamyl)-peptide + an amino acid = peptide + 5-L-glutamyl-amino acid.

-!- ENZYME REGULATION: INHIBITED BY GLUGOSE.

-!- PATHWAY: GGT PLAYS A KEY ROLE IN THE GAMMA-GLUTAMYL CYCLE, A PATHWAY FOR THE SYNTHESIS AND DEGRADATION OF GLUTATHIONE.

-!- SUBUNIT: THIS ENXYME CONSISTS OF TWO POLYPEPTIDE CHAINS, WHICH ARE SYNTHESIZED IN PRECURSOR FORM FROM A SINGLE POLYPEPTIDE (BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Acetyl-coenzyme A synthetase (EC 6.2.1.1) (Acetate--CoA ligase) (Acyl-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GAMMA-GLUTAMYLTRANSPEPTIDASE LARGE CHAIN.
GAMMA-GLUTAMYLTRANSPEPTIDASE SMALL CHAIN.
GAMMA-GLUTAMYL (POTENTIAL).
D -> V (IN REF. 3).
6BF200CBA882C4F6 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -1- SUBCELLULAR LOCATION: Secreted.
-1- DEVELOPMENTAL STAGE: EXPRESSED AT THE END OF VEGETATIVE GROWTH.
-1- SIMILARITY: STRONG, TO OTHER GGT ENZYMES AND TO GL-7ACA ACYLASES.
"The complete genome sequence of the Gram-positive bacterium Bacillus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Subtilist; BGI1838; ggt.
InterPro; IPR000101; Gglutrnspptdase.
Pfam; PF01019; G_glu_transpept; 1.
PRINTS; PF01210; GGTRANSPPA, 1.
TIGRFAMS; TIGR00066; g_glut_trans; 1.
PROSITE; PS00462; G_GLU_TRANSPEPTIDASE; 1.
Transferase; Acyltransferase; Signal; Glutathione biosynthesis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ;
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Bacteria; Proteobacteria; alpha subdivision; Rhodobacter group;
Rhodobacter.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0; Indels
                                                                                                                  SEQUENCE OF 36-52 AND 403-442, AND CHARACTERIZATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 36; DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             656 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   95;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; U49358; AAC44233.1; -. EEMBL; 299113; CAB13724.1; -. EMBL; 299114; CAB13734.1; -. MEROPS; T03.001; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         64189 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 70.68;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                          Nature 390:249-256(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STANDARD;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      587 AA;
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Best Local Similarity
Matches 5; Conser
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277 WGDYQGY 283
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SIMILARITY).
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403
467
46
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                                                                                                                                                    STRAIN=NR-1
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068040;
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ACSA_RHOCA
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ACT_SITE
ACT_SITE
METAL
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SEQUENCE
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CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CARBOHYD
CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SIGNAL
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         õ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             g
                                                                                                                                                                                                                                                                        This SWISS. PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Européan Bioinformatics Institute. There are no restrictions on its use by mon-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities meduires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@lsb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation her Burgopen Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                          Fonstein M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mus musčulus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammaliaj; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus.
NCBL_raxtp=10090;
                                                                   Vicek C., Baces V., Maltsev N., Paces J., Haselkorn R., Fonstein "Sequence of a 189 kb segment of the chromosome of Rhodobacter capsulatus Sello103.";

Proc. Natl Acad. Sci. U.S.A. 94:9384-9388(1997).

-I. CATAL XII C ACTIVITY: ATP + acetate + CoA = AMP + diphosphate
                                                                                                                                                                                      acetyl-Coa.
-!- SIMILARITY: BELONGS TO THE ATP-DEPENDENT AMP-BINDING ENZYME
FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -!- SIMILARITY: BELONGS TO THE PEROXIDASE FAMILY. XPO SUBFAMILY.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   70.6%; Score 36; DB 1; Length 656; ilarity 62.5%; Pred. No. 1.1e+02; Conservative 1; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE $ 656 AA; 72703 MW; 706EA969331D71C2 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-JUN-1994 (Rel. 29, Created)
01-JUN-1994 (Rel. 29, Last sequence update)
15-JUN-1902 (Rel. 41, Last annotation update)
Thyroid iperoxidase precursor (EC 1.11.1.8) (TPO).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            914 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRT;
SEQUENCE FROM N.A.
STRAIN-SB1003 / St Louis;
MEDLINE-97∯04404; PubMed-9256491;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PROSITE; (PS00455; AMP_BINDING; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; AFOQUO496; AAC16126.1; -. InterProciptreMO00873; AMP-bind. Pfam; PFOQS601; AMP-binding; 1. PRINTS; PRO0154; AMPBINDING.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Best Local Similarity
Matches 5% Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1:1*] | 1
495 YFGQYRGY 502
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 YYGDYEGY 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PERT_MOUSE
P35419;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
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    RRANKER RRANK RRAN
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SMART; SM00179; EGF_CA; 1.

PROSITE; PS00010: ASX_HYDROXYL; 1.

PROSITE; PS01186; EGF_2; 1.

PROSITE; PS01187; EGF_2; 1.

Oxidoreductase; Peroxidase; Iron; Heme; Transmembrane; Glycoprotein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      POTENTIAL.
THYROID PEROXIDASE.
DISTAL HISTIDINE (POTENTIAL).
DISTAL ARGININE (POTENTIAL).
IRON (PROTOHEME IX AXIAL LIGAND) (BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             POTENTIAL.

123 N-LINKED (GLCNAC. . .) (POTENTIAL).

129 N-LINKED (GLCNAC. . .) (POTENTIAL).

129 N-LINKED (GLCNAC. . .) (POTENTIAL).

134 N-LINKED (GLCNAC. . .) (POTENTIAL).

101342 MW; 595E9A0B71F3DD01 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 36; DB 1; Length >1*
Pred. No. 1.4e+02;
Transches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Search completed: December 23, 2002, 07:26:05 Job time : 3.7907 secs
send an email to license@isb-sib.ch)
                                                                        HSSP; P05164; 1car.
MGD; MGI:98813; Tpo.
InterPro; IPR002007; Anim_peroxidase.
InterPro; IPR000152; Asx_hydroxyl.
                                                                                                                                                        InterPro; IPRO001561; EGF-11ke.
InterPro; IPR001081; EGF_Ca.
InterPro; IPR002016; Peroxidase.
InterPro; IPR002016; Peroxidase.
InterPro; IPR0000436; Sushi_SCR_CCP.
Pfam; PF00008; EGF; 1.
Pfam; PF000084; sushi; 1.
Pfam; PF001084; AnPEroxidase; 1.
PRINTS; PR001057; ANPEROXIDASE.
SMART; SM00179; EGF_CA; 1.
                                        EMBL; X60703; CAA43114.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              70.6%;
75.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 75.v.
6; Conservative
                                                           JN0550; JN0550
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      914 AA;
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233
384
482
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December 23, 2002, 07:17:27 ; Search time 3.31783 Seconds (without alignments) 496.824 Million cell updates/sec
    GenCore version 5.1.3
Copyright (c) 1993 - 2002 Compugen Ltd.
                                                                                                          Total number of hits satisfying chosen parameters:
                                                                                                671580 segs, 206047115 residues
                                                                                                                                     Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                          OM protein - protein search, using sw model
                                                                               BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                sp_archea:*
sp_bacteria:*
sp_fungi:*
sp_human:*
sp_nvertebrate:*
sp_marmal:*
sp_mhc:*
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sp_vertebrate:*
sp_unclassified:*
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sp_phage:*
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Maximum DB seq length: 200000000
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sp_rodent:*
                                                          US-09-865-198-3
51
                                                                                                                                                            SPTREMBL_21:*
                                                                    1 YYGDYEGY 8
                                                                                                                                                                                 Scoring table:
                                                               Perfect score:
                                                                                                                                                           Database :
                                                                                                Searched:
                                                                     Sequence:
                                     Run on:
                                                          Title:
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Q9h719 homo sapien Q9fny5 methanosarc Q9j289 neisseria m Q9jub3 neisseria m Q9jub3 neisseria m Q23118 caenorhabdi Q95Kg1 mus musculu Q96Kg bul mus musculu Q96Kg homo sapien P90761 caenorhabdi Q92Cq8 listeria in Q97X0 listeria mo Q97X0 listeria mo Q97X0 listeria mo Q97X1 atreptococc Q8135 methanosarc Q94F135 methanosarc Q95F1 drosophila Q8syp0 drosophila Q8syp0 drosophila Q91X71 arabidopsis Q91X7 arabidopsis Q91X7 thermotoga Q95VV4 thermotoga Q95VV4 thermotoga Q95VV4 thermotoga Q95VV4 thermotoga Q95VS3 anopheles s Q96753 anopheles g

09H719 08TNY5 08TNY5 08DYZ89 029UB3 029KG1 096KC8 096KC8 097K04 09770 097751 097751 097751 097751 08770 097713 08770 097713 08770 097713 08770 097813 08770 097813 08770 097813 08770 097814 081710 091771 091771

homo sapien

Q8tci9

096753 Q9ZI87 Q8TCI9

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

sp_rvirus:*
sp_bacteriap:*
sp_archeap:*

Description	Q9pn04 campylobact	Q91eb4 nicotiana p 077328 plasmodium	Q8tjs7 methanosarc	Q9fpj8 arabidopsis	Q9ffu0 arabidopsis	067245 aquifex aeo	Q9kgk8 bacillus ha	Q98qz9 mycoplasma	062093 caenorhabdi	Q9u601 anisakis si	027163 methanobact	Q9w0hl drosophila	Q9haf2 homo sapien	Q8vvnl vibrio chol	09w098 drosophila
SUMMARIES	0.09PN04	077328	7 Q8TJS7) Q9FPJ8	O Q9FFUO		5 Q9KGK8		062093	Q90601	7 027163	Q9W0H1	Q9HAF2	Q8VVN1	860860
% Query Match Length DB	435 16	1650 5	1881 17	387 10			91 099		89 5	104 5	154 17	248 5	279 4	294 2	300 5
% Query Match	80.4	78.4	76.5	74.5	74.5	74.5	74.5	74.5	72.5	72.5	72.5	72.5	72.5	72.5	72.5
Score	41	4 4	39	38	38	38	38	38	37	37	37	37	37	37	37
Result No.		7 F	4	2	9	7	&	σ	10	11	12	13	14	15	16

RESULT 2

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	11 29P004 PRELIMINARY; PRT; 435 AA. 29P004 20P0N04; PRELIMINARY; PRT; 435 AA. 20P0N04; PRELIMINARY; PRT; 435 AA. 201-OCT-2000 (TREMBLrel. 15, Last sequence update) 201-OCT-2000 (TREMBLrel. 15, Last sequence update) 201-DEC-2001 (TREMBLrel. 15, Last sequence update) 49pothetical protein Cj1295. 201295. 201295. 201295. 201295. 201295. 201295. 201295. 201295. 201295. 201295. 201295. 201295. 2012910.	Gaps	
	r gr, 	;	
	acte Pr C J.W. A.H.	435; s	
	yloba urch enn 1iet pyloi	gth ndel:	
	ate) Camp	Length 4 0; Indels	
	pdatupdat. On; Cogen	DB 16; Length 435; 36; 0; Indels	
IIS	ared) t sequence update) t sequence update) t annotation update) on subdivision; Campylo 74; 74; 75. Relley J.M., Churc 75. Pallen M.J., Penn Therford K.M., van Vlie 1-borne pathogen Campyl 7; 7; 7; 8 9 10 11 11 12 12 13 14 15 16 17 18 18 18 18 18 18 18 18 18	DB 36; thes	
ALIGNMENTS	ated) t sequenct amotal t servenct on subdiv (04; K., Ket. Y.'s R.H. therford d-borne	41; No. smatc	
ALIG	T.1 9404 PRELIMINARY; PRT; 435 AA. 909N04; 01-OCT-2000 (TrEMBLrel. 15, Last sequence update) 10-OCT-2000 (TrEMBLrel. 19, Last sequence update) 91-OCT-2000 (TrEMBLrel. 19, Last annotation update) 91-OCT-2001 (TrEMBLrel. 19, Last annotation update) 91-DEC-2001 (TrEMBLrel. 19, Last annotation update) 91-DEC-2001 (TrEMBLrel. 19, Last annotation update) 92-ECT-2001 (TrEMBLrel. 19, Last annotation update) 93-ECT-2001 (TrEMBLrel. 19, Last annotation update) 93-ECT-2001 (TrEMBLrel. 19, Last annotation update) 94-ECT-2001 (TrEMBLrel. 19, Last annotation; Campylobacter group; Campylobacter 19, Last annotation 19, Last annotation 19, Last annotation 20, Panter 10, Wren B.W., Mungall K., Retley J.W., Churcher C., Basham D., Chillingworth T., Davies R.W., van Vliet A.H.M., Multehad S., Barrell. B.G.; Pallen M.J., Pentwell T., Pentrell. B.G., Barrell. B.G.; Pallen M.J., Pentwell A.H.M., Whitehad S., Barrell. B.G.; Pentrell. B.G., Barrell. B.G.; Pallen M.J., Pentwell S., Barrell. B.G.; Pentrell. B.G., Barrell. B.G.; Pentrell. B.G., Barrell. B.G., B	Score 41; DB Pred. No. 36; 1; Mismatches	
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	4 4 69PN04 PRELIM 09PN04; 01-OCT-2000 (TrEMB 01-OCT-2000 (TrEMB 01-DEC-2001 (TrEMB 01-DEC-2001 (TrEMB 01-DEC-2001 (TrEMB 01-DEC-2001 (TrEMB 01-DEC-2001 (TrEMB 01-DEC-2001 (TrEMB 01250 (TR	mila Cc	
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	4 4 09PN04 09PN04; 00PN04; 01-OCT-01-OCT-01-DCT-Hypothe CJ1295; CSMPY10 NCBL_TB BACTERI [1] SEQUENC STRAIN-BASHM DASHM WHITCHE PARKHIL BASHM WHITCHE PARKHIL BASHM WHITCHE NATURE REBEL; A HYPOTHE SEQUENC	/ Mat Loca nes	325 1
	SUL	Query Match Best Local Similarity Matches 6; Conserv	
	SWW RETARANGE OF SWW SWW SWW SWW SWW SWW SWW SWW SWW SW	~ 	Oy Db

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SMART; SM00220; S_TKC; 1.
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Matches 6; Conserv
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525 YFDDYEGY 532
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165 HYGDYVGY 172
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9
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Q8TJS7
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Q9FPJ8
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Bowman S. Lawson D., Basham D., Brown D., Chillingworth T.,
Bowman S., Lawson D., Basham D., Brown D., Chillingworth T.,
Churche C.M., Craig A., Davies R.M., Deviln K., Feltuell T.,
Gentleg S., Gwilliam R., Hanlin N., Harris D., Holroyd S., Hornsby T.,
Horrocks P., Jagels K., Jassal B., Kyes S., McLean J., Moule S.,
Mungal F., Murphy L., Oliver K., Quall M.A., Rajandream M.-A.,
Rutter S., Skelton J., Squares R., Squares S., Sulston J.E.,
Whitehead S., Woodward J.R., Newbold C., Barrell B.G.;
The complete nucleotide sequence of chromosome 3 of Plasmodium
                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                               Nicotiana [blumbaginifolia (Leadwort-leaved tobacco).
Mekaryota #, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Wagnoliophyta; eudicotyledons; core eudicots; Asteridae, euasterida I; Solanales; Solanaceae; Nicotiana.
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Eukaryota: Alveolata: Apicomplexa; Haemosporida; Plasmodium.
NCBI_TagID=36329;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 409;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PROSITE; #PS01102; RRM; 3.
PROSITE; #PS00030; RRM_RNP_1; UNKNOWN_1.
ERGIENCE? 409 AA; 45243 MW; 145EE701A89AF01D CRC64;
                                                01-0CT-2000 (TrEMBLrel. 15, Created)
01-0CT-2000 (TrEMBLrel. 15, Last sequence update)
01-0TN-2002 (TrEMBLrel. 21, Last annotation update)
RNA binding protein 45.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-NOV-1999 (TrEMBLrel. 12, Last sequence update) 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 40; DB 10;
Pred. No. 50;
                 409 AA.
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PFC0385©, MAL3P3.12.
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Nature#400:532-538(1999).
-! SIMILARITY: BELONGS TO THE SER/THR EMBL; 298547; CAB1112.2; --..
HSSP; 663450; 1A06.
InterPac: INTERPORTINGS TO THE SER/THR INTERPACE INTERPACE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Created)
                 PRT;
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75.08;
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                 PRELIMINARY;
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6; Conserv
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Best Local
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               Q9LEB4
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Q9LEB4
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RA Galagan J.E., Nusbaum C., Roy A., Endrizzi M.G., Macdonald P.,
RA FitzHugh W., Calvo S., Engels R., Smirnov S., Atnoor D., Brown A.,
RA Allen N., Naylor J., Stange-Thomann N., Dearellano K., Johnson R.,
A Linton L., McEwan P., McKernan K., Talamas J., Tirrell A., Ye W.,
RA Linton L., McEwan P., Cann I., Grahham D. E., Grahame D.A., Guss A.M.,
RA Leigh J.A., Li W., Liu J., Mukhopadhyay B., Grahame D.A., Guss A.M.,
RA Leigh J.A., Li W., Liu J., Mukhopadhyay B., Reeve J.N., Smith K.,
Springer T.A., Umayam L.A., White O., White R.H., de Macario E.C.,
RA Pritchett M., Sowers K.R., Swanson R.V., Zinder S.H., Lander E.,
RA Mctcalf W.W., Birren B.;
RY Mctcalf W.W., Surrell acetivorans reveals extensive metabolic
RT and physiological diversity."
RT Genome Res 12:55-542(2002).
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Arabidopsis thaliana (Mouse-ear cress).
Eukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnollophyta; eudicotyledons; core eudicots; Rosidae;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                      Gaps
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PROSITE; PSO0107; PROTEIN_KINASE_ATP; UNKNOWN_1.
PROSITE; PSO0101; PROTEIN_KINASE_DOM; 1.
PROSITE; PSO01019; PROTEIN_KINASE_ST; 1.
ATP-binding; Kinase; Serine-threonine-protein kinase; Transferase.
SEQUENCE 1650 AA; 193755 MW; D70FE19C5C640B5A CRC64;
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                                                                                                                                                                                          Length 1650;
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Last sequence update)
Last annotation update)
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Last annotation update)
                                                                                                                                                                                   78.4%; Score 40; DB 5; I
75.0%; Pred. No. 2.4e+02;
ive 1; Mismatches 1;
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Pred. No. 4.1e+02;
1; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRT; 1881 AA.
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01-MAR-2001 (TrEMBLrel. 16, Last seq
01-JUN-2002 (TrEMBLrel. 21, Last anno
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STRAIN-C2A / ATCC 35395 / DSM 2834;
MEDLINE-21929760; Pubmed-11932238;
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nilarity 75.0%;
Conservative 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Methanosarcina acetivorans.
                                                                                                                                                                                                                                                      6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRELIMINARY;
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SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-MAR-2001 (TTEMBLrel. 16, Created)
01-MAR-2001 (TTEMBLrel. 16, Last sequence update)
01-MAR-2001 (TTEMBLrel. 21, Last annotation update)
01-MIN-2002 (TTEMBLrel. 21, Last annotation update)
Similarity to polyadenylate-binding protein 5.
Arabidopsis thaliana (Mouse-ear cress).
Eukaryota, Viidiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta, Magnollophyta; eudicotyledons; core eudicots; Rosidae;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                            Shinn P., Chao Q., Brooks S., Chen H., Cheuk R., Johnson-Hopson C., Khan S., Kim C.J., Banh J., Bowser L., Chung M.K., Goldsmith A.D., Jones T., Karlin-Neumann G., Lam B., Lee J.M., Lin J., Liu S.X., Miranda M., Nguyen M., Palm C.J., Phan P.K., Quach H.L., Sakano H., Southwick A., Toriumi M., Pamada K., Yu G., Davis R.W., Theologis A.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 387;
                                                                                                                                                                                                                                                                                                                                                                                                                                      74.5%; Score 38; DB 10; Length 38
75.0%; Pred. No. 1.18+02;
tive 0; Mismatches 2; Indels
                                                                                                                                                                        Ecker J.R.;
"Arabidopsis cDNA clones.";
Submitted (MAR.2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AF324983; AAG40335.1;
                                                                                                                                                                                                                                                         HSSP; P11940; 1CVJ.
InterPro; IPR000504; RNA_rec_mot.
Pfam; PF00076; rrm; 3.
SMART; SM00360; RRM; 3.
PROSITE; PS50102; RRM; 3.
PROSITE; PS00030; RRM, RNP_1; UNKNOWN_1.
SEQUENCE 387 AA; 42324 MW; D6CF4F66DFD78DB0 CRC64;
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PROSITE; PS00030; RRM_RNP_1; UNKNOWN_1.
SEQUENCE 390 AA; 42652 MW; DD03B776CF4F66DF CRC64;
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MEDLINE-97471969; PubMed=9330910;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DNA Res. 4:215-230(1997).
EMBL; AB005232; BAB08769.1; -.
HSSP; P11940; ICVV.
INTERPO; IPR000504; RNA_rec_mot.
Pfam; PF00076; rrm; 3.
SMART; SM00360; RRM; 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 74.5
Best Local Similarity 75.0
Matches 6; Conservative
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SEQUENCE FROM N.A.
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067245
ID 06724
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Deckert G., Warren P.V., Gaasterland T., Young W.G., Lenox A.L., Graham D.E., Overbeek R., Snead M.A., Keller M., Aujay M., Huber R., Feldman R.A., Short J.W., Olson G.J., Swanson R.V.; "The complete genome of the hyperthermophilic bacterium Aquifex
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Takami H., Nakasone K., Takaki Y., Maeno G., Sasaki R., Masui N., Fuji F., Hirama C., Nakamura Y., Ogasawara N., Kuhara S., Horikoshi K.;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bacteria; Firmicutes; Bacillus/Clostridium group; Bacillales; Bacillacea; Bacillus. NCBI_TaxID=86665;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               74.5%; Score 38; DB 16; Length 595; 85.7%; Pred. No. 1.7e+02; 1:ve 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 InterPro; IPR002300; tRNA-synt_la.
InterPro; IPR002300; tRNA-synt_la.
InterPro; IPR002300; tRNA-synt_la.
InterPro; IPR002304; tRNA-synt_met.
InterPro; IPR002304; tRNA-synt_met.
InterPro; IPR002304; tRNA-synt_li.
Pfam; PF00133; tRNA-synt_l; 1.
Pfam; PF00133; tRNA-synt_li.
PRIMTS; PR001041; TRNASNTHMET.
TIGRFAMS; TIGR00399; metG. 1.
                                                                                                                                                                                              Aquifex aeolicus.
Bacteria; Aquificae; Aquificales; Aquificaceae; Aquifex.
NCBL_TaxID=63363;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Hypothetical protein; Complete proteome.
SEQUENCE 595 AA; 71080 MW; F8373F5603427F24 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-007-2000 (TrEMBLrel. 15, Created)
01-007-2000 (TrEMBLrel. 15, Last sequence update)
01-0170N-2002 (TrEMBLrel. 21, Last annotation update)
Methionyl-tRNA synthetase (EC 6.1.1.10).
METS OR BH0053.
067245;
01-AUG-1998 (TrEMBLrel. 07, Created)
01-AUG-1998 (TrEMBLrel. 07, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Hypothetical protein AQ_1185.
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STRAIN=C-125 / JCM 9153;
MEDLINE=20512582; Pubmed=11058132;
                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE-98196666; PubMed-9537320;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Nature 392:353-358(1998).
EMBL; AE000727; AAC07204.1; -.
InterPro; IPR001440; TPR.
Pfam; PF00515; TPR; 2.
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Best Local Similarity 85.7
Matches 6; Conservative
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SEQUENCE FROM N.A.
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                                                                                                                                                                                                              Anisakis simplex.
                                                             111 | 11
63 YYGGYGGY 70
                                              1 YYGDYEGY 8
                                                                                                                                                                                                                                               NCBI_TaxID=6269;
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   Query Match
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Q9U601;
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027163
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Q9U601
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                         Gaps
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Chambaud I., Hellig R., Ferris S., Barbe V., Samson D., Galisson F.,
Moszer I., Dybvig K., Wroblewski H., Viari A., Rocha E.P.C.,
Blanchard A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryoga; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
Rhabditidae; Peloderinae; Caenorhabditis.
NCBI_TagiD=6239;
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Diete genome sequence of the murine respiratory pathogen
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                                                                                                                                                                                                                      Bacteria: Firmicutes; Bacillus/Clostridium group; Mollicutes;
                                                                                                                                                                                                                                                                                                                                                                                                                              Length 3216;
  Length 660;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "Genome sequence of the nematode C.elegans: A platform for investigating blology."; science 2012-2018(1998). EMBL; #292028; CAB07335.1; -SEQUENCE 89 AA; 10003 MW; C887044842E59E25 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                             74.5%; Score 38; DB 16; Length 32
75.0%; Pred. No. 1.1e+03;
ive 1; Mismatches 1; Indels
                       1; Indels
                                                                                                                                                                                                                                                                                                                                                                      EMBL; ALMS4563; CAC13384.1; -. Mypulstsf, MYPULS210; -. Hypothetsf, MYPULS10; -. Hypothetsf, Drottein; Complete protecome. SEQUENCE 3216 AA; 359419 MW; A62ED95756BDB90C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         White S_{\mathbb{C}}; Submitted (MAR-1997) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                  01-OCT-2001 (TrEMBLrel. 18, Created)
01-OCT-2001 (TrEMBLrel. 18, Last sequence update)
01-OCT-2001 (TrEMBLrel. 18, Last annotation update)
Hypothetical protein MYPU_2110.
MYPU_2110.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   062093; ° 01-00-1998 (TrEMBLrel. 07, Created) 01-00-1998 (TrEMBLrel. 07, Last sequence update) 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
Score 38; DB 16;
Pred. No. 1.9e+02;
1; Mismatches 1;
                                                                                                                             PRT; 3216 AA
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Acids Res. 29:2145-2153(2001).
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MEDLINE#99069613; PubMed=9851916;
                                                                                                                                                                                                                              Mycoplasmataceae; Mycoplasma.
NCBI_Taxip=2107;
 74.5%;
75.0%;
                       Conservative
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C37A5.8 公
Caenorhabditis elegans.
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     Best Local Similarity
Matches 67 Conserv
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1978 YYVDYEGF 1985
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                                                          121 YLGDÝEGW 128
                                     1 YYGDYEGY 8
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Nucleic A
  Query Match
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Q98QZ9
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R. Embi, Abb00879; Abab5580.1; -.
R. Propom; PRO1881; DUF57; 1.
                                            Gaps
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Anisakidae; Anisakis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Arrieta I., Del Barrio M., Vidarte L., Del Pozo V., Pastor C., Arrieta I., Del Barrio M., Vidarte L., Del Pozo V., Pastor C., Gonzalez-Cabrero J., Cardaba B., Rojo M., Minguez A., Corteano I., Gallardo S., Aceituno E., Palomino P., Lahoz C.; "Anisakis simplex for a 12 kDa protein."; Submitted (OCT-1999) to the EMBL/GenBank/DDBJ databases. EMBL; AJ250043; CABS8174.1; -. Hypothetical protein.

SEQUENCE 104 AA; 11456 MW; 419710152ADD6FAA CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Methanobacterium thermoautotrophicum.
Archaea; Euryarchaeota; Methanobacteria; Methanobacteriales;
Methanobacteriaceae; Methanothermobacter.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 104;
Length 89;
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                                                                                                                                                                                                                                                                             01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
Hypothetical 11.5 kDa protein.
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Last annotation update)
  5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                72.5%; Score 37; DB 5; 75.0%; Pred. No. 37;
                                                                                                                                                                                                                                       104 AA.
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Score 37; DB
Pred. No. 31;
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                                            Mismatches
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01-JAN-1998 (TrEMBLrel. 05, Created)
01-JAN-1998 (TrEMBLrel. 05, Last sequ
01-JUN-2002 (TrEMBLrel. 21, Last ann
Conserved protein.
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72.5%;
75.0%;
                                          6; Conservative
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                    Best_Local Similarity
Matches 6; Conserv
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Gaps

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Length 248;

Score 37; DB 5;

72.5%; 75.0%;

Mismatches Pred. No.

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Conservative
                         Best Local Similarity
Matches 6; Conserv
                                                                        1 YYGDYEGY
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Matches
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Q9HAF2
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A Adman FLEXIBLEX;

A Adman FLEXIBLEX;

A Mannatides P.G., Scherer S.E., Holf R.A., Evans C.A., Gocayne J.D.,

BA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,

George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,

BA Brandon R.C., Rogers Y.-H.C., Blazel R.G., Champe M., Ffeiffer B.D.,

Ann K.H., Doyle C., Baxter E.G., Helf G. Nelson C.R., Miklos G.L.G.,

RA Abril J.F., Agbayani A., An H.-J., Addrews-Ffannoch C., Bladdin D.,

Ballew R.M., Benos P.V., Berman B.P., Bandari D., Bolahakov S.,

RA Beson K.Y., Benos P.V., Berman B.P., Bandari D., Bolahakov S.,

Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasiey E.M.,

Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasiey E.M.,

Ballew R.M., Cawley S., Dallke C., Davenport L.B., Davies P.,

Burtis K.C., Busam D.A., Buller H., Cadleu E., Center A., Chandra I.,

RA Cherry J.M., Cawley S., Dallke C., Davenport L.B., Davies P.,

Burtis K.C., Gabriellan A.E., Garrell J. H., Guz J., Chura P., Harris M.,

RA Glodek A., Gong F., Gorrell J. H., Guz Z., Gelbart W.M., Classer K.,

RA Hostin D., Houston K.A., Howland T.J., Herrandez J.R., Houck J.,

Alall M., Kalush F., Kalpen G. H., Ke Z., Kulp D., Hai Z.,

Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,

Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,

Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,

Muttel B. E., Kodira C. D., Kraft C., Kratt C., Kratt S.,

RA Mannel B. E.,

RA Mannel B. W.,

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                                                                                                                                                                                                                                                                                                       Drosophila melanogaster (Fruit fly).
Eukaryota, Metazoa, Arthropoda, Tracheata, Hexapoda, Insecta,
Pherygota; Neoptera, Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea, Drosophilidae; Drosophila.
                                                                        Gaps
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                                          Length 154;
                                                                        Indels
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               154 AA; 18541 MW; 9EA3B9F89F7DE210 CRC64;
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Last annotation update)
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0
                                          DB 17;
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                                                                     2; Mismatches
                                                         57:
                                          Score 37;
Pred. No.
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FlyBase; FBgn0035208; CG9184.
InterPro; IPR002965; P_rich_extensn.
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                                        72.5%;
71.4%;
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                                                                      5; Conservative
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                                          Query Match
Best Local Similarity
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Complete proteome. SEQUENCE 154 AA
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81 FYGDYDG 87
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Q9W0H1
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"Molecular Analysis of Antibiotic Resistance Gene Clusters in Vibrio cholevel en O139 and O1 SXT Constins.";
Antimicrob. Agents Chemother. 45:2991-3000(2001).
EMBL; AY034138; AAK64586.1;
Hypothetical protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TISSUE-EMBRYO;

Isogai T., Ota T., Hayashi K., Sugiyama T., Otsuki T., Suzuki Y.,
Nishikawa T., Nagai K., Sugano S., Takabashi-Fujji A., Hara H.,
Ishase T., Nomura Y., Togiya S., Komai F., Hara R., Takeuchi K.,
Arita M., Nabekura T., Ishii S., Kawai Y., Saito K., Yamamoto J.,
Wakamatsu A., Nakamura Y., Nagahari K., Masuho Y., Oshima A.;
Submitted (AuG-2000) to the EMBL/GenBank/DDBJ databases.

EMBL; AK021791; BAB13897.1;
InterPro; IPR004567; Pank_eukar.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bacteria; Proteobacteria; gamma subdivision; Vibrionaceae; Vibrio.
NCBL_TaxID=666;
                                                                                                                                                                                                                                                                                                              Hypothetical 30.7 kDa protein.
Homo sapiens (Human).
Eukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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MEDLINE-21485931; PubMed-11600347;
Hochhut B., Lotfi Y., Mazel D., Faruque S.M., Woodgate R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   72.5%; Score 37; DB 2; Length 294; 100.0%; Pred. No. 1.2e+02; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 279;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  279 AA; 30651 MW; AAD5D4A2C94AEA3C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     294 AA; 33023 MW; AOA2FA4C0173018F CRC64;
                                                                                                                                                                                                                               01-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-WAR-2002 (TrEMBLrel. 20, Created)
1-WAR-2002 (TrEMBLrel. 20, Last sequence update)
01-WAR-2002 (TrEMBLrel. 20, Last annotation update)
Hypothetical 33.0 kDa protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         72.5%; Score 37; DB 4; Ler
75.0%; Pred. No. 1.1e+02;
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                                                                                                                                                                                   279 AA
                                                                                                                                                                                   PRT;
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Matches 6; Conservative
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                                                                                                                                                                                   PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pfam; PF03630; Fumble;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               [1]
SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       163 YGGDYEGF 170
                                              160 YYGGYGGY 167
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3 GDYEGY 8 ||||||| 74 GDYEGY 79 Q 2

Search completed: December 23, 2002, 07:29:47 Job time : 6.31783 secs

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(without alignments)
248.221 Million cell updates/sec
                                                                                                                                                              December 23, 2002, 07:16:08; Search time 5.36822 Seconds
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2: /SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1981.DAT:*
3: /SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1981.DAT:*
4: /SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1983.DAT:*
5: /SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1985.DAT:*
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8: /SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1988.DAT:*
9: /SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1988.DAT:*
10: /SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1988.DAT:*
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GenCore version 5.1.3
Copyright (c) 1993 - 2002 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         908470 seqs, 133250620 residues
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Maximum Match 100%
Listing first 45 summaries
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 200000000
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48
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Perfect score:
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11: /SIDSZ/goddata/geneseqy-geneseqy-embl/AA1990.DAT:*
12: /SIDSZ/goddata/geneseqy-embl/AA1990.DAT:*
13: /SIDSZ/goddata/geneseqy-embl/AA1991.DAT:*
14: /SIDSZ/goddata/geneseqy-embl/AA1991.DAT:*
14: /SIDSZ/goddata/geneseqy-embl/AA1991.DAT:*
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16: /SIDSZ/goddata/geneseqy-embl/AA1994.DAT:*
17: /SIDSZ/goddata/geneseqy-embl/AA1994.DAT:*
18: /SIDSZ/goddata/geneseqy-embl/AA1999.DAT:*
19: /SIDSZ/goddata/geneseqy-embl/AA1999.DAT:*
20: /SIDSZ/goddata/geneseqy-embl/AA1999.DAT:*
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29: /SIDSZ/go

SUMMARIES

					COMMAKIES	
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Result						
No.	Score		Match Length DB	DB	В	Description
1	48	100.0	10	18	AAW27424	CDR1 from light ch
7	48	100.0	10	13	AAW73169	CDR1 of light chai
m	48	100.0	10	20	AAY28390	Peptide fragment f
4	48	100.0	10	21	AAY97232	Complementary dete
ß	48	100.0	10	21	AAY77582	Anti-human VEGF re
9	48	100.0	10	21	AAY77588	Anti-human VEGF re
7	48	100.0	10	22	AAE13140	Humanised antibody
80	48	100.0	10	22	AAB82706	VEGF antagonist an
6	48	100.0	10	22	AAB83163	Mouse ganglioside
10	48	100.0	10	22	AAB78851	Anti-human Flt-1 a

ALIGNMENTS

Complementarity determining region; CDR; light chain; treatment; variable region; murine; mouse; human; interleukin 5; IL-5; receptor; alpha chain; monoclonal antibody; hybridoma; detection; assay; diagnosis; allergic respiratory disease; chronic bronchitis; Antibody against alpha-chain of human interleukin 5 receptor CDR1 from light chain variable region of KM1486 antibody. Koike M; Iida A, AAW27424 standard; peptide; 10 AA. Hanai N, KYOW) KYOWA HAKKO KOGYO KK 95JP-0232384. 96WO-JP02588. (first entry) Anazawa H, Furuya A, F Nakamura K, Takatsu K; WPI; 1997-202249/18. 11-SEP-1996; W09710354-A1 11-SEP-1995; 19-DEC-1997 20-MAR-1997. AAW27424; Mus spp. RESULT 1 AAW27424

Gaps

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The sequences AAY28390 to AAY28392 replace the CDR regions of the NEWN DNA and they produce AAY28394, the hKM796L human anti-GM2 antibody light
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Chimeric human antibodies of the invention are useful in the treatment of cancer, especially that which is of neural ectodermal origin. In contrast to prior art constructs based on mouse monoclonal antibodies, the chimeric human antibodies do not cause anti-mouse immunoglobulin production.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The chimeric human antibodies have a prolonged half-life and a reduced frequency of adverse effects when compared to mouse monoclonal
                                                                                                                                                                                                                                                  Peptide fragment from the human anti-GM2 light chain in REI.
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                   Indels
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                                                                                                                                                                                                                                                                           antibody; REI; complementarity determining region; CDR; chimeric; light chain; heavy chain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Nakamura
   Pred. No. 0.0054;
Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         100.0%; Score 48; DB 20;
100.0%; Pred. No. 0.0054;
.ive. 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Chimeric human antibody expression vectors
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                                                                                                                                                        AAY28390 standard; Protein; 10 AA.
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   ilarity 100.0%; P
Conservative 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (KYOW ) KYOWA HAKKO KOGYO KK.
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93US-0116778.
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Best Local Similarity
Matches 10; Conserv
                                                 1 SASSSVSYMH 10
                                                                  1 SASSSVSYMH 10
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Matches 10; Conserv
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                                                                                                                                                                                                                                                                                                                           Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                  07-JUN-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                  07-JUN-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                              07-SEP-1993;
                                                                                                                                                                                                                                                                                                                                                      US5939532-A.
                                                                                                                                                                                                                                                                                                                                                                                    17-AUG-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Shitara K;
                                                                                                                                                                                      AAY28390;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Hanai N,
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                                                                                                                           RESULT 3
                                                                                                                                         AAY28390
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ganglioside GM2; antibody; complementarity determining region; cancer;
                                                                                                                                                                                                                                                                                                                           Gaps
                                                                        The present sequence is complementarity determining region 1 (CDR1) from the light chain variable region of the murine anti-human interleukin 5 receptor alpha chain (hIL-5R alpha) monoclonal antibody (MAD) RM1486. RM1486 is produced by the hybridoma FERM BP-5651, which was prepared by immunising Balb/c mice with hIL-5R alpha, fusing spleen cells obtained from the mice with mouse myeloma Pg-41 cells and screening the resultant hybridomas. The MAD can be used to detect or assay for hIL-5R alpha and cells expressing it on their surface, especially to disgnose allergic respiratory diseases, e.g. chronic bronchitis. It can also be used to treat such also be used.
   diagnosis and treatment of respiratory allergic diseases,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A humañ type complementarity determining region transplanted antibody against ganglioside GM2 - useful as an anti-tumour agent and as a diagnostic for related cancers
                                                                                                                                                                                                                                                                                                                        ;
                                                                                                                                                                                                                                                                                             Length 10;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CDR1 of light chain of ganglioside GM2 targeting antibody
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                                                                                                                                                                                                                                                                                        100.0%; Score 48; DB 18;
100.0%; Pred. No. 0.0054;
ive 0; Mismatches 0;
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                                               Claim 10; Page 165; 238pp; Japanese
                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAW73169 standard; peptide; 10 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim i; Page 29; 66pp; Japanese.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      97JP-0066981
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   22-JAN-1999 (first entry)
                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 100.
Matches 10', Conservative
                 e.g. chronic bronchitis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 1998-575904/49.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  anti-tumour agent.
                                                                                                                                                                                                                                                               10 AA;
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   useful for
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The invention relates to a gene recombinant antibody that has specific reaction with human vascular endothelial growth factor (VEGF) receptor Flt-1. The antibodies are useful for diagnosis and as remedies for diseases due to abnormal neovascularisation such as proliferation or metastasis of solid tumor, arthritis in rheumatoid arthritis, diabetic retinopathy, premature retinopathy and psoriasis.
                                                                                                                                                                                                                                                                                                                                                                                               Gene recombinant antibodies, useful for diagnosis and as remedies for diseases due to abnormal neovascularization e.g. proliferation or metastasis of solid tumor, rheumatoid arthritis, diabetic retinopathy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Antibody; human; vascular endothelial growth factor; VEGF receptor; Flt-1; neovascularisation; cell proliferation; metastasis; tumour; rheumatoid arthritis; retinopathy; psoriasis.
Antibody; human; vascular endothelial growth factor; VEGF receptor; Flt-1; neovascularisation; cell proliferation; metastasis; tumour; rheumatoid arthritis; retinopathy; psoriasis.
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illarity 100.0%; Pred. No. 0.0054;
Conservative 0; Mismatches 0:
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                                                                                                                                                                                                                                                                                                                     Nakamura K;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 10; Page 159; 210pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAY77588 standard; peptide; 10 AA.
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                                                                                                                                                                                                                                                                                                                   Shitara K, Ito M, Kawada Y,
                                                                                                                                                                                                                                                                               (KYOW ) KYOWA HAKKO KOGYO KK.
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Best Local Similarity
Matches 10; Conserv
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                                                                                   Mus musculus
                                                                                                                      W09960025-A1
                                                                                                                                                                                                 20-MAY-1999;
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                                                                                                                                                                                                                                        20-MAY-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New immunoglobulin molecules are described that bind kinase insert domain-containing receptor (KDR) with a comparable affinity to human vascular endothelial growth factor (VEGF). The antibodies neutralise CKDR activation. The immunoglobulin may be a multivalent single chain antibody, a humanised antibody a chimarised antibody, a diabody, a climarised antibody. The immunoglobulin molecules bind specifically to an extracellular domain of the KDR receptor with the same affinity as CKF. Overexpression of VEGF has been implicated in a number of human tumour cell lines including glioblastoma multiforme, hemangioblastoma, central nervous system neoplasms and ALDS associated Karposi's sarcoma. The antibodies therefore have applications in treating these conditions. This sequence encodes a preferred heavy chain complementary determining region of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Novel immunoglobulin molecules binding kinase insert domain-containing receptor with the same affinity as vascular endothelial growth factor, used to reduce tumour growth
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                         Immunoglobulin; antibody; complementary determing region; CDR; VBG; vascular endothelial growth factor; NDR; kinase insert domain containing receptor; multivalent; monovalent; humanised antibody; chimeric antibody; tumour; diabody; triabody; gliobhastoma multiforme; hemangloblastoma; AIDS; central nervous system neoplasms; AIDS associated Karposi's sarcoma; acquired immune deficiency syndrome; AIDS; human.
                      Complementary determining region (CDRL1) of anti-SI(KDR) antibody
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Matches 10; Conservative
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N-PSDB; AAA53764.
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29-JAN-1999;
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                                                                                                                                                                                                                                        Synthetic.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The invention relates to a method for inhibiting the growth of non-solid tumour cells that are stimulated by a ligand of vascular endothelial growth factor receptor (VECFR) in mammals particularly humans. The method involves treating the mammals with humanised VECFR monoclonal antibodies (antagonists). Humanised monoclonal antibody comprises humanised mouse variable region joined to human constant region, where the humanised mouse warlable region contains mouse complementarity determining region
                                                                                                      The invention relates to a gene recombinant antibody that has specific reaction with human vascular endothelial growth factor (VEGF) receptor Flt-1. The antibodies are useful for diagnosis and as remedies for diseases the to abnormal neovascularisation such as proliferation or metastasis of solid tumor, arthritis in rheumatoid arthritis, diabetic retinopathy, premature retinopathy and psoriasis.
                                                                                                                                                                                                                                                                                                                                                                                                                                   Vascular endothelial growth factor receptor; VEGFR; antagonist; tumour; cytostarl, light chain hypervariable region; VL; myelocytic leukaemia; lymphocytic; erythrocytic; monocytic; multiple myeloma; lymphoid cell; Hodgkin; s disease; complementarity determining region-1; CDR-1; mouse.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Inhibiting growth of non-solid tumor cells useful to treat bone marrow tumors such as leukemias or multiple myeloma comprises treatment with an antagonist of a vascular endothelial growth factor receptor -
                       Gene recombinant antibodies, useful for diagnosis and as remedies for diseases due to abnormal neovascularization e.g. proliferation or metastasis of solid tumor, rheumatoid arthritis, diabetic retinopathy
                                                                                                                                                                                                                                                                                                                                                                                                                  Humanised antibody murine light chain hypervariable region (VL) CDR1.
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                                                                                                                                                                                                               100.0%; Score 48; DB 21; Length 10; 100.0%; Pred. No. 0.0054;
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                                                                                 Claim 10; Page 161; 210pp; Japanese
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CORNELL RES FOUND INC.
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                                                                                                                                                                                                                       Local Similarity 100.
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N-PSDB AD21666.
WPI; 2000 072431/06
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                                                                                                                                                                                        10 AA;
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                                                           and psoriasis
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(CORR )
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Matches
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(CDR) grafted into human variable region. The method is useful for treating leukaemias such as acute or chronic myelocytic leukaemia, acute or chronic myelocytic leukaemia, erythrocytic or monocytic leukaemia, multiple myelomas and lymphoid cells, particularly those related to non-Hodgkin's and Hodgkin's disease. The present sequence is humanised antibody murine light chain hypervariable region (VL) CDR-1 used in the exemplification of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                IMC-1C11; chimeric antibody; mouse; human; antagonist; VEGF; vascular endothelial growth factor; anglogenesis; antianglogenic; antitumour; neoplasm; collagen-vascular disease; autoimmune disease;
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IMC-1C11, a mouse-human chimeric antibody that has vascular endothelial growth factor (VEGF) antagonist activity. The antibody, or a fragment of it, can be used as an anti-angiogenic molecule, together with a chemotherapeutic acid, for the treatment of an angiogenic dependent condition in a mammal, especially a human. The invention relates generally to a method of treating or controlling an angiogenic dependent condition by administering an anti-angiogenic molecule and a chemotherapeutic agent, to produce a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ø
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glioblastoma multiforme; melanoma; therapy; light chain; CDR;
                                                                                                                                                                                                                                                                                                                                               Length 10;
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Pred. No. 0.0054;
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31-MAR-2000; 2000US-0539692.
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                                                                                                                                                                                                                                                                                                                                                                                                              10; Conservative
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- Homo sapiens.
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                                                                                                                                                                                                                                                                                Sequence
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Best Local $
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AAB78851 standard; Peptide; 10 AA.
                                                        20-APR-2001 (first entry)
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   AAB78851
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                                                                                                                                                                   Gaps
regression or arrest of the condition while minimising or preventing significant toxicity of the chemotherapeutic agent. The anti-angiogenic molecule inhibits or blocks the action of a vascular endothelium survival factor such as VEGF or its receptor, and is especially IMC-1C11. Conditions that can be treated include a neoplasm, a collagen-vascular disease or an autoimmune disease, especially a solid tumour, including breast carcinoma, lung carcinoma, prostate carcinoma, colon carcinoma, prostate carcinoma, colon carcinoma, prostate carcinoma, ovarian carcinoma, neuroblastoma, central nervous system tumour, neuroblastoma or melanoma (all claimed).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The present invention relates to derivatives of an antibody against ganglioside GM2. The antibody may be a monoclonal antibody or its fragments. The antibody is combined with a radioactive isotope, protein or small drug in the treatment and diagnosis of cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Monoclonal antibodies against ganglioside GM2 combined with drugs, radioisotopes or proteins for treatment and diagnosis of cancer
                                                                                                                                                                                                                                                                                                                                                         Mouse; ganglioside; GM2; antibody; cytostatic; cytotoxic; cancer; complementarity determining region; CDR.
                                                                                                                                                                                                                                                                                                                                    Mouse ganglioside GM2 antibody light chain variable region CDR1.
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                                                                                                                                             Score 48; DB 22; Length 10;
Pred. No. 0.0054;
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100.0%;
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Best Local Similarity 100.
Matches 10; Conservative
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RESULT 10

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monocytes and macrophages from haematopoietic stem cells, containing a substance which binds to human vascular endothelial growth factor (VEGF) ceeptor Flt-1. The invention also includes a method for diagnosing a disease in which the differentiation of monocytes and macrophages is cipplicated, using the reagent, and an agent for the treatment of diseases diagnosed using the method, containing a substance which binds to Flt-1. Or a substance which inhibits the signal transduction of Flt-1. Diseases which inhibits the signal transduction of Flt-1. Diseases which may be diagnosed or treated include inflammation, delayed hypersensitivity, malignant tumours and arteriosclerosis.

CAP70190 - AAF70244, AAF70251 and AAF7028 represent DNA sequences encoding anti-human Flt-1 monoclonal antibody fragments, and antibody is used in the reagent of the invention. FCR primers AAF70455 antibody is used in the reagent of the invention. FCR primers AAF70455 antibody is used in the reagent of the invention of the antibody is used in the reagent of the invention. FCR primers AAF70455 of the anti-human Flt-1 antibody.
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                                                        Differentiation; monocyte; macrophage; haematopoietic stem cell; cancer; vascular endothelial growth factor; VEGF; Flt-1; inflammation; antibody; delayed hypersensitivity; malignant tumour; arteriosclerosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Substances binding to human vascular endothelial growth factor receptor Flt-1, used for diagnosis and treatment of inflammatory diseases, arteriosclerosis, cancer and delayed hypersensitivity
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Anti-human Flt-1 antibody KM1732 L chain V region CDR 1 peptide.
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Local Similarity 100.0%; Pred. No. 0.0054;
les 10; Conservative 0; Mismatches 0;
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                                                                                                                                                                                                         Mus musculus.
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14-FEB-2002 (first entry)
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Best Local Similarity 100.
Matches 10; Conservative
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WO200190192-A2.
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AAF70190. AAF70244, AAF70251 and AAF70258 represent DNA sequences on cligonuclectides used in the construction of the antibody. The monoclonal antibody is used in the reagent of the invention. PCR primers AAF70245 AAF70245 AAF70245 and AAF70246 of the invention of the antibody DNA sequences. Protein sequences AAB78848 - AAB78870 (represent fragments
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              Differentiation, monocyte, macrophage, haematopoietic stem cell; cancer; vascular endothelial growth factor; VEGF; Flt-1; inflammation, antibody; delayed hypersensitivity; malignant tumour; arteriosclerosis.
                                                                                                                                                                                                                                                                                                                                                                              Substances binding to human vascular endothelial growth factor receptor Flt-1, used for diagnosis and treatment of inflammatory diseases, arteriosclerosis, cancer and delayed hypersensitivity
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                                                                                                                                                                                                                                                                       (KYOW ) KYOWA HAKKO KOGYO KK.
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Best Local Similarity
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                                                                                                                       WO200079205-A1
                                                                                         Mus musculus.
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                                                                                                                                                                                                                                                                                                          Shitara K
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Matches

õ Q RESULT 12 AAU74409

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The invention describes an antigen-binding protein (I) comprising a complex of two polypeptides (P1) and two second polypeptides (P2) which are stably associated in an immunoglobulin like complex. Pl has an antigen-binding site located to the N terminus of immunoglobulin (Ig) indicated to the N terminus of immunoglobulin (Ig) indicated to the N terminus of the CH1 domain. (I) is useful for: neutralising the activation of a vascular endothelial growth factor (VBER) receptor; reducing tumour growth; inhibiting angiogenesis, reducing endothelial cell proliferation; inhibiting vBGF induced migration of human leukaemia cells; blocking interaction of a protein and its ligand; promoting interactions between immune cells and target cells; and in vivo and in vitro for investigative, diagnostic or treatment continuing interaction of the antigen-binding proteins production so that substantially all of the antigen-binding proteins produced are assembled in the desired configuration. (I) is bivalent and bispecific, homogeneous can din tetrament for processing in vitro to obtain the complete product. There is no requirement for processing in vitro to obtain variable domain complementarity determining region L1 (CDRL1) incorporated into an antigen-binding protein described in the method of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New bispecific immunoglobulin-like antigen-binding protein for reducing tumour growth and for inhibiting angiogenesis, comprises a complex of two polypeptides and two second polypeptides
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                                                                                                 24-MAY-2000; 2000US-206749P.
                                                                                                                                                                                                  (IMCL-) IMCLONE SYSTEMS INC
24-MAY-2001; 2001WO-US16924
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The invention relates to novel single-chain antibody recognizing human vascular endothelial growth factor receptor-2 (VEGFR-2) comprising a polypeptide having variable heavy (VH) and variable light (VL) domains connected by a linker, and their allelic variants and mutants. The antibody is useful as an immunohistochemical marker for angiogenesis or vascularisation in a human tissue from cryosection or a growing carcinoma, for vascular and stem cell targeting a drug or toxin, radionuclide, gene or viral coat protein conjugated to it, for radionuclide, gene or viral coat protein conjugated to it, for calls expressing human vascular endothelial growth factor receptor-2, cuch as human vascular endothelial cells, human megakaryocytes and their progenitor cells, human haematopoietic stem cells from bone their progenitor cells, human haematopoietic stem cells from bone their progenitor cells, human haematopoietic stem cells from bone their progenitor cells, human haematopoietic stem cells from bone their surfaces. Recombinant single chain antibodies have many advantages compared to monoclonal antibodies derived from hybridomas. The surfaces, easily purified from the bacteria periphasm or supernatant without risk of contamination with serum-components. No expensive cell:culture medium and expensive cell-culture laboratory is needed and they penetrate better into cells and tissue and are better used for in vivo imaging and in vivo diagnostic applications. The size they penetrate better into cells and tissue and are better used for in vivo imaging and in vivo diagnostic applications. The radionuclide, gene or a viral coat protein. The present sequence is the variable light chain of antibody scFvA7.
                                                                                                                                                                              Single-chain antibody that recognizes human vascular endothelial growth factor receptor-2 is useful as a marker for angiogenesis or vascularisation in human tissues and for cell sorting of vascular
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100.0%; Pred. No. 0.062;
ative 0; Mismatches 0;
(GBFB ) GES BIOTECHNOLOGISCHE FORSCHUNG MBH.
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                                                                Yayon
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                                                             Tesar M,
                                                                                                                                                                                                                                                                                                                                             Claim 1; Page 20; 35pp; English.
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Best Local Similarity 100.

Matches 10; Conservative
                                                             Weich H,
                                                                                                                       WPI; 2001-591521/67
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                                                                                                                                                                                                                                                                                   endothelial cells
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                                                             Boeldicke T,
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   The invention relates to transforming a population of cells (e.g. plant cells), comprising using a library of two different polynucleotides canding different immunoglobulin binding protein (IgBP) polypeptides canding different immunoglobulin binding protein (IgBP) polypeptides that specifically bind to a ligand or form one or more disulphide bonds with polypeptides in transferded cells, to generate an IgBP that binds to a ligand, and transformed plant cells are selected, and preparing an IgBP array in plant cells. At least one peptide sequence has at least 73% sequence identity to a framework region (FR) of a native IgM, IgG, IgA, IgD, IgE, IgY, kappa or lambda immunoglobulin molecule. The method is useful for preparing an immunoglobulin binding protein cells especially plant cells (e.g. Agrobacterium tunmefaciens or maize) cor other enkaryotic cells (e.g. insect cells or manmalian cells). The CHBP is useful for discovery of e.g. screening assays of IgBPs having desired characteristics. The present sequence is a mammalian controlled that may be incorporated into an IgBP of the cells of the control or mand into an IgBP of the control or discovery of e.g. screening assays of IgBPs of the control or discovery of e.g. screening assays of IgBPs having the control or discovery of e.g. screening assays of IgBPs of the control or discovery of e.g. screening assays of IgBPs of the control or discovery of e.g. screening assays of IgBPs of the control or discovery of e.g. screening assays of IgBPs of the control or discovery of e.g. screening assays of IgBPs of the control or discovery of e.g. screening assays of IgBPs of the control or discovery of e.g. screening assays of IgBPs of the control or discovery of e.g. screening assays of IgBPs of e.g. the mand of the control or discovery of e.g. e.g. the mand of the control or discovery of e.g. e.g. the mand of the control or discovery of e.g. e.g. the mand of the control or discovery of e.g. e.g. the control or discovery of e.g. e.g. the control or discovery of e.g. e.g. th
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                                                                                                                                                                                                                                                                                                                                                                                              Preparing immunoglobulin binding protein array in plant cells by transforming the cells with different polynucleotides encoding binding protein polypeptides specific to ligand, selecting plant cells for
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Local Similarity 100.0%; Pred. No. 0.0054;
les 10; Conservative 0; Mismatches 0; Indels
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Best Loca Matches

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Gaps

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(GBFB ) GES BIOTECHNOLOGISCHE FORSCHUNG MBH.
                                                  T, Weich H, Tesar M, Yayon A;
                                               Boeldicke
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WPI; 2001 591521/67

Single-chain antibody that recognizes human vascular endothelial growth factor receptor-2 is useful as a marker for angiogenesis or vascularisation in human tissues and for cell sorting of vascular endothelial cells

Page 20; 35pp; English Claim 1;

The invention relates to novel single-chain antibody recognizing human vascular endothelial growth factor receptor-2 (VEGER-2) comprising a polypeptide having variable heavy (VH) and variable light (VL) domains connected by a linker, and their allelic variable light (VL) domains connected by a linker, and their allelic variable light (VL) domains artibody is useful as an immunohistochemical marker for angiogenesis or vascularisation in a human tissue from cryosection or a growing carcinoma, for vascular and stem cell targeting a drug or toxin, radionucilide, gene or viral coat protein conjugated to it, for fluorescence activated cell sorting (FACS) analysis and sorting of cells expressing human vascular endothelial growth factor receptor-2, such as human vascular endothelial cells, human megakaryocytes and their progenitor cells, human haematopoietic stem cells from bone marraces. Recombinant single chain antibodies have many advantages compared to monoclonal antibodies derived from hybridomas. The surfaces medium and expensive cell-culture laboratory is needed and they penetrate better into cells and tissue and are better used for in vivo imaging and in vivo diagnostic applications. The single-chain antibodies are easily fused to a drug, toxin, radionucilide, gene or a viral coal protein. The present sequence is the variable light chain of antibody scray2.

99 AA; Sequence

Gaps ö 100.0%; Score 48; DB 22; Length 99; 100.0%; Pred. No. 0.064; tive 0; Mismatches 0; Indels Best Local Similarity 100. Matches 10; Conservative Query Match

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1 SASSSVSYMH 10 ò a

Search compléted: December 23, 2002, 07:25:05 Job time : 6%36822 secs

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(without alignments)
180.208 Million cell updates/sec
                                                                                                                          December 23, 2002, 07:30:08; Search time 0.930233 Seconds
GenCore version 5.1.3
Copyright (c) 1993 - 2002 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 2000000000
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2: /cgn2_6/ptodata/2/pubpaa/USO8_NEW_PUB.pep:*
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7: /cgn2_6/ptodata/2/pubpaa/USO8_PUBCOMB.pep:*
8: /cgn2_6/ptodata/2/pubpaa/USO8_PUBCOMB.pep:*
9: /cgn2_6/ptodata/2/pubpaa/USO8_PUBCOMB.pep:*
10: /cgn2_6/ptodata/2/pubpaa/USO9_PUBCOMB.pep:*
11: /cgn2_6/ptodata/2/pubpaa/USO9_PUBCOMB.pep:*
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Published_Applications_AA:*

Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Result Query No. Score Match Length DB ID 1 48 100.0 10 10 0S-09-976-787-4 2 48 100.0 105 9 0S-09-976-787-4 5 48 100.0 106 10 0S-09-9865-198-4 5 48 100.0 106 10 0S-09-9865-198-2 6 48 100.0 106 10 0S-09-986-198-2 7 48 100.0 107 9 0S-09-144-886-8 8 100.0 107 9 0S-09-144-886-8 9 48 100.0 107 9 0S-09-144-886-8 10 48 100.0 107 9 0S-09-144-886-8 11 48 100.0 108 10 0S-09-96-198-8 12 48 100.0 108 10 0S-09-96-198-8 13 48 100.0 238 10 0S-09-976-787-8 14 48 100.0 238 10 0S-09-976-787-8 15 48 100.0 238 10 0S-09-976-787-8 16 48 100.0 240 10 0S-09-96-198-8 17 48 100.0 240 10 0S-09-96-198-8 18 48 100.0 240 10 0S-09-96-198-8 19 48 100.0 240 10 0S-09-986-198-8 10 48 100.0 240 10 0S-09-986-198-8 11 48 100.0 240 10 0S-09-986-198-8 12 48 100.0 240 10 0S-09-986-198-8 14 48 100.0 240 10 0S-09-986-198-8 15 48 100.0 240 10 0S-09-986-198-8 16 47 97.9 239 10 0S-09-9808-037-8 18 45 93.8 107 10 0S-09-910-059-50 19 45 93.8 107 10 0S-09-910-059-50 10 45 93.8 107 10 0S-09-910-059-50

Sequence 4, Application US/09865198
Patent No. US20020103345A1
GENERAL INFORMATION:
APPLICATT: Zhu, Zhenping
TITLE OF INVENTION: Bispecific Immunoglobulin-Like Antigen Binding Proteins and Me;
TITLE OF INVENTION: Production
FILE REPERBUCE: 11245/47102
CURRENT APPLICATION NUMBER: US/09/865,198

RESULT 2 US-09-865-198-4

Sequence 61, Appl Sequence 65, Appl Sequence 71, Appl Sequence 97, Appl Sequence 52, Appl Sequence 97, Appl Sequence 97, Appl Sequence 97, Appl Sequence 14, Appl Sequence 17, Appl Sequence 17, Appl Sequence 17, Appl Sequence 17, Appl Sequence 23, Appl Sequence 23, Appl Sequence 24, Appl Sequence 54, Appl Sequence 54, Appl Sequence 54, Appl Sequence 56, Appl Sequence 66, Appl Sequence 64, Appl Sequence 64, Appl Sequence 64, Appl Sequence 64, Appl Sequence 65, Appl Sequence 66, Appl Sequence 66, Appl Sequence 66, Appl Sequence 66, Appl Sequence 65,	U	0; Gaps 0;
	nd Uses The	10; Length 10; 31; 0; Indels
US-09-910-059-61 US-09-910-059-71 US-09-910-059-71 US-09-910-059-17 US-09-910-059-17 US-09-910-059-17 US-09-910-059-18 US-09-910-059-91 US-09-910-059-91 US-09-910-059-91 US-09-771-415-19 US-09-771-415-19 US-09-771-415-19 US-09-771-415-19 US-09-996-288-56 US-09-996-288-56 US-09-996-288-56 US-09-996-288-56 US-09-996-288-56 US-09-996-288-56 US-09-996-288-56 US-09-996-288-56 US-09-996-288-56 US-09-996-288-56 US-09-996-288-56 US-09-996-288-56 US-09-996-288-56 US-09-996-288-56 US-09-996-288-56 US-09-996-288-56 US-09-996-288-56 US-09-996-288-56	ALIGNMENTS 787 Specific to KDR 2,787 2,493,539 /117,726 indows	Score 48; DB Pred. No. 0.00 0; Mismatches
.8 107 10 .8 107 10 .8 107 10 .8 235 10 .8 235 10 .9 235 10 .7 10 9 .7 106 9	6-787-4 L INFORMATION US/0997/ NO. US20020064528A1 L INFORMATION: CANT: Abu, Zhenping CANT: Witte, Larry OF INVENTION: Antibodies NT FELERENCE: 11245/46505 NT APPLICATION NUMBER: US NT FILING DATE: 2001-10- FILING DATE: 1999-01-29 APPLICATION NUMBER: US 6 APPLICATION	100.0%; rity 100.0%; nservative H 10 H 10
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100.0%; Score 48; DB 10; Length 106; 100.0%; Pred. No. 0.03;
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SOFTWARE: WordPerfect 8.0 for Windows
SEQ ID NO 23
LENGTH: 106
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, Sequence 76, Application US/09144886
; Patent No. US20020155114A1
; GENERAL INFORMATION:
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US-09-865-198-23
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US-09-982-107
US-09-982-107
Sequence 127
Patent No. US20020159958A1
Sequence 127
Patent No. US20020159958A1
GENERAL INFORMATION:
TITLE OF INVENTION: METHODS FOR PRODUCING IMMUNOGLOBULINS CONTAINING
TITLE OF INVENTION: MOTHER: 2001-10-16
CURRENT APLICATION NUMBER: US/09/982,107
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 12
SEQ ID NO 12
TYPE: PRIF
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US-09-982-107-12
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ive 0; Mismatches 0;
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          PRIOR APPLICATION NUMBER: US 60/206,749 PRIOR FILING DATE: 2000-05-24 NUMBER OF SEO ID NOS: 34 SOFTWARE: Worderfect 8.0 for Windows SEO ID NO 4 LENGTH: 10
2001-05-24
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CURRENT FILING DATE:
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Sequence 23, Application US/09865198
Patent No. US20020103345al
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: Bispecific Immunoglobulin-Like Antigen Binding Proteins and Me
TITLE OF INVENTION: Production
FILE REFERENCE: 11245/47102
CURRENT FILING DATE: 2001-05-24
PRIOR PILING DATE: 2000-05-24
PRIOR FILING DATE: 2000-05-24
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APPLICANT: Marks, James D
APPLICANT: Amersdorfer, Peter
TITLE OF INVENTION: Therapeutic Monoclonal Antibodies That Neutralize
TITLE OF INVENTION: Botulinum Neurotoxins
FILE REFERENCE: 2500.1170SO
CURRENT APPLICATION NUMBER: US/09/144,886
CURRENT FILING DATE: 1998-08-31
NUMBER OF SEQ ID NOS: 98
SOFTWARE: Patentin Ver. 2.0
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US-09-144-886-76
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0; Indels
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0; Mismatches
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Query Match
Best Local Similarity
Matches 10; Conserv
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ORGANISM: Mouse
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LENGIH: 10
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                                                                                                                         TYPE: PRT
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Sequence 82, Application US/09144886

Sequence 82, Application US/09144886

Sequence 82, Application US/09144886

SERENT INFORMATION:

APPLICANT: Marks, James D

APPLICANT: Marks, James D

TITLE OF INVENTION: Therapeutic Monoclonal Antibodies That Neutralize

TITLE OF INVENTION: Dotulinum Neurotoxins

FILE REFERENCE: 2500.117050

CURRENT APPLICATION NUMBER: US/09/144,886

CURRENT FILING DATE: 1998-08-31

NUMBER OF SEQ ID NOS: 98

SOFTWARE: Patentin Ver. 2.0

SEQ ID NO 82

LENGTH: 107
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APPLICANT: Marks, James D
APPLICANT: Amersdorier, Peter
TITLE OF INVENTION: Therapeutic Monoclonal Antibodies That Neutralize
TITLE OF INVENTION: Botulinum Neurotoxins
FILE REFERENCE: 2500.1170SO
CURRENT APPLICATION UNDBER: US/09/144,886
CURRENT FILING DATE: 1998-08-31
NUMBER OF SEQ ID NOS: 98
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 83
LENGTH: 107
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Patent No. US20020155114A1
GENERAL INFORMATION
APPLICANT: Marks, James D
APPLICANT: Marsdorfer, Peter
TITLE OF INVENTION: Fherapeutic Monoclonal Antibodies That Neutralize
FILE REFERENCE: 2500.1170SO
                                                                                                                                                                                                                                                                                                                                                                         OTHER INFORMATION: Description of Artificial Sequence: BONT/A clone; OTHER INFORMATION: 1E8 region VL epitope 1
US-09-144-886-82
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100.0%; Pred. No. 0.03;
ive 0; Mismatches 0; Indels
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US-09-144-886-83
Sequence 83, Application US/09144886
Patent No. US20020155114A1
GENERAL INFORMATION:
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ORGANISM: Artificial Sequence
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Matches 10; Conservative
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Best Local Similarity 100.0
Matches 10; Conservative
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Sequence 8, Application US/09865198

Sequence 8, Application US/09865198

Sequence 8, Application US/09865198

GENERAL NUS/002103345A1

GENERAL INFORMATION:

TITLE OF INVENTION: Bispecific Immunoglobulin-Like Antigen Binding Proteins and Me

TITLE OF INVENTION: Production

TITLE OF INVENTION: Production

FILE REFERENCE: 11245/47102

CURRENT APPLICATION NUMBER: US/09/865,198

CURRENT FILING DATE: 2000-05-24

PRIOR PRILING DATE: 2000-05-24

NUMBER OF SEQ ID NOS: 34

NUMBER OF SEQ ID NOS: 34
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                                                                                                                                                                                                                                                   ) OTHER INFORMATION: Description of Artificial Sequence: BoNT/a clone ; OTHER INFORMATION: 2G5 region VL epitope 2 US-09-144-886-88
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APPLICANT: Witte, Larry
TITLE OF INVENTION: Antibodies Specific to KDR and Uses Thereof
FITLE OF INVENTION: Antibodies Specific to KDR and Uses Thereof
FILE REFERENCE: 11245/46505
CURRENT APPLICATION NUMBER: US/09/976,787
CURRENT FILING DATE: 2001-10-12
PRIOR APPLICATION NUMBER: US 09/493,539
PRIOR FILING DATE: 2000-01-28
PRIOR FILING DATE: 1999-01-29
NUMBER OF SEQ ID NOS: 40
SOFTWARE: WordPerfect 8.0 for Windows
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 100.0%; Score 48; DB 10; Length 108; 100.0%; Pred. No. 0.03;
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CURRENT APPLICATION NUMBER: US/09/144,886
CURRENT FILING DATE: 1998-08-31
NUMBER OF SEQ ID NOS: 98
SEQ ID NO 88
LENGTH: 107
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                                                                                                                                                                                                 ORGANISM: Artificial Sequence
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GENERAL INFORMATION:
APPLICANT: Zhu, Zhenping
TITLE OF INVENTION: Bispecific Immunoglobulin-Like Antigen Binding Proteins and Me
TITLE OF INVENTION: Production
FILE OF INVENTION: Production
FILE REFERENCE: 11245/47102
CURRENT APPLICATION NUMBER: US/09/865,198
CURRENT FILING DATE: 2001-05-24
PRIOR APPLICATION NUMBER: US 60/206,749
PRIOR FILING DATE: 2000-05-24
NUMBER OF SEQ ID NOS: 34
SOFTWARE: WordPerfect 8.0 for Windows
SEQ ID NO 27
LENGTH: 240
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                                 Sequence 28, Application US/09976787; Sequence 28, Application US/09976787; Patent No. US20020064528A1
GENERAL INFORMATION:
APPLICANT: Stu, Zhenping; APPLICANT: Witte, Larry; TITLE OF INVENTION: Antibodies Specific to KDR and Uses Thereof; FILE REFERENCE: 11245/46505; CURRENT APPLICATION NUMBER: US/09/976,787; CURRENT APPLICATION NUMBER: US 09/493,539; PRIOR PILING DATE: 2000-1-28; PRIOR PELICATION NUMBER: US 60/117,726; PRIOR PELING DATE: 1999-01-29; NUMBER OF SEQ ID NOS: 40; SEQ ID NOS: 40; SEQ ID NO 28; SEQ ID NO 28; ELENTH: 240
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100.0%; Pred. No. 0.065;
iive 0; Mismatches 0;
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Best Local Similarity 100.
Matches 10; Conservative
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Best Local Similarity
Matches 10; Conserv
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APPLICANTE AND Shenping
TITLE OF INVENTION: Bispecific Immunoglobulin-Like Antigen Binding Proteins and Methor TITLE OF INVENTION: Bispecific Immunoglobulin-Like Antigen Binding Proteins and Methor TITLE OF INVENTION: Production
FILE REFERENCE: 11245/47102
CURRENT APPLICATION NUMBER: US/09/865,198
CURRENT FILING DATE: 2001-05-24
PRIOR APPLICATION NUMBER: US 60/206,749
PRIOR FILING DATE: 2000-05-24
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Sequence 29, Application US/09976787

Sequence 29, Application US/09976787

Sequence 29, Application US/09976787

Sequence 29, Application US/09976787

SETILE INFORMATION:

TITLE OF INVENTION: Antibodies Specific to KDR and Uses Thereof

TITLE OF INVENTION: Antibodies Specific to KDR and Uses Thereof

CURRENT APPLICATION NUMBER: US/09/976,787

CURRENT APPLICATION NUMBER: US 09/493,539

PRIOR FILING DATE: 2000-01-28

PRIOR FILING DATE: 1999-01-29

NUMBER OF SEQ ID NOS: 40

SOFTWARE: MORDER FELL WINDOWS
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                                          100.0%; Score 48; DB 10; Length 108; 100.0%; Pred. No. 0.03; cive 0; Mismatches 0; Indels
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; Pred. No. 0.00
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SOFTWARE; WordPerfect 8.0 for Windows
SEQ ID NO 98
LENGTH: 238
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Patent No. 10520020103345A1
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Best Local Similarity 100.
Matches 10% Conservative
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Best Local Similarity 100.
Matches 10; Conservative
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Matches $10; Conserv
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; ORGANISM: Mouse
US-09-865-198-28
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US-09-865-198-28
US-09-865-198-8
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LENGTH: 238
TYPE: PRTR
ORGANISM: MM
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PC4405 A48784 S17626 S17628

ALIGNMENTS

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December 23, 2002, 07:17:57; Search time 1.97674 Seconds (without alignments) 486.327 Million cell updates/sec
GenCore version 5.1.3
Copyright (c) 1993 - 2002 Compugen Ltd.
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Maximum DB seq length: 2000000000
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Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

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Database

kappa chain vappa Description SUMMARIES \$26341 PH1084 D38601 \$29590 \$11115 \$24214 \$29591 PS0072 S11114 S11120 KVMSX4 A30562 B30562 PT0398 PT0399 PT0400 PT0401 PT0402 ST11112 B54378 PS0071 B49049 Query Match Length DB Score Result Š.

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Gaps

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100.0%; Score 48; DB 2; Length 91; 100.0%; Pred. No. 0.0079; ive 0; Mismatches 0; Indels

Query Match 100. Best Local Similarity 100. Matches 10; Conservative

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TOUGH A A A A A A A A A A A A A A A A A A A	RESULT 1 State: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 21-Jan-2000 C; Species: Mus musculus (house mouse) C; Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 21-Jan-2000 C; Accession: S17629 R; Clackson, T; Hoogenboom, H.R.; Griffiths, A.D.; Winter, G. R; Clackson, T; Hoogenboom, H.R.; Griffiths, A.D.; Winter, G. R; Clackson, T; Hoogenboom, H.R.; Griffiths, A.D.; Winter, G. R; Clackson, T; Hoogenboom, H.R.; Griffiths, A.D.; Winter, G. R; Clackson, S17629 A; Title: Making antibody fragments using phage display libraries. A; Reference number: S17230; MUDD:91326098; PMD:1907718 A; Reference number: S17230; MUDD:91326098; PMD:1907718 A; Residues: 1-91 < CLA> CLA> C, Superfamily: immunoglobulin V region; immunoglobulin homology C; Superfamily: immunoglobulin homology < IMM> C; Keywords: heterotetramer; immunoglobulin C; Reywords: heterotetramer; immunoglobulin C;	RESULT 2 S17637 Ig Asappa chain V region - mouse C; Species: Mus musculus (house mouse) C; Species: Mus musculus (house mouse) C; Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 21-Jan-2000 C; Accession: S17637 R; Clackson, T: Hoogenboom, H.R.; Giffiths, A.D.; Winter, G. R; Clackson, T: Hoogenboom, H.R.; Giffiths, A.D.; Winter, G. R; Clackson, T: Hoogenboom, H.R.; Giffiths, A.D.; Winter, G. R; Title: Making antibody fragments using phage display libraries. A; Reference number: S17230; MUID:91326098; PMID:1907718 A; Reference tumber: S17637 A; Status: preliminary A; Molecule type: nucleic acid A; Residues: 1-91 < CLA> C; Superfamily: immunoglobulin V region; immunoglobulin homology C; Keywords: heterotetramer; immunoglobulin F; 8-B1/comain: immunoglobulin homology < C. DO CONTERNOR OF C. DO CONTENNOR OF C. DO CONTERNOR OF C. DO CONTERNOR OF C. DO CONTENNOR OF C.
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A;Title: Antibodies that are specific for a single amino acid interchange in a protei A;Reference number: S26309; WUID:91341421; PMID:1908510
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 R;Tillman, D.M.; Jou, N.T.; Hill, R.J.; Marion, T.N.
J. Exp. Med. 176, 761-779, 1992
A;Title: Both IgM and IgG anti-DNA antibodies are the products of clonally selective
A;Reference number: PH0971; MUID:92381444; PMID:1512540
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                                                                                                                                                                                                                                                                                                                                    S26341

Ig light chain V region - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Species: Mus musculus (house mouse)
C;Species: 19-War-1998 #sequence_revision 19-War-1998 #text_change 20-Jun-2000
C;Accession: S26341; S78448
R;Stark, S.E.; Caton, A.J.
J. Exp. Med. 174, 613-624, 1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ig light chain V region (clone 202.61) - mouse (fragment)
C;Species: Was musculus (house mouse)
C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 21-Jan-2000
C;Accession: PH1084
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Molecule type: mRNA
A;Residuss: 1-39,'R',41-97,'L' <CAT>
A;Cross-references: EMBL:X59179; NID:952311; PIDN:CAA41889.1; PID:91334060
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;11-84/Domain: immunoglobulin homology <IMM>
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A; Experimental source: B cell, strain [NZB x NZW]Fl
C; Superfamily: immunoglobulin V region; immunoglobulin homology
C; Keywords: immunoglobulin
F; 16-89/Domain: immunoglobulin homology <IMM>
                                                                           Length 94;
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                                                                                                                                 Indels
                                                              Score 48; DB 2; L. Pred. No. 0.0081;
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                                                                                                                            0; Mismatches
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A;Reference number: S78447
A;Accession: S78448
C;Keywords: heterotetramer; immunoglobulin F;16-89/Domain: immunoglobulin homology <IMM>
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A;Status: nucleic acid sequence not shown
                                                                        Query Match
Best Local Similarity 100.0%;
Matches 10; Conservative 0
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A;Residues: 1-97 <STA>
A;Cross-references: EMBL:X59179
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Matches 10; Conservative
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24 SASSSVSYMH 33
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Best Local Similarity
Matches 10; Conserv
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C; Species: Mus musculus (house mouse)
C; Date: 20.Peb-1995 #sequence_revision 20.Peb-1995 #text_change 23-Jul-1999
C; Accession: $20050
R; Losman, M.; Fasy, T.M.; Novick, K.E.; Monestier, M.
Submitted to the EMBL Data Library, February 1992
A; Description Relationships among antinuclear antibodies from autoimmune MRL mice react A; Reference number: $20050
A; Accession: $20050
A; Status: prepliminary
A; Molecule type: DNA
A; Residues: 1-94 <LOS>
A; Molecule type: DNA
A; Residues: 1-94 <LOS>
C; Superfamily; immunoglobulin V region; immunoglobulin homology
C; Keywords: heterotetramer; immunoglobulin
F; L6-89/Domain; immunoglobulin homology <LMM>
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(Species: Mus musculus (house mouse)
(SACCESSION: $20.Feb-1995 #sequence_revision 20-Feb-1995 #text_change 23-Jul-1999
(SACCESSION: $20.Feb-1995 #sequence_revision 20-Feb-1995 #text_change 23-Jul-1999
(SACCESSION: Relationships among antinuclear antibodies from autoimmune MRL mice react A; Reference number: $20639
(A; Reference number: $20639
(A; Residues: Breat. A; Reference number: Breat. A; Residues: Breat. X65009; NID: 952651; PIDN: CAA46142.1; PID: 952652
(Superignibly: immunoglobulin V region; immunoglobulin homology
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                                                                                                                    G. Species: Most musculus (house mouse)
C. Date: 22-Nov:1993 #sequence_revision 10-Nov-1995 #text_change 21-Jan-2000
C. Accession: 3.7639
Nature 352, 624, 628, 1991
A. Title: Making antibody fragments using phage display libraries.
A. Reference number: $17230; MUID: 91326098; PMID: 1907718
A. Accession: $17639
A. Status: preliminary
A. Molecule type: nucleic acid
A. Residues: 1-91 < CLA>
C. Superfamily: immunoglobulin V region; immunoglobulin homology
C. Keywords: heterotetramer: immunoglobulin
F: 8-81/Domain: immunoglobulin homology < NAMA>
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Pred. No. 0.0079;
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100.0%; Pred. No. 0.0081;
ive 0; Mismatches 0.
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100.0%; Pred. No. 0.00
+ive 0; Mismatches
                                                                                                   Ig kappa chain V region - mouse
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Best Local Similarity 100.
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Best Local Similarity 100.

Matches 10; Conservative
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Tyrile: Deletions of immunoglobulin (Kappa) region characterized by the circular expected type: S24214

R:Shimizu, T.; Iwasato, T.; Yamagishi, H.

R:Shimizu, T.; Iwasato, T.; Yamagishi, H.

R:Shimizu, T.; Iwasato, T.; Vamagishi, H.

R:Shimizu, T.; Iwasato, T.; Vamagishi, H.

R:Shimizu, T.; Iwasato, T.; Vamagishi, H.

R:Shimizu, T.; Iwasato, T.; Yamagishi, H.

R:Status: preliminary; translation not shown

A; Residues: 1-102 <SHY>

Residues: 1-102 <SHY>
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C; Species: Mus musculus (house mouse)
C; Species: J9-Dec-1993 #sequence_revision 18-Nov-1994 #text_change 21-Jan-2000
C; Accession: B49049
C; Accession: B49040
R; Armandola, E.A.; Mariani, S.M.; Zwickl, M.; Hardman, N.; Ferrone, S.
Eur. J. Immunol. 22, 2893-2899, 1992
A; Title: Molecular analysis of anti-idiotypic monoclonal antibodies in the HLA-DR ant
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C; Species: Mus musculus (house mouse)
C; Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 21-Jan-2000
C; Accession: S29591
R; Kavaler, J.
Submitted to the EMBL Data Library, April 1991
A; Reference number: S26459
A; Accession: S29591
A; Status: preliminary
A; Molecule type: mRNA
A; Residues: 1-103 < KAV>
                                                                           Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ouery Match 100.0%; Score 48; DB 2; Length 102; Best Local Similarity 100.0%; Pred. No. 0.0089; Matches 10; Conservative 0; Mismatches 0; Indels
100.0%; Score 48; DB 2; Length 102; 100.0%; Pred. No. 0.0089;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Cross-references: EMBL:X58204
C;Superfamily: Immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;14-87/Domain: immunoglobulin homology <IMM>
                                                                        Mismatches
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                                                                           Conservative
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Best Local Similarity
Matches 10; Conserv
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                                     Best Local Similarity
Matches 10; Conser
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   Query Match
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S24214
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                                                                                       Ig kappa chain V region (6A7) - mouse (fragment)
C; Species: Mus musculus (house mouse)
C; Species: Mus musculus (house mouse)
C; Date: 30-Aug-1991 #sequence_revision 30-Aug-1991 #text_change 21-Jan-2000
C; Accession: D38601
R; Goshorn, S.C.; Retzel, E.; Jemmerson, R.
J. Biol. Chem. 266, 2134-2142, 1991
A; Title: Common structural features among monoclonal antibodies binding the same antigen A; Reference number: A38601; MUD:91115823; PMID:1703527
A; Accession: D38601
A; Residues: preliminary
A; Molecule type: mRNA
A; Residues: 1-99 -GOS>
A; Molecule type: mRNA
A; Residues: 1-99 -GOS
C; Superfamily: immunoglobulin V region; immunoglobulin homology
C; Superfamily: immunoglobulin homology < IMM>
C; Keywords: heterotetramer; immunoglobulin homology < IMM>
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C;Species: Mus musculus (house mouse)
C;Species: Mus musculus (house mouse)
C;Date: 19-Mar-1997 #sequence_revision 18-Jul-1997 #text_change 21-Jan-2000
C;Accession: S11115
R;Kaartinen, M.; Griffiths, G.M.; Markham, A.F.; Milstein, C.
Nature 304, 320-324, 1983
A;Title: mRNA sequences define an unusually restricted IgG response to 2-phenyloxazolone
A;Reference number: S07331; MUID:83271467; PMID:6877353
A;Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Systy of kappa chain V region - mouse () Species: Mus musculus (house mouse) () Species: No. 1995 #sequence_revision 06-Jan-1995 #text_change 21-Jan-2000 () Accession: S29590 () R. Kavaler, J. Submitted to the EMBL Data Library, April 1991 () A. Reference number: S26459 () A. Status: preliminary () A. Molecule type: mRNA () A. Molecule type: mRNA () Residual () C. Kavales: 1-100 () C. Kavales: 1-100 () C. Kavales: 1-100 () C. Keywords: heterotetramer: immunoglobulin () F:16-89/Domain: immunoglobulin homology () F:16-89/Domain: immunoglobulin homology () C. Keywords: heterotetramer: immunoglobulin homology () RMA () C. Keywords: heterotetramer: immunoglobulin homology () C. Keywords: heter
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A;Residues: 1-102 <KAA.
C;Superfamily: immunoglobulin V region; immunoglobulin homology
F;16-84/Domain: immunoglobulin homology <IMMA
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Pred. No. 0.0086;
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C. Species: Musramusculus (house mouse)
C. Accession: B54378
R. Agazie, Y. M. E. Lee, J.S.; Burkholder, G.D.
J. Biol. Cham. 269, 7019-7023, 1994
A.71tle: Characterization of a new monoclonal antibody to triplex DNA and immunofluoresc
A.Reference number: A54378; MUD:94165109; PMID:7509814
A.Reference number: A54378; MUD:94165109; PMID:7509814
A.Reference number: A54378; MUD:94165109; PMID:7509814
A.Reference number: A54378
A.Reference number: A54378
A.Reference number: A54378; MUD:9545746; PIDN:ABB30096.1; PID:9545747
A.Respecimental cource: spleen and myeloma cell line MOPC 315.43
A.Rote: Sequence inconsistent with nucleotide translation
A.Note: Sequence inconsistent with nucleotide translation
A.Note: Sequence inconsistent with nucleotide translation
C. Superfamily: immunoglobulin V region: immunoglobulin homology
C. Superfamily: immunoglobulin homology <IMM>
F:16-89/Domain: immunoglobulin homology <IMM>
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A; Reference number: A49049; MUID:93049629; PMID:1425914
A; Accession: B49049
A; Status: preliminary
A; Molecule type; nucleic acid
A; Residues: 1-104
A; Residues: 1
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A; Status: translation not shown
A; Status: translation not shown
A; Molecule type: DNA
A; Residues: 1100 < LEV>
C; Superfamily: immunoglobulin V region; immunoglobulin homology
C; Keywords: heterotetramer; immunoglobulin
F; 16-89/Domain: immunoglobulin homology < IMM>
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100.0%; Pred. No. 0.0091;
ive 0; Mismatches 0; Indels
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Qy 1 SASSSVSTMH 10
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Db 24 SASSSVSTMH 33
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Search completed: December 23, 2002, 07:31:35 Job time: 1.97674 secs

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December 23, 2002, 07:16:17; Search time 0.988372 Seconds (without alignments) 419.643 Million cell updates/sec
GenCore version 5.1.3 Copyright (c) 1993 - 2002 Compugen Ltd.
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US-09-865-198-4 48 1 SASSSVSYMH 10 Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

112892 seqs, 41476328 residues Searched:

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SwissProt_40:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

STIMMARTES

	Description	P01675 mus musculu	P01676 mus musculu	P01677 mus musculu	P01678 mus musculu	P04940 mus musculu	P04941 mus musculu	PO4942 mus musculu	PO4943 mus musculu	P04944 mus musculu	P04945 mus musculu	mus	_		_	P82231 spinacia ol	homo	_	camp		P92953 arabidopsis	Q58245 methanococc	_		P54637 dictyosteli		Q9plb0 chlamydia m		O88410 mus musculu	2		Q99289 vibrio para		027509 methanobact
SUMMARIES	ΠD	KV6A_MOUSE	KV6B_MOUSE	KV6C_MOUSE .	KV6D_MOUSE	KV6F_MOUSE	KV6G_MOUSE	KV6H_MOUSE	KV61_MOUSE	KV6J_MOUSE	KV6K_MOUSE	KV6E_MOUSE	KV4A_MOUSE	ALYS_BPR1T	BGAL_MALDO	RRF_SPIOL	CBG_HUMAN	DUS4_HUMAN	SLAP_CAMFE	YLME_BACSU	ATH4_ARATH	Y835_METJA	MVIN_HELPJ	MVIN_HELPY	PTP3_DICDI	ZMS1_YEAST	PMPD_CHLMU	NUKM_ARATH	CCR3_MOUSE	CCR3_HUMAN	CBG_RABIT	HLT_VIBPA	FUT9_ARATH	COBB_METTH
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KV6B_MOUSE
ID KV6B_MOUSE STANDARD; PRT; 107 AA.
C P01676;
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 1-JUL-1999 (Rel. 38, Last annotation update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
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Pfam; PF00047; ig; 1.
SMART; SM00406; IGv; 1.
Immunoglobulin V region
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                                                                                                           Bicchemistry 17:5555-5559(1978).
-!- MISCEGLANEOUS: THIS CHAIN WAS ISOLATED FROM A MYELOMA PROTEIN THAT
BIND GALACTAN.
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MEDLINEÉRIOSATST; PubMed-6776525;
Rudikoff S., Rao D.N., Glaudemans C.P.J., Potter M.;
Rappa chain joining segments and structural diversity of antibody combining sites.";
Proc. Nätl. Acad. Sci. U.S.A. 77:4270-4274(1980).
-: MISGELLANEOUS: THE TWO SEQUENCES ARE IDENTICAL.
-: MISGELLANEOUS: THESE CHAINS WERE ISOLATED FROM MYELOMA PROTEINS
Mus musculůs (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID;10090;
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21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
15-JUL-1999 (Rel. 38, Last annotation update)
15-JUL-1999 (Rel. 38, Last annotation update)
Mus musculus (Mouse).

Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia, Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus
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MEDLINE 99082830; PubMed=103573;
Rao D.N., Rudikoff S., Potter M.;
"k Chain variable regions from three galactan binding myeloma
                                                                  MEDLINE-79082830; PubMed-103573;
Rao D.N., Rudikoff S., Potter M.;
"k Chain variable regions from three galactan binding myeloma
proteins.";
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COMPLEMENTARITY-DETERMINING-1.
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COMPLEMENTARITY-DETERMINING-2.
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HSSP, P01679; 2FBJ.
InterPro; IPR003006; Ig_MHC.
InterPro; PR003596; Ig_V.
Pfam; PF00047; ig; 1.
SMART; SMQ0406; IGV; 1.
Immunoglobulin V region.
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HSSP; P01679; ZFBJ.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_V.
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-!- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM A MYELOMA PROTEIN THAT BIND GALACTAN.
PIR, A01941; KWSX4.
HSSP; P01679; 2FBJ.
InterPro; IPR003006; Ig_MC.
InterPro; IPR003596; Ig_V.
Fam; PF00047; ig.1.
SWART; SM00406; IGv; 1.
Immunoglobulin V region.
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
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FRAMEWORK-1.
COMPLEMENTARITY-DETERMINING-1.
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COMPLEMENTARITY-DETERMINING-2.
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COMPLEMENTARITY - DETERMINING - 3.
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21-JUL-1996 (Rel. 01, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
18 Kappa chain V-VI region SAPC 10.
Mus musculus (Mouse).
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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Kaartinen M., Griffiths G.M., Markham A.F., Milstein C.;
"mRNA sequences define an unusually restricted IgG response to 2-
phenyloxazolone and its early diversification.";
Nature 304:320-324(1983).
-: FUNCTION: ANTI-2-PHENYL OXAZOLONE (PHOX) ANTIBODY.
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    !- FUNCTION: ANTI-2-PHENYL OXAZOLONE (PHOX) ANTIBODY
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13-AUG-1987 (Rel. 05, Last sequence update)
13-UUL-1999 (Rel. 38, Last annotation update)
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SMART; SM00406; IGv; 1.
Immunoglobulin V region; Hybridoma.
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InterPro: IPR003006; Ig_MHC.
InterPro: IPR003596; Ig_v.
Pfam: PF00047; Ig; 1.
SMART; SM00406; IGv; 1.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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MEDLINE-83271465; PubWed-6877353;
Kaartinen M., Griffiths G.M., Markham A.F., Milstein C.;
"mRNA sequences define an unusually restricted IgG response to 2-phenyloxazolone and its early diversification.";
Nature 304:320-324(1983).
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Kaartinen M., Griffiths G.M., Markham A.F., Milstein C.;
"mRNA sequences define an unusually restricted IgG response to
phenyloxazzolone and its early diversification.";
Nature 304:320-324(1983).
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Pred. No. 0.0034;
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                                     13-AUG-1987 (Rel. 05, Created)
13-AUG-1987 (Rel. 05, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  73-74.7.
13-AUG-1987 (Rel. 05, Last sequence update)
13-AUG-1999 (Rel. 38, Last annotation update)
15-UUL-1999 (Rel. 38, Last annotation update)
Mus musculus (Mouse).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               107 AA.
107 AA
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BY SIMILARITY.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FRAMEWORK-2
                                                                                                             Ig kappa chain V-VI region NQ2-17.4.1.
PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Immunoglobulin V region; Hybridoma
DOMAIN 1 23 FRAME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     11561 MW;
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InterPro; IPR003596; Ig_V.
Pfam; PF00047; ig; 1.
SMART; SM00406; IGv; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       100.08;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STANDARD;
  STANDARD;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   107 AA;
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es 10; Conser'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 SASSSVSYMH 10
                                                                                                                                                                                                   NCBI_TaxID=10090;
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  KV6F_MOUSE
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NON_TER
SEQUENCE
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DOMAIN
DOMAIN
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Gaps

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24 SASSSVSYMH 33
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P04945;
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KV6K_MOUSE
                                    KV6J_MOUSE
                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches
                            RESULT 9
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                                                                                                             Gaps
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                                                                                                                                                                                                                                             Eukaryota: Metazoa; Chordata; Cranlata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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                                                                                          ; Score 48; DB 1; Length 107;
; Pred. No. 0.0034;
0; Mismatches 0; Indels
FRAMEWORK-1.
COMPLEMENTARITY-DETERMINING-1.
                FRAMEWORK-2.
COMPLEMENTARITY-DETERMINING-2.
                                 FRAMEWORK-3.
COMPLEMENTARITY-DETERMINING-3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPLEMENTARITY-DETERMINING-1. FRAMEWORK-2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     100.0%; Score 48; DB 1; Length 107; 100.0%; Pred. No. 0.0034; Ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPLEMENTARITY - DETERMINING - 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FRAMEWORK-3.
COMPLEMENTARITY-DETERMINING-3.
                                                                          11605 MW; CA6C4284ECFCB550 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     11572 MW; 6F694824ECF0C8E6 CRC64;
                                                                                                                                                                                                    13-AUG-1987 (Rel. 05, Created)
13-AUG-1987 (Rel. 05, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
Ig kappa chain V-VI region NQ6-8.3.1
                                                                                                                                                                                      107 AA
                                                           BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FRAMEWORK-4.
BY SIMILARITY.
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                                                  FRAMEWORK-4
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HSSP; P01679; ZFBJ.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_V.
                                                                                           100.0%;
                                                                                                             Conservative
                                                                                                                                                                                      STANDARD;
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DOMAIN 1 23
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23
33
48
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87
96
106
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SMART; SM00406; IGv; 1.
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33
87
87
106
107
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88
97
23
107
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nes 10; Conserv
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DOMAIN
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                                         DOMAIN
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Matches
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                                                                                                                                                                                                                                                         [1]

MEDLINE-83271467; PubMed=6877353;
Kaartinen M., Griffiths G.M., Markham A.F., Milstein C.;
Kaartinen M., Griffiths G.M., Markham A.F., Milstein C.;

MENA Sequences define an unusually restricted 1gG response to 2-

"mENA Sequences and its early diversification.";

Phenyloxazolone and its early diversification.";

Nature 304:320.324(1983).

-I FUNCTION: ANTI-2-PHENYL OXAZOLONE (PHOX) ANTIBODY.
                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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                                                                           13-AUG-1987 (Rel. 05, Last sequence update)
15-UUL-1999 (Rel. 38, Last annotation update)
15 kappa chain V-VI region NQ5-78.2.6.
Mus musculus (Mouse).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Add-1987 (Rel. 05, Created)
13-AdC-1987 (Rel. 05, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
18 Kappa chain V-VI region NQ2-6.1.
Mus musculus (Mouse).
     107 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SMART; SM00405; 16v, ...
Immunoglobulin V region; Hybridoma.
23 FRAMEWORK-1.
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                                                   13-AUG-1987 (Rel. 05, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; K00744; AAA38689.1; -. HSSP; P01679; 2FBJ.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_v.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local Similarity 100.
mes 10; Conservative
     STANDARD;
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SMART; SM00406; IGv; 1.
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SEQUENCE FROM N.A.
                                                                                                                                                                                                                                       NCBI_TaxID=10090;
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KV6J_MOUSE
P04944;
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KV4A_MOUSE
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DISULFID
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                                                          This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch/
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -!- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM A MYELOMA PROTEIN THAT
                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "The galactan-binding immunoglobulin Fab J539: an X-ray diffraction study at 2.6-A resolution.";
Proteins 1:74-80(1986).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Suh S.W., Bhat T.N., Navia M.A., Cohen G.H., Rao D.N., Rudikoff S., Davies D.R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Rudikoff S., Rao D.N., Glaudemans C.P.J., Potter M.;
"Kappa Chain joining segments and structural diversity of antibody
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
MEDLINE-83271467; PubMed-6877353;
Kaartinen M., Griffiths G.M., Markham A.F., Milstein C.;
mrNa sequences define an unusually restricted IgG response to 2-
phenyloxazolone and its early diversification.";
Nature 304:320-324(1983).
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0
                                                                                                                                                                                                                                    FRAMEWORK - 2.
COMPLEMENTARITY - DETERMINING - 2.
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COMPLEMENTARITY-DETERMINING-3.
                                                                                                                                                                                                                          COMPLEMENTARITY - DETERMINING - 1.
                                                                                                                                                                                                                                                                                                                            Score 42; DB 1; Length 108; Pred. No. 0.061;
                                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                         DABF235CD9680AC6 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
18 Appa chain V-VI region J539.
Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                          107 AA
                                                                                                                                                                                                                                                                                      BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                       Pred. No. 0.06
1; Mismatches
                                                                                                                                                                                                                FRAMEWORK-1.
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MEDLINE-88217852; PubMed-3449853;
                                                                                                                                                                              Pfam; PF00047; 19; 1.
SMART; SM00406; IGV; 1.
Immunoglobulin V region; Hybridoma
                                                                                                                                                                                                                                                                                                                                                                                                                                          PRT;
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                                                                                                                                                                                                                                                                                                          11713 MW;
                                                                                                                                         EMBL; K00746; AAA38691.1; -. HSSP; P01679; 2FBJ.
                                                                                                                                                                                                                                                                                                                            87.5%;
90.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PDB; 2FBJ; 15-OCT-90.
InterPro; IPR003006; Ig_MHC.
                                                                                                                                                            InterPro; IPR003006; Ig_MHC InterPro; IPR003596; Ig_v.
                                                                                                                                                                                                                                                                                                                                       Local Similarity 90.0 nes 9; Conservative
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PIR; A01942; KVMSJ5.
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P01679;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -i- MISCELLANEOUS: THIS PROTEIN, IN WHICH THERE IS A DELETION OF TWO AMINO ACIDS AT THE V-J RECOMBINATION SITE (AFTER POSITION 118), IS SYNTHESIZED BUT NOT SECRETED IN CELLS THAT EXPRESS AND SECRETE THE NORMAL KAPPA CHAIN S107.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
MEDLINE-82115300; PubMed-6799208;
Kwan S.-P., Max E.E., Seidman J.G., Leder P., Scharff M.D.;
Kwan Kappa immunoglobulin genes are expressed in the myeloma $107.";
Cell 26:57-66(1981).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ;
0
                                                                                             COMPLEMENTARITY - DETERMINING - 1.
                                                                                                                                                 FRAMEWORK - 3.
COMPLEMENTARITY - DETERMINING - 3.
FRAMEWORK - 4.
                                                                                                                              COMPLEMENTARITY - DETERMINING - 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 36; DB 1; Length 107; Pred. No. 1.1; 1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             11502 MW; EA30C9A3E903979C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          21-JUL-1986 (Rel. 01, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
19 kappa chain V-IV region S107B precursor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     129 AA.
                                                                            FRAMEWORK - 1.
                                                                                                              FRAMEWORK-2
                                                         3D-structure
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last seq
15-JUL-1999 (Rel. 38, Last anno
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  75.0%;
80.0%;
InterPro; IPR003596; Ig_v. Pfam; PF00047; ig; 1. SMART; SM00406; IGv; 1. Immunoglobulin V region; 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 75.0
Best Local Similarity 80.0
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STANDARD;
                                                                                                                                                                                                                                     233
333
348
87
87
87
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87
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 SASSSVSYMH 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           24 SASSSVSSLH 33
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Gaps

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Indels

5

Mismatches

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Conservative
 9:
                                                                                                  BGAL_MALDO
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ACT_SITE
ACT_SITE
SEQUENCE
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                                                                            RESULT 14
BGAL_MALDO
                                                                                                             P48981
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RRF_SPIOL
                                           40
 Matches
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                                                                                                                                                                                                                                                                           ij
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Venema G., Nauta A.;
"Sequence analysis and molecular characterization of the temperate lactococcal bacteriophage rlt.";
MOI. Migrobiol. 19:1343-1355(1966).
--I- CATALYTIC ACTIVITY: Hydrolyzes the link between N-acetylmuramoyl resigues and L-amino acid residues in certain bacterial cell-wall
                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     glygopeptides.
SIMILARITY: BELONGS TO THE N-ACETYLMURAMOYL-L-ALANINE AMIDASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE 96332669; PubMed-8730875;
Van Sinderen D., Karsens H., Kok J., Terpstra P., Ruiters M.H.,
                                                                                                                                                                                                                                                                           5
                                                                                                                     IG KAPPA CHAIN V-IV REGION S107B.
                                                                                                                                           COMPLEMENTARITY - DETERMINING - 1.
                                                                                                                                                                 COMPLEMENTARITY - DETERMINING - 2.
                                                                                                                                                                                       COMPLEMENTARITY - DETERMINING - 3.
                                                                                                                                                                                                                                                   Score 34; DB 1; Length 270; Pred. No. 7.7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             InterPropi IPR002502; Amidase_2.
Pram. pr01510; Amidase_2; 1.
Hydrolase; Cell Wall.
SEQUENÇE 270 AA; 30214 MW; 80A5E38F7F2A6675 CRC64;
                                                                                                                                                                                                                                13833 MW; E4BB73072DCF6BE4 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                           01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
N-acetylmuramcyl-L-alanine amidase (EC 3.5.1.28).
Bacterloghage rlt.
                                                                                                                                                                                                            BY SIMILARITY.
                                                                                                                                                                             FRAMEWORK - 3
                                                                                                                                                                                                 FRAMEWORK - 4
                                                                                                                                                                                                                                                                                                                                                                          PRT;
                              PIR; A01943; KVMS7B.
HSSP; P01679; ZFBJ.
InterPro; TPR003006; Ig_MHC.
InterPro; TPR003596; Ig_W.
Pfam; PP00047; Ig; 1.
Pfam; SM00406; IGv; 1.
Immunoglobulin V region; Signal.
          EMBL; J00577; AAA38780.1; -. EMBL; V00780; CAA24157.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   70.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; U38906; AAB18724.1;
                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                          STANDARD;
                                                                                                                                                                                                                                                                                                           46 SASSSVSSSYLH 57
                                                                                                                                                                                                                    129
129 AA;
                                                                                                                                                                                                                                                              Local Similarity
es 9; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                               SASSSV - - SYMH
                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_Tax ID-43685;
                                                                                                                                                                                                                                                                                                                                                                        ALYS_BPR1T
Q38135;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FAMÎLY
                                                                                                                                                                                                                      NON_TER
SEQUENCE
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                                                                                                           SIGNAL
                                                                                                                                           DOMAIN
                                                                                                                                                       DOMAIN
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
STRAIN-CV. Granny Smith; TISSUE-Fruit cortical tissue;
STRAIN-CV. Granny Smith; TISSUE-Fruit cortical tissue;
MFDLINE-9508375; Pubmed-7991682;
Ross G.S., Wegrzyn T., Macrae E.A., Redgwell R.J.;
Ross G.S., Wegrzyn T., Macrae E.A., Redgwell R.J.;
Apple beta-galactosidase. Activity against cell wall polysaccharides and characterization of a related cDNA clone.";
Plant Physiol. 106:521-528(1994).
-!- FUNCTION: Involved in cell wall degradation. Degrades polysaccharides containing beta-(1->4)-linked galactans, acting as an exo-(1->4)-beta-D-galactanase.
-!- CATALYIC ACTIVITY: Hydrolysis of terminal, non-reducing beta-D-galactose residues in beta-D-galactosides.
-!- SIMILARITY: BELONGS TO FAMILY 35 OF GLYCOSYL HYDROLASES.
                                                                                                                                                                                                                                                                                            01-FEB-1996 (Rel. 33, Created)
01-FEB-1996 (Rel. 33, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
15-JUN-2002 (Rel. 41, Last annotation update)
Beta-galactosidase precursor (EC 3.2.1.23) (Lactase) (Acid beta-galactosidase) (Exo-(1-->4)-beta-D-galactanase).
Malus domestica (Apple) (Malus sylvestris).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids I; Rosales; Rosaceae; Malus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
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302231; 09X697;
30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Ribosome recycling factor, chloroplast precursor (Ribosome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   70.8%; Score 34; DB 1; Length 731; ilarity 70.0%; Pred. No. 22; Conservative 2; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               BETA-GALACTOSIDASE.
PROTON DONOR (POTENTIAL).
NUCLEOPHILE (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FAB65D24A0D30BD4 CRC64;
                                                                                                                                                                                                                                          731 AA.
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Pfam: PF01301; Glyco_hydro_35; 1.
PRNUTS; PR00742; GLHVDRAASB35.
PROSITE: PS01182; GLYCOSYL_HYDROL_F35; 1.
Hydrolase; Glycosidase; Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               POTENTIAL
                                                                                                                                                                                                                                          PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      80995 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; L29451; AAA62324.1;
                                                                                                                                                                                                                                          STANDARD;
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1 SASSSVSYMH 10
                                          ||:: ||||
SATNEASYMH 49
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Matches 7; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 SASSSVSYMH 10
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21 AASASVSYDH 30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=3750;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             Yamaguchi K., Subramanian A.R.; The plastid ribosomal proteins. Identification of all the proteins in the plastid ribosomal proteins. Identification of all the proteins in the 50 s.mbunit of an organalle ribosome (chloroplast)."; J. Biol. Chem. 275:28466-28482(2000).
J. Biol. Chem. 275:28466-28482(2000).
FUNCTION: RESPONSIBLE FOR THE RELEASE OF RIBOSOMES FROM MESSENGER RNA AT THE TERMINATION OF CHLOROPLASTIC PROTEIN BIOSYNTHESIS (BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SIMILARITY).

- SUBCELLULAR LOCATION: CHLOROPLAST. THE MAJOR PART WAS FOUND IN THE STROMA AND SOME PROTEIN WAS IN THE ENVELOPE SUBFRACTION, BUT NO PROTEIN WAS DETECTED IN THE THYLAKOIDS.
- TISSUE SPECIFICITY: RESTRICTED TO PHOTOSYNTHETIC TISSUES.
- MISCELLANEOUS: EXPRESSION SCEMS TO BE LIGHT-INDEPENDANT.
- SIMILARITY: BELONGS TO THE RRP FAMILY.
                                                                                                                                                                                                                                        Rolland N., Janosl L., Block M.A., Shuda M., Teyssier E., Miege C., Cheniclet C., Carde J.-P., Kaji A., Joyard J.;

Cheniclet C., Carde J.-P., Kaji A., Joyard J.;

"Plant ribosome recycling factor homologue is a chloroplastic protein and is bactericidal in Escherichia coli carrying temperature-sensitive ribosome recycling factor."

Proc. Natl. Acad. Sci. U.S.A. 96:5464-5469(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                       Spinacia oleracea (Spinach).
Eukaryota: Viridiplantae: Streptophyta: Embryophyta: Tracheophyta;
Eukaryota: Magnoliophyta; eudicotyledons; core eudicots;
Caryophyllidae: Caryophyllales: Chenopodiaceae; Spinacia.
NCBI_TaxID=3562;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
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Pred. No. 12;
2; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                InterPro; IPR02561; RRF.
Pfam; PF01765; RRF; 1.
TIGRFAMS; TIGR00496; fir: 1.
Protein biosynthesis; Transit peptide; Chloroplast.
TRANSIT 78 CHLOROPLAST.
CHAIN 79 271 RIBOSOME RECYCLING FACTOR.
SEQUENCE 271 AA; 30431 MW; F7D3012BB90AD175 CRC64;
releasing factor, chloroplast) (RRF) (CpFrr) (RRFHCP).
                                                                                                                                                                            SEQUENCE FROM N.A., AND SEQUENCE OF 79-88.
                                                                                                                                                                                              TISSUE-Leaf;
MEDLINE-99254063; PubMed=10318906;
                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE OF 79-99 AND 194-217.
STRAIN=cv. Alwaro; TISSUE=Leaf;
PubMed=10874046;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; AJ133751; CAB41419.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     68.8%;
60.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   5 SLSSATSYLH 14
                      RRF OR FRRHCP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches
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Search completed: December 23, 2002, 07:26:06 Job time : 1.98837 secs

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Q951C7 arabidopsis
017720 caenorhabdi
09vc32 drosophila
018137 caenorhabdi
095zy7 caenorhabdi
09m3c7 arabidopsis
09m3c7 arabidopsis
09wk13 drosophila
09kk12 bacillus ha
09kvy9 vibrio chol
                                                                                                                                                                                                                                                                                                     Q9nswl homo sapien
Q9k9pl bacillus ha
Q8x0d9 neurospora
                                                                                                                                                                                                                                                              Q9sa31 arabidopsis
Q19536 caenorhabdi
O74060 cenarchaeum
                                                                                                                                                                                                                                                                                                                                           Q13649 homo sapien
Q9rk08 streptomyce
Q9k3j1 streptomyce
              Q9s197 arabidopsis
                                                                             Q991c4 mus musculu
Q97tf8 clostridium
                                       094664 schizosacch
                                                   Q9mm74 acanthodact
Q9amn1 clostridium
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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0
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Pred. No. 0.026;
1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "Targeting T cells to the CNS.";
Submitted (JAN-2002) to the EMBL/GenBank/DDBJ databases.
EMBL, A416331; CAC94866.1; -.
InterPro; IPR003599; Ig.
InterPro; IPR003599; Ig.
InterPro; IPR003599; Ig.
Flam: PF00047; ig. 1.
SMART; SM00409; IG; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Chernajovsky Y.; Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             134 134 AA; 14525 MW; CFDF8E2236E2D0CF CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 08VDD0,
01-MAR-2002 (TrEMBLrel. 20, Created)
01-MAR-2002 (TrEMBLrel. 20, Last sequence updi
01-JUN-2002 (TrEMBLrel. 20, Last sequence updi
01-JUN-2002 (TrEMBLrel. 21, Last annotation updi
MATI-MOG Z12 variable light chain (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                              ALIGNMENTS
                                                                                                                                                                                  Q9M3C7
Q9SIH6
Q9VK13
                                                                                                                                                                                                                        Q9KBL2
Q9KRV9
O97455
Q9SA31
Q19536
Q94LS3
Q9SL97
Q9JL78
O94664
                                                               Q9AMN1
Q99LC4
Q97TF8
Q95LC7
Q17720
Q9VC32
Q18137
Q95ZY7
                                                                                                                                                                                                                                                                                                                                                          Q9RK08
                                                                                                                                                                                                                                                                                                                   Q9K9P1
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                                                   Q9MM74
                                                                                                                                                                                   97.9%;
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 SASSSVSYMH 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
 NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRAIN-BALB/C;
 Sembi P.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 1
  08VDD0
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Q9j176 mus musculu
Q91w12 mus musculu
                                                                                                      (without alignments)
496.824 Million cell updates/sec
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                                                                                        December 23, 2002, 07:17:27 ; Search time 4.14729 Seconds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Description
             GenCore version 5.1.3
Copyright (c) 1993 - 2002 Compugen Ltd
                                                                                                                                                                                                                                                             Potal number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                     671580 seqs, 206047115 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SUMMARIES
                                                                                                                                                                                                                                                                                                                             Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                 OM protein - protein search, using sw model
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091102
091102
090410
0990429
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008003
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098115
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sp_mammal:*
sp_mhc:*
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sp_vertebrate:*
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sp_archeap:*
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sp_bacteria:*
sp_fung1:*
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Maximum DB seq length: 200000000
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sp_rodent:*
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Match Length DB
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48
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46 SASSSVSHMH 55
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=1665;
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NON_TER
SEQUENCE
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                                                                090410;
                                                      Q9U410
                                     RESULT 4
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                                                                                                                                                                                                                                                                                                                                                                                                                             091W12 PRELIMINARY, PRT; 235 AA.
091W12;
091W12;
091W12;
091W12;
091W12;
091W12;
091W12;
01-DEC-2001 (TEMBLrel. 19, Last sequence update)
01-MAR-2002 (TEMBLrel. 20, Last annotation update)
01-MAR-2002 (TEMBLrel. 20, Last annotation update)
Mus musculus (Mouse).
Mus musculus (Mouse).
EUKAryota: Metazoa, Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus.
                                                                                                                 Mus musculus (Mouse).
Eukaryotaj Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                 ö
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Pred. No. 0.34;
1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                              Score 44; DB 11; Length 97;
Pred. No. 0.082;
0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Strausberg R.;
Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases.
Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; BC006643 AAH0643.1;
InterPro; IPR003006; Ig_MHC.
Pfam; PF00047; Ig; 2.
PROSITE; PS002090; IG_MHC; UNKNOWN I.
SEQUENÇE 235 AA; 26021 MW; 5FC73BDEBD5E8FEF CRC64;
                                                                      01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-DCC-2001 (TrEMBLrel. 19, Last annotation update)
Anti-myosan immunoglobulin 11ght chain variable region
                                                                                                                                                                                                                                                                                                    97 97
97 AA; 10542 MW; C9EE1FFEJF49DA1C CRC64;
                                                      97 AA.
                                                      PRT;
                                                                                                                                                                                 MEDLINE-20448942; PubMed-10992488;
                                                                                                                                                                                                                                                                                                                       91.7%; Scur
100.0%; Pred
0; N
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        89.68;
90.08;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ouery Match
Best Local Esimilarity 90.0
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                   Local Similarity 100.
                                                      PRELIMINARY;
                                                                                                                                                                                                                                                                           Pfam; PF00047; ig; 1.
SMART; SM00406; IGv; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENĈE FROM N.A.
TISSUE≜BREAST TUMOR;
46 SASSŠISYMH 55
                                                                                                                                                       [1] SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                  2 ASŠSVSYMH 10
                                                                                                                                            NCBI_TaxID-10090;
                                                                                                                                                                                                                                                                                                                                                                                   15 ASSSVSYMH 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=10090;
                                                                                                                                                                         STRAIN-DBA/2
                                                                                                            (Fragment)
                                                                                                                                                                                                                                                                                         NON_TER
NON_TER
SEQUENCE
                                                                09JL76;
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                                                     971760
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                                   RESULT 2
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SASSSVSYMH 10

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variable region (Fragment).
Schistosoma japonicum (Blood fluke).
Bukaryota; Metazoa; Platyhelminthes; Trematoda; Digenea; Strigeidida; Schistosomatoidea; Schistosomatoidea; Schistosomatoidea; Schistosomatidae; Schistosomatoidea; Schistosomat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                      01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
Monoclonal anti-idiotypic antibody NP30 immunoglobulin light chain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A. SON, Qiu Z.N., Li Y.Q., Huang H.L., Guan X.H.; Song X.T., Feng Z.Q., Qiu Z.N., Li Y.Q., Huang H.L., Guan X.H.; "Amplification, cloning and sequence analysis of the light chain variable region gene of monoclonal anti-idiotypic antibody NP30 of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE-96145502; PubMed-8555454; Deshium P., Los D.A., Hayashi H., Mustardy L., Murata N.; Transformation of Synechococcus with a gene for choline oxidase enhances tolerance to salt stress.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 547;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 106;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Schistosoma japonicum.";
Submitted (NOV-1999) to the EMBL/GenBank/DDBJ databases.
EMBL; AF207620; AAF19434.1; --
HSSP; P01679; ZPBJ.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        11478 MW; F20F544426BAE63E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              58865 MW; 589175892034B3BE CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
Choline oxidase (EC 1.1.3.17).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 38; DB 5;
Pred. No. 1.7;
2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     77.1%; Score 37; DB 2; 77.8%; Pred. No. 16;
     106 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             547 AA.
     PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Plant Mol. Biol. 29:897-907(1995)
EMBL; X84895; CAA59321.1; -.
HSSP; P22637; 3COX.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       InterPro; IPR000172; GMC_oxred.
Pfam; PF00732; GMC_oxred; 1.
PROSITE; PS00624; GMC_OXRED_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               79.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_v.
Pfam; PF00047; ig; 1.
SMART; SM00406; IGv; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ouery Match 79.2
Best Local Similarity 80.0
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Arthrobacter globiformis.
PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   106 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 SASSSVSYMH 10
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Gaps

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Length 858; Indels

Score 37; DB 5; Pred. No. 26;

77.18; 70.08;

1; Mismatches

96291 MW; 95030ED5FE096139 CRC64;

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7; Conservative
                                                                                                                     366 STEASVSYMH 375
                858 AA;
                                           Query Match
Best Local Similarity
                                                                                                     1 SASSSVSYMH 10
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                SEQUENCE
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                                                                        Matches
                                                                                                                                                                        RESULT 7
Q9VIF5
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RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Adams M.D., Celniker S.E., Richards S., Ashbuncen M., Hedderson S.N.,
Radon R.C., Mortas J.E., Nandell M.D., Zhang Q., Chen L.X.,
Burdon R.C., Rogers Y.H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Button G.G., Worthan J.R., Wandell M.D., Zhang Q., Chen L.X.,
Radon R.C., Rogers Y.H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Abril J.F., Agbayani A., An H.J., Andrews-Pfannkoch C., Baldwin D.,
RA Beeson K.Y., Beanes P.V., Barman B.P., Bhandari D., Bolahako S.,
Rokova D., Botchan M.R., Bouled J., Baytektarglu L., Beasley E.M.,
RA Burtis R.C., Busam D.A., Buller C., Davenport L.B., Davies P.,
RA Burtis R.C., Busam D.A., Dahlke C., Davenport L.B., Davies P.,
RA Burtis R.C., Dablike C., Davenport L.B., Davies P.,
RA Burtis R.C., Dablike C., Perraz C., Ferriar S., Fleischman W.,
RA Burtis N.L., Evangelista C.C., Ferraz C., Ferriara S., Fleischman W.,
RA Burtis N.L., Harvey D., Hehman T.J., Herrandez J.R., Hookey J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
Jalahi M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
Jasko P., Lei Y., Levitsky A.A., Li J., J., Liang Y., Lia Z.,
Liang V., Lei Y., Levitsky A.A., Li J., J., Wolneris J., Moshrefi A.,
Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
Ralazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
Ralazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Rese M.G.,
Spier E., Spradling A.C., Stapleton M., Stupski M.P., Smith H.O.,
Spier E., Spradling A.C., Stapleton M., Stupski M.P., Smith H.O.,
Ralamer K., Waesserman D.A., Welsenbach J.,
Rhilams S.M., Woodage T., Worley K., Wu D., Yang S., Yao Q.A.,
Rhilams S.M., Woodage T., Worley K., Wu D., Yang S., Yao Q.A.,
Rhilams S.M., Woodage T., Worley W. D., Yang S., Yao Q., S.,
Rhilams S.M., Woodage T., Worley W. D., Yang S., Zhao O., Zhao G., Shao C., Shan H.,
Rhilams S.M
                ö
                                                                                                                                                                                                                                Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pteryota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE=20296724; PubMed=10837029;
Hatini V., Bokor P., Goto-Mandeville R., DiNardo S.;
"Tissue- and stage-specific modulation of Wingless signaling by the
                ;
0
                Indels
                                                                                                                                                                    01-MXY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
CG11770 protein (LINES).
LIN OR CG11770.
                ö
                                                                                                                                             858 AA.
                Mismatches
                                                                                                                                             PRT;
                                                                                                                                                                                                                                                                                                                                              STRAIN=BERKELEY;
MEDLINE=20196006; PubMed=10731132;
                2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     segment polarity gene lines.";
Genes Dev. 14:1364-1376(2000).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FlyBase; FBgn0002552; lin.
7; Conservative
                                                                                                                                             PRELIMINARY;
                                                            208 SSSSVSYIH 216
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                                          2 ASSSVSYMH 10
               Matches
                                                                                                               RESULT 6
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Addam Serkelber;

RATAIN SERKELBER;

RAGIN SERVELBER;

RAGIN SERVELBER;

RAGIN SERVELBER;

RA Amanatides P. C. Glinker S.E., Hill R.A., Evans C.A., Gocayne J.D.,

RA Amanatides P. C. Scherer S.E., Hill P.W., Hoskins R.A., Galle R.F.,

George R.A., Lewis S.E., Richards S.. Ashburner M., Henderson S.N.,

RA Brandon R.C., Rogers Y.-H.C., Blazel R.G., Champe M., Pfeiffer B.D.,

RA Brandon R.C., Rogers Y.-H.C., Blazel R.G., Champe M., Pfeiffer B.D.,

RA Abril J.F., Agbayani A., Am H.-J., Androws-Frankoch C., Bladwin D.,

Ballew R.M., Basu A., Baxendale J., Bayzaktaroglu L., Beasley E.M.,

Ballew R.M., Basu A., Baxendale J., Bayzaktaroglu L., Beasley E.M.,

Ballew R.M., Benco P.V., Berman B.P., Bhandari D., Bolahakov S.,

RA Borkova D., Botchen M.R., Bouck J., Brokstein P., Brottler P.,

Burtis R.C., Busam D.A., Buller H., Cadleu E., Center A., Chandra I.,

RA Cherry J.M., Cawley S., Dahke C., Davenport L.B., Davies P.,

RA Cherry J.M., Cawley S., Dahke C., Davenport L.B., Davies P.,

RA Durbin K.J., Evangelista C.C., Ferraz C., Ferriera S., Fleischmann W.,

RA Durbin K.J., Evangelista C.C., Ferraz C., Ferriera S., Fleischmann W.,

RA Harris M.L., Harvey D., Hahman T.J., Hermandez J.R., Houck J.,

RA Harris N.L., Harvey D., Hahman T.J., Hermandez J.R., Rottle M.,

RA Jalali M., Kalush F., Karpen G.H., Wei M.-H., Ibegwam C.,

RA Alali M., Kalush F., Karpen G.H., Wei M.-H., Ibegwam C.,

RA Alali M., Kalush F., Karpen G.H., Wei M.-H., Ibegwam C.,

RA Mentel B., McIntosh T.C., Morris J., Morleson D.L.,

RA Mentel B., McIntosh T.C., Morris J., Morleson D.L.,

RA Spier E., Sperdling A.C., Stapleton M., Stucski M.P., Smith T.,

Shue B.C., Siden Klamme G.S., Pan S., Pollar J., Wen S.,

RA Spier E., Sperdling A.C., Stapleton M., Strong R., Wallsenberden J.,

RA Spier E., Spordling A.C., Stapleton M., Strong R., Wallsenberden S., Wallsham S.M., Woodage T., Worley K.C., Wu D., Yu Wu Y., Smith H.O.,

RA Spier E., Spradling A.C., Stapleton M., Strong R., Shue S., Shen K., Wassarman D.A., Weller E., Wallsham S.H., Woolage T., Worl
                                                                                                                                                                                                                                                                                                Drosophila melanogaster (Fruit fly).
Bukaryota, Metazoa, Arthropoda, Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 36; DB 5; Length 991;
Pred. No. 50;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         111757 MW; FFD72B5E86384155 CRC64;
                               01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAY-2000 (TrEMBLrel. 13, Last annotation update)
020522 protein.
991 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FBgn0032920; CG9252.
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EMBL; AE003669; AAF53964.1;
PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=7227;
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\$15.4

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Schizosaccharomyces
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255 SSSLSYLH 263
                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN-SP.011;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRAIN-972H-;
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                                                                                                                                                                                GLUCONATE.
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084646;
                                                                   014367
                       RESULT 10
014367
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084646
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Bukaryota, Metazoa: Arthropoda; Tracheata; Hexapoda; Insecta;
Pteryota: Neoptera; Endopteryota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A. STRSUE-OVARY;
STRAIN-OREGON R; TISSUE-OVARY;
TZOLOVSKY G., Bownes M., Millo H., Pathirana S., Wood T.;
"Identification and phylogenetic analysis of Drosophila melanogaster
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                         Saccharomyces cerevisiae (Baker's yeast).

Bukaryota Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Saccharomyces.
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0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            72.9%; Score 35; DB 5; Length 689; 60.0%; Pred. No. 56; ive 4; Mismatches 0; Indels
  2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Submitted (MAY-1996) to the EMBL/GenBank/DDBJ databases EMBL; 273245; CAA97630.1; -. SGD; SOOQ4063; YLR073C, SEQUENCEF 200 AA; 22850 MW; 1C93378ED78C41A4 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pohl T.M. Submitted (MAY-1996) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             myosins;'';
Mol. Biol. Evol. 0:0-0(2002).
EMBL; AP454349; AAL91723.1; -.
SROUENCE 689 AA; 74009 MW; 9525A3C5B928FD2A CRC64;
                                                                                                                                                                                                                                            01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Chromosome XII reading frame ORF YLR073C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-JUN-2002 (TrEMBLrel. 21, Created)
01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Unconventional myosin 29D short isoform.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     689 AA.
                                                                                                                                                                                                       200 AA.
    Mismatches
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                                                                                                                                                                                                       PRT;
  1;
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Best Locals Similarity 60.0
Matches 36; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Best Local Similarity 70.0
Matches 🐉 Conservative
7; Conservative
                                                                                                                                                                                                       PRELIMINARY;
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                                                                   613 AASSAVSFLH 622
                                            1 SASSSVSYMH 10
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|:|∭| ||:|
75 SSSSSSYIH 84
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                                                                                                                                                                                                                            008003;
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                                                                                                                                                                                                  00800
  Matches
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31

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Stephens R.S., Kalman S., Lammel C.J., Fan J., Marathe R., Aravind L., Mitchell W.P., Olinger L., Tatusov R.L., Zhao Q., Koonin E.V.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                Caspari T.; "Onset of gluconate-H+ symport in Schizosaccharomyces pombe is regulated by the kinases Wisl and Pkal, and requires the gtil+ gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "Genome sequence of an obligate intracellular pathogen of humans:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Zimmermann W., Wambutt R., McDougall R.C., Rajandream M.A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    72.9%; Score 35; DB 3; Length 720; 66.7%; Pred. No. 58; 0; Indels ative 3; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Barrell B.G.;
Submitted (NOV-1999) to the EMBL/GenBank/DDBJ databases.
EMBL; X92655; CAA63345.1; -.
EMBL; ALI33154; CAB61447.1; -.
SEQUENCE 720 AA; 78725 MW; 5CC2CD58ACE7CD87 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      BB89266ED55F1496 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Caspari T.;
Submitted (OCT-1995) to the EMBL/GenBank/DDBJ databases
                                                                                                                                         Schizosaccharomyces pombe (Fission yeast).
Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
Schizosaccharomycetales; Schizosaccharomycetaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         08, Created)
08, Last sequence update)
19, Last annotation update)
                                                           Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Chlamydia trachomatis.
Bacteria; Chlamydiales; Chlamydiaceae; Chlamydia.
NCBI_TaxID-813;
720 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRT; 1004 AA.
                                        Created)
PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
STRAIN-D/UW-3/CX;
MEDLINE-99000809; PubMed-9784136;
                                                                                                                                                                                                                                                                                        STRAIN-SP.011;
MEDLINE-98039718; PubMed-9372449;
                                                                                                                                                                                                                                                                                                                                                                                                                Cell Sci. 110:2599-2608(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1004 AA; 114401 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Chlamydia trachomatis.";
Science 282:754-759(1998).
EMBL; AEO01334; AAC68244.1; -.
Complete proteome.
SEQUENCE 1004 AA; 114401 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Exodeoxyribonuclease V, gamma.
                                      01-JAN-1998 (TrEMBLrel. 05, 01-JAN-1998 (TrEMBLrel. 05, 01-MAY-2000 (TrEMBLrel. 13,
  PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 72.9
Best Local Similarity 66.7
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRELIMINARY;
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01-NOV-1998 (TrEMBLrel.
01-DEC-2001 (TrEMBLrel.
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Length 537;

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58507 MW; 250E2948450EC19D CRC64;
                                           Score 34; DB 16;
Pred. No. 70;
2; Mismatches 0
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STRAIN-CV. COLUMBIA;
MEDLINE-21016719; Pubmed-11130712;
                                           70.8%;
75.0%;
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Best Local Similarity 70.0
Matches 7; Conservative
                                                                                   Conservative
                                                                                                                                                                                                                                                                   PRELIMINARY;
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    537 AA;
                                         Query Match
Best Local Similarity
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                                                                                                                                                                  192 SSAVSYLH 199
                                                                                                                          3 SSSVSYMH 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=3767;
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      SEQUENCE
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Q9AYS1;
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                                                                                   Matches
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MEDLINE-21082930; PubMed=11214968;
MEDLINE-21082930; PubMed=11214968;
Manacko T., Nakamura Y., Sato S., Asamizu E., Kato T., Sasamoto S., Watanabe A., Idesawa K., Ishikawa A., Kawashina K., Kimura T., Kishida Y., Kiyokawa C., Kohara M., Matsumoto M., Matsuno A., Mochizuki Y., Nakayama S., Nakazaki N., Shimpo S., Sugimoto M., Takeuchi C., Yamada M., Tabata S.;
"Complete genome structure of the nitrogen-fixing symblotic bacterium
                                                                                                                                                                                                                                                                                                                                                                                  Drosophila melanogaster (Fruit fly).
Bukaryota, Metazoa, Arthropoda, Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Rhizobium loti (Mesorhizobium loti).
Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
Phyllobacteriaceae; Mesorhizobium.
                                                                ;
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                        DB 16; Length 1004;
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Pred. No. 1.18+02;
4; Mismatches 0; Indels
                                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MOI. Biol, Evol. 0:0-0(2002).
EMBL; AF454348; AAL91722.1; -.
SEQUENCE 1313 AA; 142708 MW; 1A164E5A073D9450 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-OCT-2001 (TrEMBLrel. 18, Created)
01-OCT-2001 (TrEMBLrel. 18, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Probable dehydrogenase.
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Last annotation update)
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                                                              1; Mismatches
                    Score 35; DB
Pred. No. 83;
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InterPro; IPR000172; GMC_oxred.
Pfam; PF00732; GMC_oxred; 1.
PROSITE; PS00624; GMC_OXRED_2; 1.
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                    72.9%;
70.0%;
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60.0%;
Query Match
Best Local Similarity 70.0.
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DNA Res. 7:331-338(2000).
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                                                                                                                              108 SSSEVSYSH 117
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Q8T6L9;
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Q98LI5
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SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

A Tateishi, A., Inoue H., Shiba H., Yamaki S.;

A Tateishi A., Inoue H., Shiba H., Yamaki S.;

Tholecular cloning of beta-galactosidase from Japanese pear (Pyrus Tronicular cloning of beta-galactosidase from Japanese pear (Pyrus Tronicular cloning of beta-galactosidase from Japanese pear (Pyrus Tronicular) and its gene expression with fruit ripening.",

Submitted (JUL-2000) to the EMBL/GenBank/DDBJ databases.

CALACTOSE RESIDUES IN BETA-D-GALACTOSIDES.

CALACTOSE RESIDUES IN BETA-D-GALACTOSIDES.

CALACTOSE RESIDUES IN BETA-D-GALACTOSIDES.

SEMBL, RABG46543; BAB21492.1; -..

SEMBL, RABG46543; BAB21492.1; -..

DR FAINTS; PRO01301; GIYCO., Mydro., 35; 1.

PRINTS; PRO0142; GLHYDRLASE35.

DR PRINTS; PRO142; GLHYDRLASE35; 1.
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01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
10-JUN-2002 (TrEMBLrel. 21, Last annotation kinase)
10-JUN-2002 (Mouse-ear cress)
10-JUN-2002 (Mouse-ear cres
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Spermatophyta, Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids I; Rosales; Rosaceae; Maloideae; Pyrus.
Gaps
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Pred. No. 97;
      Indels
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01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
Beta-galactosidase (EC 3.2.1.23) (Lactase).
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RA Buehler E., Chan A., Chao Q., Chen H., Cheuk R.F., Chin C.W.,
RA Chung M.K., Conn L., Conway A.B., Conway A.R., Creasy T.H., Dewar K.,
Dunn P., Edud P., Feldblyum T.V., Feng J.-D., Fong B., Fuji C.Y.,
RA Gill J.E., Goldsmith A.D., Haas B., Huizar E.,
RA Hunter J.E., Jenkins J., Johnson-Hopson C., Khan S., Khaykin E.,
RA Langin-Högper S., Lee A., Lee J.M., Lenz C.A., Li J.H., Li Y.-P.,
RA Lin X., Liu S.X., Liu Z.A., Luros J.S., Maiti R., Marziali A.,
RA Millischef J., Miranda M., Nguyen M., Neoney T., Rowley B.I.,
RA Pai G., Peterson J., Pam P.K., Shinn P., Southwick A.M.,
RA But G., Peterson J., Tambunga G., Toriumi M.J., Town C.D.,
RA Utterback T., Van Aken S., Vaysberg M., Vysotskala V.S., Walker M.,
Ru D., Yul G., Fraser C.M., Venter J.C., Davis R.W.;
Thallana J.,
Thal
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Yamada K., Liu S.X., Sakano H., Pham P.K., Banh J., Chung M.K.,

A Goldsmith A.D. Lee J.M., Quach H.L., Toriumi M., Yu G., Bowser L.,

A Carnincia P., Chen H., Cheuk R., Hayashizaki Y., Ishida J., Jones T.,

Kamiya A., Karilin-Neumann G., Kawai J., Kinc., Lam B., Lin J.,

A Kamiya A., Karilin-Neumann G., Kawai J., Kinc., Lam B., Lin J.,

A Miranda M., Narusaka M., Nguyen M., Palm C.J., Sakurai T., Satou M.,

A Arabidopis A., Narusaka M., Shinozaki K., Davis R.W., Ecker J.R.,

Theologis A.,

"Arabidopis P. Couthwick A., Shinozaki K., Davis R.W., Ecker J.R.,

"Arabidopis P. Couthwick A., Shinozaki K., Davis R.W., Ecker J.R.,

"Arabidopis P. Couthwick A., Shinozaki K., Davis R.W., Ecker J.R.,

"Arabidopis P. Couthwick A., Shinozaki K., Davis R.W., Ecker J.R.,

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"Arabidopis P. Couthwick A., Shinozaki K., Davis R. Linerprof, IPR001291; ERR_Lyp.

"Interprof, IPR001291; ERR_Lyp.

"Interprof, IPR001245; Tyr_pkinase.

"A Pfam; Prof0069; Prinse. I."

"A Pfam; Prof0069; Prinse. I."
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Search complèted: December 23, 2002, 07:29:50 Job time : $7_{\tilde{\gamma}}14729~\text{secs}$

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                        GenCore version 5.1.3
Copyr,ight (c) 1993 - 2002 Compugen Ltd.
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VILHPVI
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VYES, SCHOUSE
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NP11, ASPOR
YK51, YERST
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NP11, ASPOR
YK51, YERST
ARS, HUMAN
MHP1, YERST
FAS, HUMAN
MHP1, YERST
YERST HUMAN
MHP1, YERST HUMAN
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	i i	01-FEB-1995	(Rel.	31, 1	ast	sequence	DI 01-FEB-1995 (Rel. 31, Last sequence update)			
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	8	Eukaryota;	Fungi;	Ascom	ycot	a; Sacche	romycotina; Sacc	haromycet	tes;	
	2 8	Saccharomyc	etales 4932.	, sacc	naro	мусетасе	e; saccharomyces			
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	RA	Gentles S.,	Hamly	n N.	Hors	nell T.S.	, Hunt S., Jagel	s K., Jor	nes M.,	
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	RA Pa	Rajandream	M.A., White	Riles head c	; ;	Rowley N.	., Skelton J., Sm	ith V.,		
	Z.	Submitted (DEC-19	nead a	the	EMBL/Ger	Bank/DDBJ databa	ses,		
	ပ္ပ	-1- SIMILAR	ITY: T	O YEAS	T YK	R100C.	-1- SIMILARITY: TO YEAST YKR100C,			
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		orsities re	quires	to lic	ense	agreemer	nt (see nttp://ww ch)	W.ISD-SIL	o.cn/anno	/eoun
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	DR	EMBL; 23805	9; CAA	86120.	1; -					
	A G	PIR; S483/6	, 5483	76.						
	X Z	Hypothetica	l prot	ein: T	rans	membrane				
	FT	TRANSMEM	9	26		POTENTI	TRANSMEM 6 26 POTENTIAL.			
	ÖS	SEQUENCE	204 AA	; 228	40 M	W; 7B861	A9F125F19BF CRC6	4;		
	Ď	atch		90	38;	SG	DB	h 204;		
	W D	Matches 6;	Conse	Similarity 63.7%; 6; Conservative	• •	1;	9./; thes 0;	Indels (0; Gaps	0;
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Wood VV, Gwilliam R., Rajandream M.A., Lyne M., Lyne R., Stewart A., Sgouros J., Peat N., Hayles J., Baker S., Bowman S., Bornors K., Bownon B., Brown S., Chillingworth T., Churcher C.M., Collins M., Connor R., Cronin A., Davis P., Feltwell T., Fraser A., Gentles S., Goble A., Hamlin N., Harris D., Hidalgo J., Hodgson G.,
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                                                                                                                                                              MEDLINE-85246220; PubMed-2990099;
Seedorf K., Krammer G., Durst M., Suhai S., Rowekamp W.G.;
"Human papillomavirus type 16 DNA sequence.";
Virology 145:181-185(1985).
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85.7%; Pred. No. 29;
ive 1; Mismatches 0; Indels
                                    Human papillomavirus type 16.
Viruses; dgbNA viruses, no RNA stage; Papillomaviridae;
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EMBL; M96285; AAA4024.1; ---
EMBL; A06331; CAA00546.1; ---
EMBL; A06331; CAA00546.1; ---
EMBL; A06331; CAA00546.1; ---
FIR, A03640; PHRO02210; PV. capsid_L1.
PRINTS; PRO08065; HPVCAPSIDL1.
Propon; PD0000544; PV_capsid_L1; 1.
Coat protein: Late protein.
SEQUENCE 531 AA; 59554 MW; 5B3402587093B380 CRC64;
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Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
Schizosaccharomycetales; Schizosaccharomycetaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    15-JUL-1998 (Rel. 36, Created)
16-CCT-2001 (Rel. 40, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
19-pothetical protein C167.05 in chromosome I.
SPAC167, 05 OR SPAC57A7.01
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Matches 6; Conservative
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Major caps@d protein L1.
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NCBI_TaxID=4896;
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                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                      NCBI_TaxID=10581;
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And James K., Jones L., Jones M., Leather S., McDonald S., McLean J., Radaes K., Jones L., Jones M., Leather S., McDonald S., McLean J., Radoney P., Moule S., Mungall K., Murphy L., Nibbett D., Odell C., Radoney P., Moule S., Mungall K., Murphy L., Nibbett D., Odell C., Radoney P., Moule S., Saudres S., Saudres B., Saudres S., Stevens K., Sharp S., Skelton J., Simmonds M., Squares R., Squares S., Stevens K., Sharp S., Rador M., Taylor K., Taylor K., Taylor K., Taylor K., Taylor K., Melsh S.V., Marren T., Whitehead S., Radolovard J., Volckaert G., Aert R., Robben J., Grymonprez B., Weltjens I., Vanstreels E., Rieger M., Schaefer M., Mueller-Auer S., Rabel C., Fuchs M., Fritzc C., Holzer E., Moestl D., Hilbert H., Rabel C., Fuchs M., Fritzc C., Holzer E., Moestl D., Hilbert H., Rabel C., Fuchs W., Fatzc C., Holzer E., Dernalle B., Hilbert H., Radole C., Fuchs W., Wedler H., Wambutt R., Purnelle B., Active S., Grigeau A., Cadleu E., Dreano S., Gloux S., Lelaure V., Mocter S., Anibert F., Aves S.J., Xiang Z., Hunt C., Moore K., Hurst S.M., Lucas M., Rochet M., Gaillardin C., Tallada V.A., Garzon A., Thode G., Radoninguez A., Revuelta J.L., Moreno S., Armstrong J., Forsburg S.L., Ashary C., Williamer Z., Moninguez A., Revuelta J.L., Moreno S., Armstrong J., Forsburg S.L., Radoninguez A., Revuelta J.L., Moreno S., Armstrong J., Forsburg S.L., The genome sequence of Schizosaccharomyces pombe.";

R. Nature 415:871-880(2002).
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Holroyd S., Hornsby T., Howarth S., Huckle E.J., Hunt S., Jagels K.,
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Eukaryota; Fungi; Ascomycota; Saccharomycetes; Saccharomycetales; Saccharomycetaceae; Saccharomyces.
NCBI_TaxID=4932;
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15-DEC-1998 (Rel. 37, Last annotation update)
Hypothetical 81.2 kDa protein in NMD5-HOM6 intergenic region.
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Submitted (SEP-1995) to the EMBL/GenBank/DDBJ databases.
-! SIMILARITY: SOME, TO PARAMYOSINS AND MYOSINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         l protein.
601 AA; 65947 MW; 13FAACABDCE14239 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; AL035248; CAA22850.1; -.
EMBL; 295396; CAB08759.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-FEB-1996 (Rel. 33, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       InterPro; IPR000041; Usp. Pfam; PF00582; Usp; 1. Hypothetical protein. SEQUENCE 601 AA; 65947
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
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YRP2_IRV6
                         P18306;
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                    MEDLINE-83271467; PubMed-6877353;
Kaartinen M., Griffiths G.M., Markham A.F., Milstein C.;
"mRNA sequences define an unusually restricted IgG response to
phenyloxazolone and its early diversification.";
Nature 304:320-324(1983).
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COMPLEMENTARITY-DETERMINING-1.
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COMPLEMENTARITY-DETERMINING-2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPLEMENTARITY - DETERMINING - 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 1; Length 108;
8.1;
                                                                                         90.3%; Score 28; DB 1; Length 707; 85.7%; Pred. No. 41;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0; Indels
                                                                                                                Indels
                                                                   BA47D1A7265BF3D9 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  11713 MW; DABF235CD9680AC6 CRC64;
EMBL; 249634; CAA89665.1; -.
EMBL; 249635; CAA89667.1; -.
SGD; S0003895; YJR134C.
Hypothetical protein; Coiled coil.
DOMAIN 122 473 COLLED COIL (POTENTIAL).
DOMAIN 594 706 COILED COIL (POTENTIAL).
                                                                                                                0;
                                                                                                                                                                                                                                      13-AUG-1987 (Rel. 05, Created)
13-AUG-1987 (Rel. 05, Last sequence update)
12-UUL-1999 (Rel. 38, Last annotation update)
15 kappa chain V-VI region NQ2-6.1.
                                                                                                                                                                                                                    108 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0; Mismatches
                                                                                                                1; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FRAMEWORK-4
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Pred. No.
                                                                                                                                                                                                                    PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SMART; SM00406; ÍGv; 1.
Immunoglobulin V region; Hybridoma
DOMAIN 1 23 FRAMES
                                                                   707 AA; 81171 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        87.1%;
100.0%;
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HSSP; P01679; 2FBJ.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_v.
                                                                                                                6; Conservative
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                                                                                                                                                                                                                                                                                   Mus musculus (Mouse).
                                                                                                  Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=10090;
                                                                                                                                                  |||||:|
STSNLSS 31
                                                                                                                                    1 STSNLAS 7
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|TSNLAS 55
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NON_TER
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DOMAIN
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Matches
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RESULT 6

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Darai G.; "DNA nucleotide sequence analysis of the PvuII DNA fragment L of the genome of insect iridescent virus type 6 reveals a complex cluster of multiple tandem, overlapping, and interdigitated repetitive DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musince; Mus.
NCBI_TaxID=10090;
                                                                                                                                                                                                          SEQUENCE FROM N.A.
MEDLINE-89073753; PubMed-3201751;
Fischer M., Schnitzler P., Scholz J., Roesen-Wolff A., Delius H.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ;
0
                                                                                                     Repetitive protein ORF2.
Chilo iridescent virus (CIV) (Insect iridescent virus type 6).
Viruses; dsDNA viruses, no RNA stage; Iridoviridae; Iridovirus
NCBI_TaxID=10488;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CONSERVED MOTIF IN THE FIVE ORFS 2C927AlD41C41471 CRC64;
                                                                                                                                                                                                                                                                                                                                                                            Virology 167:497-506(1988).
-1- SIMILARITY: A CONSENSUS SEQUENCE MANLX(6)IGSSSTX(6)LX(1)
LGSX(1)LQISGX(2)LX(1)VN WAS FOUND IN ALL FIVE ORFS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 27; DB 1; Length 126;
Pred. No. 9.7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
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(Rel. 38, Last annotation update)
                                     (Rel. 16, Created)
(Rel. 16, Last sequence update)
(Rel. 16, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  129 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                126 AA; 13371 MW;
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21-JUL-1986 (Rel. 01, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             87.1%;
85.7%;
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STANDARD;
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Hypothetical protein.
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                                     01-NOV-1990 (
01-NOV-1990 (
01-NOV-1990 (
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE
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REVISIONS.
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MEDLINE—21664186; PubMed-11805826;
A Gavin A.C. Bosch M., Krause R., Grandi P., Marzioch M., Bauer A., Gavin A.C., Bosch M., Michon A.M., Cruciat C.M., Remor M., Hofert C., Schultz, J., Rick J.M., Michon A.M., Cruciat C.M., Remor M., Hofert C., Schelder M., Brajenovic M., Ruffner H., Merino A., Klein K., Hudak M., Dickson M., Rajin W., Bauch A., Kopley R.R., Edelmann A., Querfurth E., Rybin V., Drewes G., Raida M., Bouwmeester T., Bork P., Seraphin B., Kuster B., Neubauer G., Superti-Furga G.;
Rybin V., Drewes G., Superti-Furga G.;
Rybin V., Drewes G., Raida M., Poure G., Superti-Furga G.;
Rybin V., Drewes G., Raida M., Poure G., Superti-Furga G.;
Rybin V., Drewes G., Raida M., Robinse G.;
Rybin V., Drewes G., Raida M., Robinse G.;
Rybin V., Drewes G., Raida M., Robinse G.;
Rybin V., Drewes G., Raida M., Colley R.R., Edelmann A., Courfurth E., Rybin V., Drewes G., Superti-Furga G.;
Rybin V., Drewes G., Raida M., Robinse S., Caraphin B.,
Rybin V., Drewes G., Raida M., Robinse G., Superti-Furga G.;
Rybin V., Drewes G., Raida M., Robinse S., Caraphin B.,
Rybin V., Drewes G., Raida M., College R.R., Edelmann A., Courfurth E.,
Rybin V., Drewes G., Raida M., Robinse R.R., Edelmann A., Courfurth E.,
Rybin V., Drewes G., Raida M., Robinse R.R., Edelmann A., Courfurth E.,
Rybin V., Drewes G., Raida M., Robinse R.R., Edelmann A., Courfurth E.,
Rybin V., Drewes G., Raida M., Robinse R.R., Edelmann A., Courfurth E.,
Rybin V., Drewes G., Raida M., Robinse R.R., Edelmann A., Robinse R.R., Edelmann A., Robinse R.R., Edelmann A., Robinse R.R., Edelmann A., Robinse R.R., Robinse R.R., Robinse R.R., Edelmann A., Robinse R.R., Robi
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   and for commercial
                                 (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               15-JUN-2002 (Rel. 41, Created)
15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Transport protein particle 23 kDa subunit (TRAPP 23 kDa subunit).
TRS23 OR TRANSAGW OR YD0419.13.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SUBĎNIT: Part of multisubunit complex composed of BET3, BET5, TRS20, TRS23, TRS31, TRS33, TRS65, TRS85, TRS120 and TRS130. SIMŪLARITY: BELONGS TO THE TRAPP SMALL SUBUNITS FAMILY.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               IG KAPPA CHAIN V-IV REGION S107B. FRAMEWORK-1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPLEMENTARITY - DETERMINING - 2.
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STRAIN-S288C / AB972;
Oliver K., Harris D., Barrell B.G., Rajandream M.A.;
Submitted (MAY-1995) to the EMBL/GenBank/DDBJ databases.
   Usage by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              13833 MW; E4BB73072DCF6BE4 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       87.1%; Scor.
100.0%; Pred. No. 10.
modified and this statement is not removed.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              BY SIMILARITY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Saccharomyces cerevisiae (Baker's yeast).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FRAMEWORK - 3
                                 entities requires a license agreement (
or send an email to license@isb-sib.ch)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRT;
                                                                                                                                                                                                                                                                                                                           Pfam; PF00047; 1g; 1.
SMART; SM00406; IGV; 1.
Immunoglobulin V region; Signal.
                                                                                                                                                            EMBL; V00780; CAA24157.1; -. PIR; A01943; KVWS7B. HSSP, P01679; 2FBJ. InterPro; IPR0033006; Ig_MHC. InterPro; IPR003596; Ig_V.
                                                                                                                                EMBL; J00577; AAA38780.1; -.
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TRS23 SUBFAMILY
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Q03784;
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SEQUENCE
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                  between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
This SWISS-PROT entry is copyright. It is produced through a collaboration
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "Whole-genome random sequencing and assembly of Haemophilus influenzae
                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE-55350630; PubMed=7542800;
Relachmann R.D., Adams M.D., White O., Clayton R.A., Kirkness E.F.,
Relachmann R.D., Adams M.D., White O., Clayton R.A., Kirkness E.F.,
Kerlavage A.R., Bult C.J., Tomb J.-F., Dougherty B.A., Merrick J.M.,
McKenney K., Sutton G., Fitzhugh W., Fields C.A., Gocayne J.D.,
Scott J.D., Shirley R., Liu L.I., Glodek A., Kelley J.M.,
Weidman J.E., Phillips C.A., Spriggs T., Hedblom E., Cotton M.D.,
Ulterback T.R., Hanna M.C., Nguyen D.T., Saudek D.M., Brandon R.C.,
Fine L.D., Fritchman J.L., Fuhrmann J.L., Geoghagen N.S.M.,
Gnehm C.L., McDonald L.A., Small K.V., Fraser C.M., Smith H.O.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              White O., Clayton R.A., Kerlavage A.R., Fleischmann R.D.;
Submitted (SEP-1996) to the EMBL/GenBank/DDBJ databases.
--- SUBCELLULAR LOCATION: Integral membrane protein (Potential).
--- SIMILARITY: STRONG, TO E.COLI YFCA.
                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bacteria; Proteobacteria; gamma subdivision; Pasteurellaceae;
Haemophilus.
                                                                                                                                                                                                                                                                                  87.1%; Score 27; DB 1; Length 219;
100.0%; Pred. No. 19;
Live 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        InterPro, IPR002781; DUF81.
Pfam; PF01925; DUF81; 1.
Hypothetical protein; Transmembrane; Complete proteome.
                                                                                                                                                                                                                            Transport; Endoplasmic reticulum; Golgi stack.
SEQUENCE 219 AA; 24863 MW; 8B32B1D5FE3846ED CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-NOV-1995 (Rel. 32, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
10-LUN-2002 (Rel. 41, Last annotation update)
Hypothetical protein H10198.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               255 AA.
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                                                                                                                                                                                EMBL; Z49701; CAA89732.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Rd.";
Science 269:496-512(1995).
                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STANDARD;
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                                                                                                                                                                                                          SGD; S0002654; TRS23
                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
Matches 6; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                               166 STSNLA 171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=727;
                                                                                                                                                                                                                                                                                                                                                                                      1 STSNLA 6
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P46490;
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YBO3_YEAST
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RAY Dunham I. Hunt A.R., Collins J.E., Blueskiewich R., Beare D.M.,

Bunnam I., Hunt A.R., Collins J.E.,

Bunnam I., Hunt A.R., Collins J.E.,

Bagguley C., Bailey J., Barlow K.F., Bates K.N., Beasley O.P.,

RA Bagguley C., Bailey J., Barlow K.F., Bates K.N., Beasley O.P.,

Blud C.P., Bladew S.E., Bridgeman A.M., Burgess J.,

RA Burrill W.D., Burton J., Carder C., Carter N.P., Chen Y., Clark G.,

RA Conroy D., Corbly N.E., Coylle G.G., Collier R.E., Connor R.,

Conroy D., Corby N.R., Coylle G.J., Cox A.V., Davis J., Dawson E.,

RA Dhami P.D., Dockree C., Dodsworth S.J., Durbin R.M., Ellington A.G.,

RA Ball R.E., Hall-Tamlyn G., Heathcott R.W., Ho S., Holmes S.,

A Hall R.E., Hall-Tamlyn G., Heathcott R.W., Ho S., Holmes S.,

RA Hall R.E., Hall-Tamlyn G., Heathcott R.W., Ho S., Holmes S.,

RA Hall R.E., Mashreqhi-Mohammadi M., Matthews L.H., Mccann O.T.,

RA Martyn I.D., Mashreqhi-Mohammadi M., Matthews L.H., Mccann O.T.,

RA Martyn I.D., Mashreqhi-Mohammadi M., Watthews L.H., Mccann O.T.,

RA Martyn I.D., Pavitt R., Shuce C.D., Smalley S., Smith M.L.,

RA Moclay J., Mclaren S., McMurray A.A., Millines S.H., Wollimore B.J.,

RA Moclay J., Mclaren S., McMurray A.A., Milliams D., Phillimore B.J.,

RA Scott C.E., Sepra H.K., Skuce C.D., Smalley S., Smith M.L.,

RA Williams L., Williams S.A., Williamson H., Wilmer T.E., Wilming L.,

RA Williams L., Williams S.A., Williamson H., Wilmer T.E., Wilming L.,

RA Milliams L., Williams S.A., Williamson H., Wilmer T.E., Wilming L.,

RA Milliams L., Williams S.A., Williamson H., Wilmer T.E., Wilming L.,

RA Milliams L., Williams K., Yoshizaki Y., Asakawa S., Rodoh J.,

RA Milliams L., Williams S.A., Williamson H., Wilmer T.E., Wilming L.,

RA Milliams S., Kawasaki R., Sasaki T., Asakawa S., Rodoh J.,

RA Milliams S., Lewis S., Libuya K., Yoshizaki Y., Abeki N., Mitsuyama S.,

Roe B.A., Chen F., Chu L., Crabtree J., Deschamps S., Do A., Do T.,

RA Meng Y., Mang Y., Mang Z., Milliams D., Willimph D., Williams D., Well R., Wang S., Williams D., Williams D
                                                                                                                                                           ö
                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "Cloning, chromosome mapping and functional characterization of a human homologue of murine Gtse-1 (B99) gene."; Gene 254:229-236(2000).
                                                                                                                                                                                                                                                                                                                                                                                               Craniata; Vertebrata; Euteleostomi;
Catarrhini; Hominidae; Homo.
                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Monte M., Collavin L., Lazarevic D., Utrera R., Dragani T.A., Schneider C.;
                                                                                                                               Score 27; DB 1; Length 255;
Pred. No. 22;
                                                                                                                                                           0; Indels
                                                                                        POTENTIAL.
7C0936C07F7B58F5 CRC64;
                                                                                                                                                                                                                                                                                 GTSE_HUMAN STANDARD; PRT; 720 AA. Q9NY23; Q9BRED; Q9Y557; Q9UG29; 15-JUN-2002 (Rel. 41, Created) 15-JUN-2002 (Rel. 41, Last sequence update) 15-JUN-2002 (Rel. 41, Last annotation update) G2 and S phase expressed protein 1 (B99 homolog).
                                                                                                                                                           Mismatches
                                  POTENTIAL. POTENTIAL.
                                                             POTENTIAL. POTENTIAL.
                      POTENTIAL
          POTENTIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=20432105; PubMed=10974554;
                                                                                                                      87.1%; Scc...
100.0%; Pre/
0; P
48
99 119
2 152
173
211
255
27608 MW;
                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens (Human).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
                                                                                                                                                           Conservative
       76
76
99
132
153
191
235
AA;
                                                                                                                                            Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TISSUE=Placenta;
                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID-9606;
                                                                                                                                                                                                                185 TSNLAS 190
                                                                                                                                                                                     2 TSNLAS 7
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                                                                       TRANSMEM
TRANSMEM
SEQUENCE
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Fulton R., Johnson D., Bemis G., Bentley D., Bradshaw H., Bourne S., Cordes M., Du Z., Fulton L., Goela D., Graves T., Hawkins J., Hinds K., Kemper K., Layman D., Ozersky P., Rohlfing T., Scheet P., Walker C., Wamsley A., Wohldmann P., Pepin K., Nelson J., Rorf I., Bedell J.A., Hillier L., Mardis E., Waterston R., Wilson R., Emanuel B.S., Shaikh T., Kurahashi H., Saitta S., Budarf M.L., McDermid H.E., Johnson A., Wong A.C.C., Morrow B.E., Edelmann L., Kim U.J., Shizuya H., Simon M.I., Dumanski J.P., Peyrard M., Kedra D., Seroussi E., Fransson I., Tapia I., Bruder C.E., O'Brien K.P., Hilahun Y., Wright H.;
Tilahun Y., Wright H.;
The DNA sequence of human chromosome 22.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: May be involved in p53-induced cell cycle arrest in G2/M phase by interfering with microtubule rearrangements that are required to enter mitosis. Overexpression delays G2/M phase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     progression.
-!- SUBCELLULAR LOCATION: Cytoplasmic. Associated with microtubules.
-!- DEVELOPMENTAL STAGE: Expressed in G2/M phase. Not detected in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-0CT-1994 (Rel. 30, Last sequence update)
16-0CT-2001 (Rel. 40, Last annotation update)
Putative 103.4 kDa transcriptional regulatory protein in RPL4A-HWT1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Saccharomyces cerevisiae (Baker's yeast).
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Saccharomyces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ;
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R -> W (IN REF. 2; CAB38415).
ACD91CCCD008A89C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             87.1%; Score 27; DB 1; Length 720; 100.0%; Pred. No. 74;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      quiescent cells.
-!- PTM: Phosphorylated in mitosis (By similarity).
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Smits P.H.M., de Haan M., Maat C., Grivell L.A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         919 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                100.0%; Pred. No. 74; ive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 POLY-SER.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL, AL022325, CAB63079.1; --
EMBL, BC006325, AAH06325.1; --
MCCTCLUDULES; Phosphorylation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; AF223408; AAF31459.1; -. EMBL; AL031588; CAB38415.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-OCT-1994 (Rel. 30, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  720 AA; 76614 MW;
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                                                                                                                                                                                                                                                                                                                                                                                                                  Nature 402:489-495(1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       intergenic region.
YBR033W OR YBR0318.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sest Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              303 STSNLA 308
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TISSUE-Muscle;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Strausberg R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 STSNLA 6
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P38073;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CONFLICT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; L08483; AAA53472.2; -.
EMBL; AE003657; AAF53651.1; ALT_SEQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   InterPro; IPR000210; BTB_POZ.
InterPro; IPR001798; Kelch.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; L08483; AAA53471.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FlyBase; FBgn0001301; kel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Q05516; 1CS3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D., Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F., George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N., Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X., Brandon-R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D., Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G., Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Kue F., Cooley L.;
*Relch encodes a component of intercellular bridges in Drosophila egg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRT; 1477 AA.

004652; Q04653; O9VJA2;
01-FEB-1994 (Rel. 28, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
15-JUN-2002 (Rel. 41, Last monotation update)
15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last sequence update)
16-OCT-2001 (Rel. 28, Created)
16-OCT-2001 (Rel. 28, 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
"The complete sequence of a 33 kb fragment on the right arm of chromosome II from Saccharomyces cerevisiae reveals 16 open reading
                                                                                                                                                                                                                                                                                                                                                                  R EMBL; X76078; CAA83688.1; -
R EMBL; X35902; CAA84975.1; -
R PEMBL; Z35902; CAA84975.1; -
PIR; S45889; S45889.
SGD; S0000237; YBR033W.
R InterPro; IPR001138; Fungi_TrN.
R Pfam; PF00172; Zn_clus; 1.
R PROSTIE; PS0046; ZAL2; 1.
R PROSTIE; PS50048; ZN2_CY6_FUNGAL_1; 1.
R PROSTIE; PS50048; ZN2_CY6_FUNGAL_2; 1.
W Hypothetical protein; Transcription regulation; DNA-binding; Nuclear protein; Zinc; Metal-binding.
W Nuclear protein; Zinc; Metal-binding.
ZN(2)-CYS(6), FUNGAL-TYPE.
SEQUENCE 919 AA; 103396 MW; 18DDZE37A042E246 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               87.1%; Score 27; DB 1; Length 919; 100.0%; Pred. No. 99; 0; Indels tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRAIN-Berkeley;
MEDLINE-20196006; PubMed-10731132;
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MEDLINE-93201592; PubMed-8453663;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best Local Similarity 100.
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 cell 72:681-693(1993).
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RA Bellew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Becson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottler P.,
Burtis K.C., Busam D.A., Buller H., Cadieu E., Center A., Chandra I.,
RA Burtis K.C., Busam D.A., Buller H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Dodson K., Gong F., Gorrell J.H., Gu Z., Guan P., Harriss M.,
RA Barris N.L., Harvey D., Helman T.J., Hernandez J.R., Houck J.,
RA Harris N.L., Harvey D., Helman T.J., Well M.-H., Ibegwam C.,
RA Harris N.L., Harvey D., Helman T.J., Well M.-H., Ibegwam C.,
RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
A Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Ralazzolo M., Pittman G.S., Pan N., Nelson D.L.,
RA Ralazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Spier E., Saben H., Saunders R.D.C., Scheeler F., Shen H.,
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Williams S.M., Woodage T., Worlex E., Wang S., Yao Q., Zhong X.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q., Zhong X.,
RA Zheng X.H., Zhong W., Zhong W., Zhou X., Zhu S., Zhu X., Zhu S., Zhon X.,
R. Zience 287:2185-2195(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              BINDS ACTIN.
SUBCELLULAR LOCATION: INNER SURFACE OF CYTOPLASMIC BRIDGES OR RING
CANALS PRESENT IN EGG CHAMBERS. SUBCORTICALLY IN IMAGINAL DISK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                --- TISSUE SPECIFICITY: BOTH PROFEINS ARE EXPRESSED IN OVARIES, MALE TESTIS, OVARECTOMIZED FEMALES, CUTICLE, SALIVARY GLAND AND IMAGINAL DISKS. RELCH ORFI IS THE PREDOMINANT PROTEIN AND IS ALSO EXPRESSED IN FAT BODIES. ON ENTRY INTO METAMORPHOSIS LEVELS OF FULL LENGTH PROTEIN INTORRASE IN TESTIS AND IMAGINAL DISKS.
---- SHMILARITY: CONTAINS 1 BTB/POZ DOMAIN.
---- SIMILARITY: CONTAINS 6 KELCH REPEATS.
---- SIMILARITY: CONTAINS 6 KELCH REPEATS.
---- CAUTION: Ref. 2 sequence differs from that shown due to erroneous
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Robinson D.N., Cooley L.; "Examination of two kelch proteins generated by stop
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Development 124:1405-1417(1997).
-!- FUNCTION: COMPONENT OF RING CANALS THAT REGULATES THE FLOW OF CYTOPLASM BETWEEN CELLS. MAY BE INVOLVED IN THE REGULATION OF CYTOPLASM FLOW FROM NURSE CELLS TO THE OCCYTE DURING OGGENESIS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TISSUE-Embryo;
MEDLINE-97236487; PubMed-9118811;
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Gaps

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Length 87; Indels

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83.9%;

Mismatches Score 26; Pred. No.

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Conservative
   Query Match
Best Local Similarity
Matches 6; Conserv
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                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A
                                                                                                                                                                                                               NCBI_TaxID=4932;
                                                     STSDLAS 11
                                         1 STSNLAS 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 STSNLAS 7
                                                                                                             SP12_YEAST
P17123;
                                                                                                                                                                                                                                                                                                                                                                                              Vaudin M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
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                                                                                                  SP12_YEAST
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                                                                                          RESULT 14
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                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Saccharomyces.
NCBI_TaxID=4932;
                                                                                                                                                                                                                                                                                                     ô
                                                    Selenium; Selenocysteine; Repeat.
                                                                                                                                                                                                                                                                                                                                                                                                             16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Mitochondrial import inner membrane translocase subunit TIM8.
TIM8 OR YJR135W-A OR YJR135BW.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            InterPro; IPR004217; Znf Tim10/DDP.
Pfam; PF02953; Zf-Tim10_DDP; 1.
Transport; Protein transport; Translocation; Mitochondrion;
                                                                                                                                                                                                                                                                                 DB 1; Length 1477;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Rose M., Koetter P., Entian K.D.;
Submitted (SEP-1995) to the EMBL/GenBank/DDBJ databases.
-!- SUBCELLULAR LOCATION: Mitochondrial inner membrane (By
                                                                                                                                                                                                                                                              4851EEAE9D9DBA47 CRC64;
                                                                                                                                                                                                                                                                                                     0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     87 AA; 9764 MW; B91D1DD41707EA24 CRC64;
                                                                                                                                                                                                                                                                             87.1%; Score 2/; Lb 1,
100.0%; Pred. No. 1.7e+02;
tive 0; Mismatches 0;
                                                            KELCH PROTEIN.
KELCH SHORT PROTEIN
                                                                                                                                                                                                                      -> L (IN REF. 1).
-> D (IN REF. 1).
-> R (IN REF. 1).
-> G (IN REF. 1).
                                                                                                                                                                                                                                                                                                                                                                                            87 AA
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POLY-GLN.
                                                                                                                                                  ASN-RICH.
GLN-RICH.
                                                                                        KELCH 1.
KELCH 2.
KELCH 3.
KELCH 4.
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KELCH 6.
                                                                                                                                                                                           PROBABLE
                                                                                                                                                                                                                                                                                                                                                                                            PRT;
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                                                                                                                                                                                                                                                              160086 MW;
Pfam; PF00651; BTB; 1.
Pfam; PF01344; Kelch; 6.
PRINTS; PR00501; KEICHREPEAT.
SMART; SM00225; BTB; 1.
PROSITE; PS50097; BTB; 1.
Cytoskeleton; Actin-binding; Se
                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                            STANDARD;
                                                                                                                                                                                                                                          1083
1086
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                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
Matches 6; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          similarity).
                                                                                                                                                                                                                                                                                                                                  2 TSNLAS 7
                                                                                                                                                                                                                                                                                                                                                                                           IM08_YEAST
P57744;
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CONFLICT
CONFLICT
SEQUENCE
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REPEAT
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REPEAT
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                                                                     CHAIN
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IMO8_YEAST
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Science 265:2077-2082(1994).
-!- FUNCTION: IT IS REQUIRED FOR MEIOSIS I CHROMOSOME DIVISION DURING SPORULATION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Johnston M., Andrews S., Brinkman R., Cooper J., Ding H., Dover J., Du Z., Favello A., Fulton L., Gattung S., Gelsel C., Kirsten J., Kucaba T., Hillier L., Jier M., Johnston L., Langston Y., Latreille P., Louis E.J., Macri C., Mardis E., Menezes S., Mouser L., Nhan M., Rifkin L., Ribes L., St Peter H., Trevaskis E., Vaughan K., Vignati D., Wilcox L., Wohldman P., Waterston R., Wilson R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "Complete nucleotide sequence of Saccharomyces cerevisiae chromosome
                                                                                                                                                                                                                                Saccharomyces cerevisiae (Baker's yeast).
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -!- MISCELLANEOUS: ITS NEGATIVE TAIL IS FUNCTIONALLY IMPORTANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ó
                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
MEDLINE=90258869; PubMed=2188099;
Malavasic M.J., Elder R.T.;
"Complementary transcripts from two genes necessary for normal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 173;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   E114394516451F60 CRC64;
                                                                                                                                                                                                                                                                                                         Saccharomycetales; Saccharomycetaceae; Saccharomyces.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             meiosis in the yeast Saccharomyces cerevisiae.";
Mol. Cell. Biol. 10:2809-2819(1990).
                                                               01-AUG-1990 (Rel. 15, Created)
01-AUG-1990 (Rel. 15, Last sequence update)
01-0CT-1996 (Rel. 34, Last annotation update)
Sporulation protein SPO12.
SPO12 OR YHR152W.
173 AA
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85.7%; Pred. No. 25;
.ive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN-S288c / AB972;
MEDLINE-94378003; Pubmed-8091229;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; M32653; AAA35076.1; -. EMBL; U10397; AAB68979.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                6; Conservative
   STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PIR; B36321; B36321.
PIR; S46756; S46756.
SGD; S0001195; SP012.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "Three-dimensional structures of two plant beta-glucan endohydrolases with distinct substrate specificities.";
Proc. Natl. Acad. Sci. U.S.A. 91:2785-7789(1994).
-!- FUNCAION: MAY PROVIDE A DEGREE OF PROPECTION AGAINST MICROBIAL INVASION OF GERMINATED BARLEY GRAIN THROUGH ITS ABILITY TO DEGRADE FUNGAL CELL WALL POLYSACCHARIDES.
-!- CATAMIYTIC ACTIVITY: Hydrolysis of 1,3-beta-D-glucosidic linkages in 1,3-beta-D-glucans.
-!- SIMMIARITY: BELONGS TO FAMILY 17 OF GLYCOSYL HYDROLASES.
                             01-APR-1990 (Rel. 14, Created)
01-APR-1990 (Rel. 14, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Glucan endo-1,3-beta-glucosidase GII precursor (EC 3.2.1.39) ((1->3)-beta-glucan endo-hydrolase GII) ((1->3)-beta-glucanase isoenzyme GII)
                                                                                                                                                                                                                                                                               STRAIN-CY. Clipper;
MEDLINE-93357431; PubMed-2562758;
MEDLINE-93357431; PubMed-2562758;
Hoej P.B. Hartman D.J., Morrice N.A., Doan D.N.P., Fincher G.B.;
"Purification of (1-->3)-beta-glucan endohydrolase isoenzyme II from germinated barley and determination of its primary structure from a
                                                                                                                                      Hordeum vilgare (Barley).

Eukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae;
Triticeae? Hordeum.
NCBI_TaxIp=4513;
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MEDLINE-20,1107649;
Leah R. "Towned. Svendsen I., Mundy J.;
Menter and molecular characterization of three barley seed proteins with antifungal properties.";
J. Biol. Chem. 266:1564-1573(1991).
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MEDLINE-94195828; PubMed-8146192;
Varghesefjin., Garrett T.P.J., Colman P.M., Chen L., Hoej P.B.,
Fincher G.B.;
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   334 AA.
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   PRT;
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EMBL; X16274; CAA34350.1; -.
EMBL; M23548; AAA32958.1; -.
   STANDARD;
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PIR; A31800; A31800
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                                                                   GLUCAN ENDO-1, 3-BETA-GLUCOSIDASE GIL
                                            Hydrolase; Glycosidase; Signal; Multigene family; 3D-structure.
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L -> V (IN REF. 2).
'552D66A29A08C703 CRC64;
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                     Pfam; PF00332; Glyco_hydro_17; 1.
PROSITE; PS00587; GLYCOSYL_HYDROL_F17; 1.
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            InterPro; IPR000490; Glyco_hydro_17.
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Best Local Similarity 85.7
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Search completed: December 23, 2002, 07:26:08 Job time : 2.69186 secs

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094456 human papil
094282 human papil
094hs6 human papil
094h46 human papil
09444 human papil
09644 uromyces fa
000330 human papil
082093 anabaena sp
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Q24262 drosophila
Q8vkn2 mycobacteri
Q9178 mus musculu
Q9410 schistosoma
Q95275 ostertagia
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007232 mycobacteri
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STRAIN-16M / ATCC 23456 / BIOTYPE 1;

STRAIN-16M / ATCC 23456 / BIOTYPE 1;

STRAIN-16M / ATCC 23456 / BIOTYPE 1;

DELVECCHIO V.G., Kapatral V., Redkar R.J., Patra G., Mujer C., Los T.,

Delvecchio V.G., Kapatral V., Redkar R.J., Lykidis A., Reznik G.,

Jablonski L., Larsen N., D'Souza M., Bernal A., Mazur M., Goltsman E.,

Selkov E., Elzer P.H., Haglus S., O'Callaghan D., Letesson J.-J.,

Haselkorn R., Kyrpides N., Overbeek R.;

The genome sequence of the facultative intracellular pathogen

Brucella melitensis.
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Brucellaceae; Brucella.
NCBI_TaxID=29459;
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                       Length 265;
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01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
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Matches 7; Conservative
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1333
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 Brucella melitensis
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Copyright (c) 1993 - 2002 Compugen Ltd
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Bourg (§, Foulongne V., Frutos P., Kulakov Y., Ramuz M.;
Bourg (§, Foulongne V., Frutos P., Kulakov Y., Ramuz M.;
A homologue of the Agrobacterium tumefaciens VirB and Bordetella
pertussis plt type IV secretion systems is essential for intracellular
survival for Brucella suis.";
Mol. Microbiol. 33:1210-122(1999).
EMBL: ARI41604; AAD56620.1;
SEQUENCE 391 AA, 41453 MW; AGDCA4C9AFBB490D CRC64;
                                                                                                                                                       STRAIN-2308;
MEDLINB-20388168; PubMed-10940027;
Sieitra R.; Comerci D.J., Sanchez D.O., Ugalde R.A.;
Almologue of an Operon Required for DNA Transfer in Agrobacterium
Is Required in Brucella abortus for Virulence and Intracellular
Multiplication...;
J. Bacteriol. 182:4849-4855(2000).
EMBL; AF226278; AAF73903.1;
SEQUENCE 388 AA; 41193 MW; D8A63372B267E7F3 CRC64;
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Brucellaceae; Brucella.
NCBL_TaxID-235;
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342 STSNLAS 348
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                                                                 VirB10.
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Q37901
ID Q379
AC Q379
DT 01-N
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Q9KIS6
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           ID DT ACCOOC OCCOOC OCCO
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"The Drosophila neurogenic gene neuralized encodes a novel protein and is expressed in precursors of larval and adult neurons.";
EMBO J. 12:2586-2586(1993).
-!- SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGER.
EMBL, 562597, AABZ7151.1;
-!- Flybase: Fegnon02932: neur.
InterPro; IPR001841; Znf_ring.
Pfam: PF00097; zf-C3HC4: 1.
SMART; SM00184; RING; 1.
Zinc-finger.
SEQUENCE 753 AA; 82307 MW; 45056A93EDDA7B41 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota, Metazoá, Arthropoda, Tracheata, Hexapoda, Insecta, Pteryyota, Neoptera, Endopterygota, Diptera, Brachycera, Muscomorpha, Ephydroidea, Drosophilidae, Drosophila, NCBI_TaxID=7227;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                        MEDLINE-96204568; PubMed-8623528; Medidien M., Holz T., Heller K.J.; Medidien M., Holz T., Heller K.J.; Medidien of the receptor-binding regions of pb5 proteins of bacteriophages T5 and BF23."; Virology 219:19-28(1996). EMBL; L42820; AAB05216.1; SEQUENCE 595 AA, 63909 MW; E79B717F88EA2099 CRC64;
                                                                                                                              Viruses; dsDNA viruses, no RNA stage; Caudovirales; Siphoviridae;
T5-like viruses.
NCBI_TaxID=10707;
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100.0%; Score 31; DB 9; Length 595;
Best Local Similarity 100.0%; Pred. No. 50;
Matches 7; Conservative 0; Mismatches 0; Indels
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Last annotation update)
01, Last sequence update)
19, Last annotation update)
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Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             753 AA.
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MEDLINE-93285130; PubMed=8508781;
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01,
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01,
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01-NOV-1996 (TrEMBLrel. 01
01-DEC-2001 (TrEMBLrel. 15
NEU-NEURALIZED.
NEUR OR NEU OR CG11988.
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01-NOV-1996 (TrEMBLrel.
01-NOV-1996 (TrEMBLrel.
01-JUN-2002 (TrEMBLrel.
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Yamada K., Liu S.X., Pham P.K., Banh J., Banno F., Dale J.M.,
A Goldsmith A.D., Jiang P.X., Lee J.M., Ondera C.S., Quach H.L.,
A Goldsmith A.D., Jiang P.X., Lee J.W., Ondera C.S., Quach H.L.,
A Tang C., Toriumi M., Yamamura Y., Yu G., Yu S., Bowser L.,
A Carninci P., Chen H., Cheuk R., Hayashizaki Y., Ishida J., Jones T.,
A Kamiya A., Karlin-Neumann G., Kavai J., Kim C., Koesema E., Lam B.,
Lin J., Meyers M.C., Miranda M., Narusaka M., Nguyen M., Palm C.J.,
Sakurai T., Satou M., Seki M., Shinn P., Southwick A., Tracy S.E.,
Shinozaki K., Davis R.W., Ecker J.R., Theologis A.;
T'Ll Length CDNA of gene F22D1.70/AT5q20900.";
Submitted (AUG-2001) to the EMBL/GenBank/DDBJ databases.

EMBL; AR560184; AAK25894.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Yamada K., Liu S.X., Sakano H., Pham P.K., Banh J., Chung M.K.,
Yamada K., Liu S.X., Sakano H., Pham P.K., Banh J., Chung M.K.,
Goldsmith A.D., Lee J.M., Quach H.L., Toriumi M., Yu G., Bowser L.,
Carninci P., Chen H., Cheu K., Hayashizaki Y., Ishida J., Jones T.,
Kamiya A., Karlin-Neumann G., Kawai J., Kim C., Lam B., Lin J.,
Miranda M., Narusaka M., Nguyen M., Palm C.J., Sakurai T., Satou M.,
Skinn P., Shinn P., Southwick A., Shinozaki K., Davis R.W., Ecker J.R.,
"Full Length cDNA of gene F22D1.70/AT5920900.";
Submitted (MAR-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                Hypothetical 19.9 kDa protein.
F22D1.70/ATSG20900.
Arabidopsis thaliana (Mouse-ear cress).
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
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Neurospora crassa.
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes; Sordariales; Sordariaceae; Neurospora.
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                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Hypothetical protein.
SEQUENCE 187 AA; 19933 MW; 4FOC66DECBB4F0E1 CRC64;
                                                                                                                                                                                                                                           01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
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01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
Related to vegetative cell wall protein gpl.
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PROSITE; PS00152; ATPASE_ALPHA_BETA; UNKNOWN_1.
                                                                                                                                                                                                       187 AA.
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    ed. No. 44;
Mismatches
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    Pred. No.
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85.7%;
85.78;
  Best Local Similarity 85.7
Matches 6; Conservative
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|112 STSNVAS 118
                                                                                                   39 ATSNLAS 45
                                                           1 STSNLAS 7
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Q8X084;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mus musculus (Mouse).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                     Paces V.,
                                    Saccharomyces cerevisiae (Baker's yeast).
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Saccharomyces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ;
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                                                                                                                                                             Benes V., Andrade M.A., Rechmann S., Teodoru C., Banrevi A., Sander C., Valencia A., Ansorge W., Voss H.; Submitted (JAN-1996) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   100.0%; Score 31; DB 3; Length 1107; 100.0%; Pred. No. 91;
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                                                                                                                                                                                                                                       Voss H., Benes V., Rechmann S., Teodoru C., Schwager C.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1107 AA; 124576 MW; 1E024F15085261EA CRC64;
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01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-OCT-2001 (TrEMBLrel. 19, Last annotation update)
Anti-myosin immunoglobulin light chain variable region
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                                                                                                                                                                                                                                                                                                                                                                MIPS;
Submitted (JUL-1996) to the EMBL/GenB EMBL; X94335; CAA64029.1; EMBL; Z75017; CAA99307.1; SGD; S0005635; INPS3.
InterPro: IPR005135; Exo_endo_phos. InterPro: IPR000300; IPPC.
InterPro: IPR0020135; Syja_N.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            with cardiac myosin.";
Infect. Immun. 68:5803-5808(2000).
EMBL; AF206030; AAF69328.1; -.
HSSP, P01679; 2FBJ.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_v.
Pfam, PF00047; Ig; 1.
SMART; SM00406; IG; 1.
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YOR3231W from chromosome XV. INP53 OR YOR3231W OR YOR109W
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Matches 7; Conservative
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                                                                                                                                          SEQUENCE FROM N.A.
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                                                                                                   NCBI_TaxID=4932;
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SEQUENCE
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Q9JL76
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01-NOV-1996 (TrEMBLrel. 01, Last sequence update) 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
                         Late major capsid protein L1 (Fragment).
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                                                                                                                           STRAIN-NM 9999;
MEDLINE-96079021; Pubmed-7494284;
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MEDLINE=96079021; PuḥMed=7494284;
                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRELIMINARY;
                                                  Human papillomavirus.
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Best Local Similarity
6; Conserva
                                                                                                              SEQUENCE FROM N.A.
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273 STANLAS 279
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Farmer A.D.;
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Q80998
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                                  Schulte U., Aign V., Hoheisel J., Brandt P., Fartmann B., Holland R., Nyakatura G., Mewes H.W., Mannhaupt G., Submitted (MAY-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                        Gaps
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MEDLINE-96079021; PubMed-7494284;
MEDLINE-96079021; PubMed-7494284;
Yamada T., Wheeler C.M., Halpern A.L., Stewart A.C., Hildesheim A., Jenison (S.A.);
"Human papillomavirus type 16 variant lineages in United States "Human papillomavirus type 16 variant lineages in United States populations characterized by nucleotide sequence analysis of the E6,
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Pred. No. 2.1e+02;
1; Mismatches 0; Indels
                                                                                                                                                             90.3%; Score 28; DB 3; Length 401;
85.7%; Pred. No. 1.7e+02;
iive 1; Mismatches 0; Indels
                                                                                                  German Neŭrospora genome project;
Submitted{{\dan-2002} to the EMBL/GenBank/DDBJ databases.
EMBL; AL356173; CABJT53.2;
SEQUENCE \(\frac{1}{2} 401 AA; 42038 MW; 0933A161C07B92EA CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human papillomavirus.
Viruses; %dsDNA viruses, no RNA stage; Papillomaviridae;
Papillomavirus.
NCBI_TaxiD=10566;
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01-NOV-1396 (TrEMBLrel. 01, Created)
01-NOV-1396 (TrEMBLrel. 01, Last sequence update)
01-JUN-2301 (TrEMBLrel. 17, Last annotation update)
Late major capsid protein L1 (Fragment).
                                                                                                                                                                                                                                                                                                   494 AA.
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01-NOV-1996 (TrEMBLrel. 01, Created)
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85.7%;
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Best Local, Similarity 85.7;
Electron 16, Conservative
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                                                                                   SEQUENCE EROM N.A.
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 NCBI_TaxID=5141;
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RESULT 10 Q80996

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"Human papillomavirus type 16 variant lineages in United States
populations characterized by nucleotide sequence analysis of the E6,
L2, and L1 coding segments.";
J. Virol. 69:7743-7753(1995).
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"Human papillomavirus type 16 variant lineages in United States
populations characterized by nucleotide sequence analysis of the
L2, and L1 coding sequents.";
J. Virol. 69:7743-7753(1995).
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Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
Papillomavirus.
NCBI_TaxID=10566;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Submitted (AUG-1995) to the EMBL/GenBank/DDBJ databases EMBL; U34166; AAA91713.1;
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Pfam; PF00500; late_protein_L1; 1.
Pr00500; PR00565; HPVCAPSID_L1; 1.
Pr000m; PD000544; PV_capsid_L1; 1.
NON_TER 1 1 494
SEQUENCE 494 AA; 55063 MW; 735F7C2B86CAC58F CRC64;
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01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-UNV-2001 (TrEMBLrel. 17, Last annotation update)
Late major capsid protein L1 (Fragment).
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85.7%; Pred. No. 2.1e+02;
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SEQUENCE FROM N.A.
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Q81001;
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                                                  Length 494;
                                                90.3%; Score 28; DB 12; Length 49
85.7%; Pred. No. 2.1e+02;
Live 1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                      Submitted (AUG-1995) to the EMBL/GenBank/DDBJ databases.
EMBL: U34169; AAA91716.1; -.
Interpro: IPR002210; PU-capsid_L1.
Pfam: PF005001 late_protein_L1; 1.
PRINTS; PR00865; HPVCARSIDI1.
PRODOM: PD000544; PV_capsid_L1; 1.
                                                                                                                                                                                                                                     Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
Papillomavirus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human papillomavirus.
Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
                    494
55021 MW; E446FD38994FB3DD CRC64;
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01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
Late major capsid protein L1 (Fragment).
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01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
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ProDom; PD000544; PV_capsid_L1; 1.
                                                                                                                                                                                                                                                                                    STRAIN=NM T455;
MEDLINE=96079021; PubMed=7494284;
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J. Virol. 69:7743-7753(1995).
                                              Query Match 90.3
Best Local Similarity 85.7
Matches 6; Conservative
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                             494 AA;
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NCBI_TaxID=10566;
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MEDLINE=96079021; PubMed=7494284;
Yamada T., Wheeler C.M., Halpern A.L., Stewart A.C., Hildesheim A.,
Jenison S.A.;
"Human papillomavirus type 16 variant lineages in United States
populations characterized by nucleotide sequence analysis of the E6,
I.2. and I.1 coding sequents";
J. Virol. 69:7743-7753(1995).
                                                                                                      "Human papillomavirus type 16 variant lineages in United States populations characterized by nucleotide sequence analysis of the E6, L2, and L1 coding segments.";
STRAIN=NM T529;
MEDLINE=96079021; PubMed=7494284;
Yamada T., Wheeler C.M., Halpern A.L., Stewart A.C., Hildesheim A.,
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Submitted (AUG-1995) to the EMBL/GenBank/DDBJ databases.
EMBL, 34172; AAA91719.1;
InterPro: IRR002210; PV_capsid_Ll.
Pfam; PF00500; Late_protein_Ll: 1.
PRINTS; PR00865; HPVCAPSIDL1.
PROMP. PR00865; HPVCAPSIDL1.
NON_TER 494 494
SEQUENCE 494 AA; 55094 MW; ECB31B09E8EFB4E3 CRC64;
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EMBL: U34170; AAA91717.1; -.
InterPro; IPR002210; PV_capsid_L1.
Pfam; PF00500; Hate_protain_L1; 1.
PRINTS: PR00865; HPVCAPSIDL1.
Probom; PD000544; PV_capsid_L1; 1.
NON_TER
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Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
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01-NOV-1996 (TrEMBLrel. 01, Last seq
01-JUN-2001 (TrEMBLrel. 17, Last ann
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NCBI_TaxID=10566;
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1 STSNLAS 7 ||:|||| 273 STANLAS 279 qq ٥y

Search completed: December 23, 2002, 07:29:52 Job time : 4.9031 secs

us-09-865-198-6.rai

Title: Perfect score:

Sequence:

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OM protein

Run on

Scoring table:

Searched:

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44, Appl
35, Appl
34, Appl
112, Appl
112, Appl
102, Appl
93, Appl
93, Appl
7, Appl
85, Appl
90, Appl
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/116,778E
FILING DATE: 07-SEP-93
CLASSIFICATION: 424
ATTONNEY/AGENT INFORMATION:
NAME: WILSON, MARY J.
REGISTRATION NUMBER: 32,955
REFERENCE/DOCKET NUMBER: 249-59
TELEPANONICATION NUMBER: 249-59
TELECOMMUNICATION NUMBER: 240-60
TELEPANONICATION NUMBER: 240-60
TELEPANONICATION INFORMATION:
TELEPANONICATION OF 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 9 amino acids
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Pred. No. 1.9e+05;
1; Mismatches 0;
                            US-09-423-439-51
US-08-378-939-32
US-08-378-939-34
US-08-314-000A-12
US-09-485-737B-102
US-09-485-737B-93
US-09-485-737B-93
US-09-485-737B-91
US-09-485-737B-91
US-09-485-737B-91
US-09-485-737B-91
US-09-485-737B-90
US-09-485-737B-90
US-09-485-737B-90
US-09-485-737B-90
US-09-85-737B-90
US-08-85-867-2
US-08-85-867-2
US-08-85-868-18
US-08-85-868-18
US-08-85-869-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:

APPLICANT: NAKAMURA, KAZUYASU
APPLICANT: KOIKE, MASAMICHI
APPLICANT: KOIKE, MASAMICHI
APPLICANT: HANAI, NOBUO
APPLICANT: HASEGAMA, MANORU
COUNTERS: ADDRESS:
ADDRESSEE: ALINGYON & VANDERHYE P.C.
STREET: 1100 NORTH GLEBE ROAD
CITY: ARLINGTON
STATE: VIRGINIA
COUNTRY: U.S.A.
ZIP: 22201-4714
COMPUTER: REABABLE FORM:
MEDIUM TYPE: FLOPPY disk
COMPUTER: LEM PC COMPATIBLE
COMP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 11, Application US/08116778E Patent No. 5830470
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Best Local Similarity 88.9%;
Matches 8; Conservative
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881.2
779.22
779.22
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US-08-116-778E-11
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Sequence 110, App
Sequence 2, Appli
Sequence 92, Appli
Sequence 111, Appl
Sequence 1113, Appl
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16, Appl
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28, Appl
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113, App
37, Appl
37, Appl
                                                                                                                                                                                                                                                      December 23, 2002, 07:20:23 ; Search time 1.62209 Seconds (without alignments) 163.250 Million cell updates/sec
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/cgn2_6/ptodata/1/iaa/5B_COMB.pep:*
/cgn2_6/ptodata/1/iaa/6A_COMB.pep:*
/cgn2_6/ptodata/1/iaa/6B_COMB.pep:*
/cgn2_6/ptodata/1/iaa/pcTUS_COMB.pep:*
/cgn2_6/ptodata/1/iaa/pcTUS_COMB.pep:*
                                    GenCore version 5.1.3 GenCore version 5.1.3 Copyright (c) 1993 - 2002 Compugen Ltd
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US-08-393-3858-110
US-08-148-562-2
US-08-483-5288-92
US-08-393-3858-111
US-09-393-3858-111
US-09-393-3858-113
US-08-116-7788-37
US-08-116-7788-37
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US-08-652-507-2
US-08-661-052-16
US-09-188-082-16
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US-09-171-945-52
US-09-171-945-97
US-09-171-945-99
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US-09-171-945-50
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Maximum Match 1008
Listing first 45 summaries
                                                                                                                                                                                              protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 2000000000
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48
1 QQRSSYPFT 9
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Length 9;
                                                                                                         CITY: AKLINOJO...
STATE: VIGGINIA
COUNTRY: U.S.A.
ZIP: 22201-4714
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
SOFTWARE: Patentin Release #1.0, Version #1.25
SOFTWARE: OT-UN-95
SOFTWARE: OT-UN-95
SOFTWARE: OT-UN-95
TELECOMMUNICATION NUMBER: US/08/483,528B
FILING DATE: 07-UN-95
CLASSIFICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEFAX: (703)816-4000
TELEFAX: (703)816-4000
TELEFAX: (703)816-4000
TELEFAX: (703)816-4000
TELEFAX: (703)816-4000
SEQUENCE CHARACTERISTICS:
LENGTH: 9 amino acids
TWARE AMINO ACIDS
TELENGTH: 9 amino acids
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPAtible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        93.8%; Score 45; DB 2; Le
88.9%; Pred. No. 1.9e+05;
tive 1; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 110, Application US/09393385B

Patent No. 6423511

GENERAL INFORMATION:
APPLICANT: NAKAMURA, KAZUYASU
APPLICANT: KOIKE, MASAMICHI
APPLICANT: KOIKE, MASAMICHI
APPLICANT: KOWANA, YOSHIHISA
APPLICANT: KWANA, NOBUO
APPLICANT: HANAI, NOBUO
TITLE OF INVENTION: HUMANIZED ANTIBODIES
NUMBER OF SEQUENCES: 113
CORRESPONDENCE ADDRESS:
ADDRESSEE: NIXON & VANDERHYE P.C.
STREET: 1100 NORTH GLEBE ROAD
CITY: ARLINGTON
STATE: VIRGINIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: US/09/393,385B FILING DATE: 27-JUN-96
                                                               STREET: 1100 NORTH GLEBE ROAD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEPHONE: (703)816-4000
TELEFAX: (703)816-4100
INFORMATION FOR SEQ ID NO: 11
SEQUENCE CHARACTERISTICS:
LENGTH: 9 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 93.8
Best Local Similarity 88.9
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; TOPOLOGY: linear; MOLECULE TYPE: peptide US-08-483-528B-99
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STRANDEDNESS: single
                                                                                           CITY: ARLINGTON
STATE: VIRGINIA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPREME PATENTIAL PC-DOS/MS-DOS
SOFTWARE: PATENTIAL NATION DATA:
APPLICATION NUMBER: US/08/438,562
CLASSIFICATION: 424
PRIOR APPLICATION 1424
PRIOR APPLICATION NUMBER: 08/116,778
FILING PATENT INFORMATION:
APPLICATION NUMBER: 32,955
REFIRENCE/POCKET NUMBER: 32,955
REFERENCE/POCKET NUMBER: 32,955
REFERENCE/POCKET NUMBER: 32,955
REFERENCE/POCKET NUMBER: 32,957
TELEPHÓNE: (703)816-4000
TELEPHÓNE: (703)816-4100
TELEPHÓNE: (703)816-4100
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US-00-483-528B-99
Sequence 99, Application US/08483528B
Patent No.5 5939532
GENERAL INFORMATION:
APPLICANT: NORKAMURA, KAZUYASU
APPLICANT: SHITARA, KENYA
APPLICANT: HANAI, NOBUO
APPLICANT: HANAI, NOBUO
APPLICANT: HASEGAMA, MAMORU
APPLICANT: HASE
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Pred. No. 1.9e+05
1; Mismatches
                                                                                                                                                                                                                         GENERAL INCOMATION:
APPLICANT ROINE, MASAMICHI
APPLICANT ROINE, MASAMICHI
APPLICANT ROINE, MASAMICHI
APPLICANT ROINE, MASAMICHI
APPLICANT ROINE, MOBUO
APPLICANT HANAI, NOBUO
TITLE OF INVENTION: HUMANIZED ANTIBODIES
NUMBER OF GENOUENCES: 49
CORRESPONDENCE ADDRESS: 49
CORRESPONDENCE ADDRESS: 40
CITY: ARLINGTON & VANDERHYE P.C.
STREET: 1100 NORTH GLEBE ROAD
CITY: ARLINGTON
STREET: VIRGINIA
COUNTRY: VIRGINIA
COUNTRY: VIRGINIA
COUNTRY: VIRGINIA
COUNTRY: WEBADABLE FORM:
COUNTRY: WEBADABLE FORM:
COUNTRY: WEBADABLE FORM:
COUNTRY: WEBADABLE FORM:
                                                                                                                                                                    Sequence 11, Application US/08438562
Patent No. 5874255
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SEQUENCE CHARACTERISTICS:
LENGTH: 9 amino acids
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Best Local Similarity 88.9
Matches 8, Conservative
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1 QORSSYPYT 9
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                                                                                                  RESULT 2
US-08-438-562-1
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Gaps

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; NAME/KEY: domain
; LOCATION: 88..96
; LOCATION: 88..96
; IDENTIFICATION METHOD: BY SIMILARITY
; IDENTIFICATION METHOD: WITH KNOWN SEQUENCE OR TO AN ESTABLISHED
; IDENTIFICATION METHOD: CONSENSUS
; OTHER INFORMATION: /product= "HYPERVARIABLE REGION 3"
US-08-116-778E-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         BY SIMILARITY WITH KNOWN SEQUENCE TO TO AN ESTABLISHED CONSENSUS
                                                                                                                                                                                                                                                                                          Length 129;
                        /product= "HYPERVARIABLE REGION 2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: PATENTIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/438,562
FILLING DATE: 10-MAY-95
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/116,778
FILLING DATE: 07-SEP-93
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: WILSON, MARY: 32,955
REGISTATION NUMBER: 32,955
RECISTATION NUMBER: 32,955
RECISTATION NUMBER: 249-76
TELEPHONE: (703)816-4000
TELEFAX: (703)816-4100
INPORMATION FOR SEQ ID NO: 2:
SEQUENCE (ARRACTERISTICS:
LENGTH: 129 mmino acids
TYPE: mmino acids
                                                                                                                                                                                                                                                                                          93.8%; Score 45; DB 2;
88.9%; Pred. No. 0.12;
iive 1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: NAKAMURA, KAZUYASU
APPLICANT: KOIKE, MASAMICHI
APPLICANT: SHITARA, KENYA
APPLICANT: HANAI, NOBUO
APPLICANT: HASEGAMA, MANORU
TITLE OF INVENTION: HUMANIZED ANTIBODIES
OORRESPONDENCE ADDRESS:
ADDRESSEE: NIXON & VANDERHYE P.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADDRESSEE: NIXON & VANDERHYE P.C.
STREET: 1100 NORTH GLEBE ROAD
CITY: ALLINGTON
STATE: VIRGINIA
COUNTRY: U.S.A.
ZIP: 22201-4714
COMPUTER READABLE FORM:
MEDIUM TYPE: ELOAPY disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
  CONSENSUS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 2, Application US/08438562
Patent No. 5874255
IDENTIFICATION METHOD: OTHER INFORMATION: /prc
                                                                                                                                                                                                                                                                                                                                                    8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LOCATION: -22. -1
IDENTIFICATION METHOD:
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                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
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LOCATION: 24..33
IDENTIFICATION METHOD: BY SIMILARITY
IDENTIFICATION METHOD: WITH KNOWN SEQUENCE OR TO AN ESTABLISHED
IDENTIFICATION METHOD: CONSENSUS
OTHER INFORMATION: /product= "HYPERVARIABLE REGION 1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           BY SIMILARITY WITH KNOWN SEQUENCE OR TO AN ESTABLISHED
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                                                                                                      Score 45; DB 4; Length 9;
Pred. No. 1.9e+05;
1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STATE: VIRGINIAN
COUNTRY: U.S.A.
ZIP: 22201-4714

ZIP: 22201-4714

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
RPLING DATE: 07-SEP-93
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
REFERENCE/DOCKET NUMBER: 249-59
TELECOMMUNICATION INFORMATION:
TELEFAX: (703)816-4100
                                                                                                                                                                                                                                                                                                                                                                                        Sequence 2, Application US/08116778E
Patent No. 5830470
GENERAL INFORMATION:
APPLICANT: NARAMURA, KAZUYASU
APPLICANT: KOIKE, MASAMICHI
APPLICANT: HANAI, NOBUO
APPLICANT: HANAI, NOBUO
APPLICANT: HANAI, NOBUO
APPLICANT: HASEGAWA, MAMORU
TITLE OF INVENTION: HUMANIZED ANTIBODIES
NUMBER OF SEQUENCES: 49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 BY SIMILARITY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CORRESPONDENCE ADDRESS:
ADDRESSEE: NIXON & VANDERHYE P.C.
STREET: 1100 NORTH GLEBE ROAD
                                                                                                      93.8%;
88.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          : 129 amino acids
amino acid
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IDENTIFICATION METHOD:
IDENTIFICATION METHOD:
IDENTIFICATION METHOD:
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LOCATION: 49..55
IDENTIFICATION METHOD:
IDENTIFICATION METHOD:
                                                                                                   Query Match 93.8
Best Local Similarity 88.9
Matches 8; Conservative
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                ; MOLECULE TYPE: peptide US-09-393-385B-110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MOLECULE TYPE: protein
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TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CITY: ARLINGTON STATE: VIRGINIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         VIRGINIA
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US-08-116-778E-2
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Gaps
BY SIMILARITY WITH KNOWN SEQUENCE TO TO AN ESTABLISHED CONSENSUS
                                                                                                NAME/KEY: domain
LOCATION: 24.33
IDENTIFICATION METHOD: BY SIMILARITY
IDENTIFICATION METHOD: WITH KNOWN SEQUENCE OR TO AN ESTABLISHED
IDENTIFICATION METHOD: CONSENSUS
OTHER INFORMATION: /product= "HYPERVARIABLE REGION 1"
                                                                                                                                                                                                                                                                                                                           NAME/KEY: domain
LOCATION: 49.25
LOCATION 49.25
LIDENTIFICATION METHOD: BY SIMILARITY
LIDENTIFICATION METHOD: WITH KNOWN SEQUENCE OR TO AN ESTABLISHED
LIDENTIFICATION METHOD: CONSENSUS
OTHER INFORMATION: /product= "HYPERVARIABLE REGION 2"
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME/KEY: domain
LOCATION: 88..96
LIDENTIFICATION METHOD: BY SIMILARITY
LIDENTIFICATION METHOD: WITH KNOWN SEQUENCE OR TO AN ESTABLISHED
LIDENTIFICATION METHOD: CONSENSUS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/393,385B
FILING DATE: 27-JUN-96
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             93.8%; Score 45; DB 2;
88.9%; Pred. No. 0.12;
live 1; Mismatches (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
APPLICANT: NAKAMURA, KAZUYASU
APPLICANT: KOIKE, MASAMICHI
APPLICANT: SHITARA, KENYA
APPLICANT: SHITARA, KOBUO
APPLICANT: KUWANA, YOSHHHISA
APPLICANT: HANGAI, WAMORU
ITITLE OF INVENTION: HUMANIZED ANTIBODIES
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADDRESSEE: NIXON & VANDERHYE P.C. STREET: 1100 NORTH GLEBE ROAD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 111, Application US/09393385B Patent No. 6423511
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEPHONE: (703)816-4000
TELEFAX: (703)816-4100
INFORMATION FOR SEQ ID NO: 111:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELECOMMUNICATION INFORMATION:
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Best Local Similarity 88.2.
Fra 8; Conservative
      IDENTIFICATION METHOD: IDENTIFICATION METHOD:
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MOLECULE TYPE: protein
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STRANDEDNESS: sin
TOPOLOGY: linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        VIRGINIA
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US-09-393-385B-111
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                                                                                                                                                                                          NAME/KEY: domain
LOCATION: 49..55
IDENTIFICATION METHOD: BY SIMILARITY
IDENTIFICATION METHOD: WITH KNOWN SEQUENCE OR TO AN ESTABLISHED
IDENTIFICATION METHOD: CONSENSUS
OTHER INFORMATION: /product= "HYPERVARIABLE REGION 2"
FEATURE: #
                                                                  BY SIMILARITY WITH KNOWN SEQUENCE OR TO AN ESTABLISHED CONSENSUS
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OD: WITH KNOWN SEQUENCE OR TO AN ESTABLISHED
OD: CONSUSSUS
OPTOCOLCL "HYPERVARIABLE REGION 3"
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                                                                                                                                                                      /product= "HYPERVARIABLE REGION 1"
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APPLICANE: NARAMICHI
APPLICANE: NARAMICHI
APPLICANE: SHITARA, KENYA
APPLICANE: HANAI, NEUNO
APPLICANE: HANAI, NEUNO
APPLICANE: HANAI, NEUNO
APPLICANE: HARBGAWA, MAMORU
APPLICANE: HASEGAWA, MAMORU
APPLICANE: HASEGAWA, MAMORU
ATTLE OF INVENTION: HUMANIZED ANTIBODIES
NUMBER OF SEQUENCES: 103
CORRESPONDENCE ADDRESS:
ADDRESSE: NIXON & VANDERHYE P.C.
STREET, 1100 NORTH GLEBE ROAD
CITY: FALINGTON
STATE, VIRGINIA
COMPUTER: FALINGTON
MEDIUM TYPE: Floppy disk
COMPUTER: READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: PARENTIN RELEASE #1.0, Version #1.25
SOFTWARE: PALENTION DATA:
COMPUTER: PALENTION NUMBER: US/08/483,528B
FILING DATE: O'-UN-95
CLASSMELCATION INFORMATION:
TELEBRAM: (703)816-4100
TELEBRAM: AMILO ACID
NOTE: AMILO ACID
TELEBRAM: AMILO ACID
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Patent No. 5939532
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                                                                                                                                                                                                                                                                                                                                                                                                                        LOCATION: 88.36
; LOCATION: 88.36
; IDENTIFICATION METHOD: B.
; IDENTIFICATION METHOD: W1
; IDENTIFICATION METHOD: CO.
; OTHER INFORMATION: /production: /product
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                                       LOCATION: 24..33
IDENTIFICATION METHOD:
IDENTIFICATION METHOD:
IDENTIFICATION METHOD:
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Matches 8; Conservative
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LOCATION: -22...1
IDENTIFICATION METHOD:
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                                                                                                                                                                  OTHER INFORMATION:
FEATURE: Comain
             domain
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         NAME/KEY#:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Patent No. 5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                          SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/116,778E
FILING DATE: 07-SEP-93
CLASSIFICATION: 424
AUTONNEY/AGENT INDOC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
APPLICANT: NAKAMURA, KAZUYASU
APPLICANT: KOLKE, MASAMICHI
APPLICANT: SHITARA, KENYA
APPLICANT: HANAI, NOBUO
APPLICANT: HANAI, NOBUO
APPLICANT: HASEGAWA, MAMORU
APPLICANT: HASEGAWA, MAMORU
APPLICANT: HASEGAWA, MAMORU
APPLICANT: ABSEGAWA, MAMORU
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1: Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADDRESSEE: NIXON & VANDERHYE P.C. STREET: 1100 NORTH GLEBE ROAD
   NUMBER OF SEQUENCES: 49
CORRESSPONDEMESS:
ADDRESSEE: NIXON & VANDERHYE P.C.
STREET: 1100 NORTH GLEBE ROAD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: US/08/438,562
FILING DATE: 10-MAY-95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-08-438-562-37; Sequence 37, Application US/08438562; Patent No. 5874255
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PRIOR APPLICATION DATA:
FILING DATE: 08/116,778
                                                                                                           COUNTRY: U.S.A.
ZIP: 22201-4714
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPAtible
OPERATING SYSTEM: PC-DOS/MS-D
SOFTWARE: PatentIn Release #1
                                                                                                                                                                                                                                                                                                                     ATTORNEY/AGENT INFORMATION:
NAME: WILSON, MARY J.
REGISTRATION NUMBER: 249-
REFERENCE/CDCKET NUMBER: 249-
TELEPHONE: (703)816-4000
                                                                                                                                                                                                                                                                                                                                                                                                                                                          INFORMATION FOR SEO ID NO: 37: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             93.8%;
88.9%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LENGTH: 133 amino acids TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 88.9
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CITY: ARLINGTON
SPATE: VIRGINIA
COUNTRY: U.S.A.
ZIP: 22201-4714
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy di
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; MOLECULE TYPE: protein US-08-116-778E-37
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           110 QQRSSYPYT 118
                                                                        CITY: ARLINGTON STATE: VIRGINIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 QQRSSYPFT
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TOPOLOGY:
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                                         DB 4; Length 130;
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                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CITY: ARLINGTON
STATE: VIRGINIA
COUNTRY: US.A.
ZIP: 22201-4714
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Ploppy disk
COMPUTER: Ploppy disk
COMPUTER: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/393,385B
FILING DATE: 27-JUN-96
CLASSIFICATION:
                                                                                                                                                                                                                                       Sequence 113, Application US/09393385B
Patent No. 6423511
GENERAL INFORMATION:
APPLICANT: NAKAMURA, KAZUYASU
APPLICANT: SHITARA, KENYA
APPLICANT: HANAL, NOBBO
APPLICANT: HANAL, NOBBO
TITLE OF INVENTON: HUMANIZED ANTIBODIES
NUMBER OF SEQUENCES: 113
CORRESPONDENCE ADDRESS:
ADDRESSEE: NIXON & VANDERHYE P.C.
STREET: 1100 NORTH GLEBE ROAD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 45; DB 4;
Pred. No. 0.12;
                                                            Pred. No. 0.12
1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: SHITARA, NEWL.
APPLICANT: HANAI, NOBUO
APPLICANT: KUWANA, YOSHIHISA
APPLICANT: KUWANA, YOSHIHISA
APPLICANT: HASEGAWA, MAMORU
                                           Score 45;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 37, Application US/08116778E Patent No. 5830470 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAKAMURA, KAZUYASU
KOIKE, MASAMICHI
SHITARA, KENYA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELECOMMUNICATION INFORMATION:
TELEPHONE: (703)816-4000
TELEFAX: (703)816-4100
INFORMATION FOR SEQ ID NO: 113:
SEQUENCE CHARACTERISTICS:
                                       93.8%;
88.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LENGTH: 130 amino acids
TYPE: amino acid
STRANDEDNES: single
TOPOLOGY: linear
MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        93.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 93.8
Best Local Similarity 88.9
Matches 8; Conservative
                                     Query Match 93.8
Best Local Similarity 88.9
Matches 8; Conservative
                                                                                                                                     110 QQRSSYPYT 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    110 QQRSSYPYT 118
                                                                                                               1 QQRSSYPFT 9
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US-09-393-385B-111
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT:
APPLICANT:
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Gaps
                                                                                                                                        TITLE OF INVENTION: ANTIBODY AGAINST CARCINOEMBRYONIC ANTIGEN TITLE OF INVENTION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1; Indels
                                                                                                                                                                                                                                                                                                                                                                                    OPERATION SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)
CURREWY APPLICATION DATA:
APPLICATION NUMBER: US/08/652,507
FILING DATE: 02-Jul-1996
CLASSIFICATION: 530
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 16, Application US/08661052
Petent No. 5837243
GENERAL INFORMATION:
APPLICANT: Yashwant M. Deo
APPLICANT: Toel Goldstein
APPLICANT: Robert Graziano
APPLICANT: Robert Graziano
APPLICANT: The Compounds COMPRISED
TITLE OF INVENTION: THERAPEUTIC COMPOUNDS COMPRISED
TITLE OF INVENTION: OF ANTI-FC RECEPTOR ANTIBODIES
                                                                                                                                                                                                                     ADDRESSEE: Nixon & Vanderhye, P.C.
STREET: 1100 No. 5876691th Glebe Road, 8th Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 42; DB 2;
Pred. No. 0.92;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD
STREET: 60 State Street, Suite 510
CITY: Boston
STATE: Massachusetts
                                                             Sequence 2, Application US/08652507 Patent No. 5876691 GENERAL INFORMATION: APPLICANT:
                                                                                                                                                                                                                                                      CITY: Arlington
STATE: Virginia
COUWTRY: USA
ZIP: 22201-4714
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STATE: Massachusetts
COUNTRY: USA
ZIP: 02109-1875
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-D
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ATTORNEY/AGENT INFORMATION:
NAME: Arthur R. Crawford
REGISTRATION NUMBER: 25,327
REFERENCE/DOCKET NUMBER: 117-
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-816-4100
TELEFAX: 703-816-4100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               87.5%;
88.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEFAX: 703-816-4100
INFORMATION FOR SEQ ID NO: 2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  : 270 amino acids amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 88.99
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-652-507-2
                                                                                                                                                                               NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1111111 |
249 QQRSSYPLT 257
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                           RESULT 13
US-08-652-507-2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STATE: VIRGINIA
COUNTRY: U.S.A.
ZINE: $2201-4714
COMPUTER: FALABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: FLOPPY disk
COMPUTER: FINE FOOMBAILE
COMPUTER: FINE FOOMBAILE
COMPUTER: PATENTIAL PLOS/MS-DOS
SOFTWARE: PATENTIAL Release #1.0, Version #1.25
CURRENT APPLICATION NUMBER: US/08/483,528B
FILING DATE: 07-JUN-95
CLESSETICATION INFORMATION:
TELEPRAM: (703)816-4000
TELEPRAM: (703)816-4100
                                                                                                                                                                                                                                                                                                             Score 45; DB 2;
Pred. No. 0.12;
l; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 45; DB 2;
Pred. No. 0.12;
1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: NAKAMURA, KAZUYASU
APPLICANT: KOIKE, MASAMICHI
APPLICANT: SHITARA, KENYA
APPLICANT: HARAI, NOBUO
APPLICANT: HASEGAWA, MAMORU
TITLE OF, INVENTION: HUMANIZED ANTIBODIES
NUMBER OF SEQUENCES: 103
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADDRESSEE: NIXON & VANDERHYE P.C. STREET: 1100 NORTH GLEBE ROAD CITY: ARLINGTON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-08-483-5288-101
; Sequence 10%, Application US/08483528B
; Patent No. 5939532
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: WILSON, MARY J.
REGISTRATION NUMBER: 32,955
REFERENGE/DOCKET NUMBER: 249-
TELECHOMINICATION INFORMATION:
TELEPHONE: (703)816-4000
TELEFAXE (703)816-4100
INFORMATION FOR SEQ ID NO: 37:
SEQUENCE GHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEFAX: (703)816-4100
INFORMATION FOR SEQ ID NO: 101:
                                                                                                                                                                                                                                                                                                           93.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       93.8%;
88.9%;
                                                                                                                                                                                           LENGTH: 133 amino acids TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE CHARACTERISTICS:
LENGTH: 133 amino acids
TYPE: amino acid
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                                                                                                                                                                                                                                                    YPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TOPOWOGY: linear
MOLECUWE TYPE: protein
                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                            110 QORSSYPYT 118
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MOLECULE TYPE
US-08-438-562-37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-08-483-528B-101
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                                                                                                                                                                                                                                                                                                                                                                  1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 16, Application US/09188082
Patent No. 6370765
CEMERAL INFORMATION
APPLICANT: Yeahwant M. Deo
APPLICANT: Joel Goldstein
APPLICANT: Robert Graziano
APPLICANT: Chezian Somasundaram
TITLE OF INVENTION: THERAPEUTIC COMPOUNDS COMPRISED
TITLE OF INVENTION: OF ANTI-FC RECEPTOR ANTIBODIES
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD
STREET: 60 State Street, Suite 510
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                0; Mismatches
                                                                                                                 NAME: Arnold, Beth E.
REGISTRATION NUMBER: 35,430
REFERNEC/POCKET NUMBER: MXI-043CP
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)227-7400
TELEFAX: (617)227-541
INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
LENGTH: 553 amino acids
                                         FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/484,172
FILING DATE: 07-JUNE-1995
ATTORNEY/AGENT INFORMATION:
                            APPLICATION NUMBER: US/08/661,052
                                                                                                                                                                                                                                                                                                                                    87.5%;
88.9%;
                                                                                                                                                                                                                                          ; LENGTH: 553 amino acids
; TYPE: amino acid
TYPE: amino acid
TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-661-052-16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             553 amino acids
                                                                                                                                                                                                                                                                                                                                  Query Match 87.55
Best Local Similarity 88.99
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CITY: Boston
STATE: Massachusetts
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LENGTH: 553 amino TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                 499 QQRSSYPLT 507
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US-09-188-082-16
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/cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep:*
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GenCore version 5.1.3
Copyright (c) 1993 - 2002 Compugen Ltd.
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                                                                                                                                                                                                                                                                                                                                                                                                        106657 seqs, 16763532 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Published_Applications_AA:*
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Maximum Match 100%
Listing first 45 summaries
                                                                                           - protein search, using sw model
                                                                                                                                                                                                                                                                                                                                  BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Minimum DB seq length: 0
Maximum DB seq length: 200000000
                                                                                                                                                                                                                                  US-09-865-198-6
48
1 QORSSYPFT 9
                                                                                                                                                                                                                                    Title:
Perfect score:
Sequence:
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                                                                                         OM protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Database :
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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SUMMARIES

Description	iland A equences			Sequence 23, Appl	-	Sequence 8, Appli	Sequence 6, Appli	Sequence 29, Appl	Sequence 28, Appl		Sequence 27, Appl			7	Sequence 19, Appl	28,	ď,	_	
B ID	10 IIS-09-976-787-6	10 US-09-865-198-6	10 US-09-976-787-24	10 US-09-865-198-23	10 US-09-976-787-8	10 US-09-865-198-8	10 US-09-881-823-6	10 US-09-976-787-29	10 US-09-865-198-28	10 US-09-976-787-28	10 US-09-865-198-27	9 US-09-144-886-88	9 US-09-144-886-89	10 US-09-808-037-17	10 US-09-808-037-19	10 US-09-808-037-28	10 US-09-808-037-6	10 US-09-808-037-18	9 US-09-144-886-75
% Query Match Length DB ID	6 0 00	0.0	100.0 106	0.00								93.8 107	3.8 112	6 9.6	. 6 9.6	119.6	19.6 239	13.3	13.3 107
% Qu Score Ma	48 10	48 10	48 10	48 10	48 10	48 10	48 10	48 10	48 10	48 10	48 10	45 9	45 9	43 8	43 8	43 8	43 8	40 8	40 8
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Sequence 28, Appl Sequence 50, Appl Sequence 61, Appl Sequence 71, Appl Sequence 17, Appl Sequence 17, Appl Sequence 97, Appl Sequence 97, Appl Sequence 12, Appl Sequence 12, Appl Sequence 16, Appl Sequence 16, Appl Sequence 16, Appl Sequence 16, Appl Sequence 16, Appl Sequence 16, Appl Sequence 79, Appl Sequence 79, Appl Sequence 79, Appl Sequence 79, Appl Sequence 6, Appl Sequence 6, Appl Sequence 176, Appl Sequence 17, Appli Sequence 17, Appli Sequence 17, Appli Sequence 17, Appli Sequence 17, Appli
10 US-09-910-059-28 10 US-09-910-059-50 10 US-09-910-059-61 10 US-09-910-059-61 10 US-09-910-059-9 10 US-09-144-886-78 10 US-09-144-886-78 10 US-09-144-886-78 10 US-09-144-886-78 10 US-09-144-15-5 10 US-09-144-15-5 10 US-09-910-51 10 US-09-910-51 10 US-09-910-51 10 US-09-910-51 10 US-09-910-51
11000 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0
8811.2 8811.2 8811.2 8811.2 8811.2 8811.2 8811.2 8811.2 8812.2 8813.2 88
01022222222222222222222222222222222222

ALIGNMENTS

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Sequence 6, Application US/09865198
Patent No. US20020103345A1
GENERAL INFORMATION:
APPLICANT: Zhu, Zhenping
TITLE OF INVENTION: Bispecific Immunoglobulin-Like Antigen Binding Proteins and Me
TITLE OF INVENTION: Production
FILE REPERENCE: 11245/47102
CURRENT APPLICATION NUMBER: US/09/865,198
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                                                         Sequence Seq
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Best Local Similarity
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US-09-865-198-6
9-184-976-60-SU
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Sequence 8, Application US/09865198
Patent No. US20020103345A1
GENERAL INCORMATION:
GENERAL INCORMATION:
TITLE OF INVENTION: Bispecific Immunoglobulin-Like Antigen Binding Proteins and Me
TITLE OF INVENTION: Production
TITLE OF INVENTION: Production
FILE REFERENCE: 11245/47102
CURRENT APPLICATION NUMBER: US/09/865,198
CURRENT FILING DATE: 2001-05-24
PRIOR FILING DATE: 2000-05-24
NUMBER OF SEQ ID NOS: 34
SOFTWARE: WordPerfect 8.0 for Windows
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US-09-976-787-8
US-09-976-787-8
Sequence 8, Application US/09976787
Sequence 8, Application US/09976787
Sequence 10. US2020064528A1
GENERAL INFORMATION:
APPLICANT: Zhu, Zhenping
APPLICANT: Witck, Larry
TITLE OF INVENTION: Antibodies Specific to KDR and Uses Thereof
FILE REFERENCE: 11245/46505
CURRENT APPLICATION NUMBER: US/09/976,787
CURRENT FILING DATE: 2001-10-12
PRIOR PILING DATE: 2000-01-28
PRIOR PLING DATE: 1999-01-28
PRIOR PLING DATE: 1999-01-29
NUMBER OF SEQ ID NOS: 40
SOFTWARE: WordPerfect 8.0 for Windows
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Query Match
100.0%; Score 48; DB 10; Length 106;
Best Local Similarity 100.0%; Pred. No. 0.014;
Matches 9; Conservative 0; Mismatches 0; Indels
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Best Local Similarity 100.0%; Score 48; DB 10; Length 108;
Best Local Similarity 100.0%; Pred. No. 0.014;
Matches 9; Conservative 0; Mismatches 0; Indels
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Best Local Similarity 100.0%; Score 48; DB 10; Length 108;
Best Local Similarity 100.0%; Pred. No. 0.014;
Matches 9; Conservative 0; Mismatches 0; Indels
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; ORGANISM: Mouse
US-09-865-198-8
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LENGTH: 108
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US-09-865-198-8
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LENGTH: 108
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US-09-881-823-6
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APPLICANT: Witte, Larry
APPLICANT: Witte, Larry
TITLE OF INVENTION: Antibodies Specific to KDR and Uses Thereof
FILE REFERENCE: 11245/46505; CURRENT APPLICATION NUMBER: US/09/976,787
CURRENT FILMG DATE: 2001-10-12; PRIOR APPLICATION NUMBER: US 09/493,539
PRIOR FILLNG DATE: 2000-01-28
PRIOR FILLNG DATE: 1999-01-29
NUMBER OF SEQ ID NOS: 40
SOFTWARE: WordPerfect 8.0 for Windows
SEQ ID NO 240;
LENGTH: 106
LENGTH: 106
TYPE: PRIOR
US-09-976-787:24
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100.0%; Pred. No. 8.9e+04;
tive 0; Mismatches 0;
   CURRENT FILING DATE: 2001-05-24
PRIOR APPLICATION NUMBER: US 60/206,749
PRIOR FILING DATE: 2000-05-24
NUMBER OF SEQ ID NOS: 34
SOFTWARE: WordPerfect 8.0 for Windows
SEQ ID NO 6
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Best Local Similarity
Matches 9% Conserva
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; TYPE: PRT ;
; ORGANISM: Mouse
US-09-865-198-6
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US-09-865-198-23
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US-09-976-787-24
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Sequence 27, Application US/09865198
Patent No. US20020103345a1
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: Bispecific Immunoglobulin-Like Antigen Binding Proteins and Me
TITLE OF INVENTION: Production
TITLE OF INVENTION: Production
FILE REFERENCE: 11245/47102
CURRENT APPLICATION NUMBER: US/09/865,198
CURRENT FILING DATE: 2001-05-24
PRIOR FILING DATE: 2000-05-24
NUMBER OF SEQ ID NOS: 34
NUMBER OF SEQ ID NOS: 34
SOFTWARE: WordPerfect 8.0 for Windows
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Fatent No. US200200645281
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Zhu, Zhenping
TITLE OF INVENTION: Antibodies Specific to KDR and Uses Thereof
FILE REFERENCE: 11245/45505
CURRENT APPLICATION NUMBER: US/09/976,787
CURRENT FILING DATE: 2001-10-12
PRIOR APPLICATION NUMBER: US 60/493,539
PRIOR PLICATION NUMBER: US 60/117,726
PRIOR PLICATION NUMBER: US 60/117,726
PRIOR FILING DATE: 1999-01-29
NUMBER OF SEQ ID NOS: 40
SOFTWARE: WordPerfect 8.0 for Windows
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, 0.03;
0; Indels
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100.0%; Pred. No. 0.03;
Live 0; Mismatches 0;
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100.0%; Pred. No. 0.0
Live 0; Mismatches
CURRENT APPLICATION NUMBER: US/09/865,198;
CURRENT FILING DATE: 2001-05-24
PRIOR APPLICATION UNMBER: US 60/206,749;
PRIOR FILING DATE: 2000-05-24
NUMBER OF SEQ ID NOS: 34
SOFTWARE: WordPerfect 8.0 for Windows SEQ ID NO 28
LENGTH: 238
TYPE: PRT
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Best Local Similarity 100.
Matches 9; Conservative
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Best Local Similarity
Matches 9; Conserv
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220 QQRSSYPFT 228
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; ORGANISM: Mouse
US-09-865-198-27
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US-09-976-787-28
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LENGTH: 240
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LENGTH: 240
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Patent No. US20020103345A1
GENERAL INFORMATION:
APPLICANT: Zhu, Zhenping
TITLE OF INVENTON: Bispecific Immunoglobulin-Like Antigen Binding Proteins and Methoric Professional Proteins Production
FILE REFERENCE: 11245/47102
                                                                                                                                                                                                  APPLICANT: CHEN, LI
TITLE OF INVENTION: Method for the Treatment and Prevention of Dental Caries
FILE REFERENCE: 22851-032
CURRENT APPLICATION NUMBER: US/09/881,823
CURRENT FILING DATE: 2001-06-15
PRIOR FILING DATE: 1999-08-20
NUMBER OF SEQ ID NOS: 32
SOFTWARE: Patentin version 3.0
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US-09-976-787-29
i Sequence 29, Application US/09976787
j Patent No. US20020064528A1
i GENERAL INFORMATION:
    APPLICANT: Zhu, Zhenping
    APPLICANT: Witte, Larry
    TITLE OF INVENTION: Antibodies Specific to KDR and Uses Thereof
    TITLE OF INVENTION: Antibodies Specific to KDR and Uses Thereof
    TITLE OF INVENTION: Antibodies Specific to KDR and Uses Thereof
    TITLE OF INVENTION: Antibodies Specific to KDR and Uses Thereof
    PRIOR FILING DATE: 12040-10-12
    PRIOR PILING DATE: 2000-10-12
    PRIOR FILING DATE: 1999-01-29
    NUMBER OF SEQ ID NOS: 40
    SOFTWARE: WordPerfect 8.0 for Windows
    SEQ ID NO 29
    LEWING THE STATES SEQ ID NOS: 40
    SOFTWARE: WordPerfect 8.0 for Windows
    LEWING THE STATES SEQ ID NOS: 40
    SOFTWARE: WordPerfect 8.0 for Windows
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    SOFTWARE: WordPerfect 8.0 for Windows
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    MADELLE STATES SEQ ID NOS: 40
    SOFTWARE: WordPerfect 8.0 for Windows
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; Pred. No. 0.03;
0; Mismatches 0; Indels
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  Application US/09881823
US20020068066A1
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100.0%;
                                                   GENERAL INFORMATION:
APPLICANT: SHI, WENYUAN
APPLICANT: ANDERSON, MAXWELL
APPLICANT: WERNE, SHERIE
APPLICANT: TRINH, KYAN
APPLICANT: WINS, LETITIA
APPLICANT: CHEN, LI
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Best Local Similarity 100.۱
نامع 9; Conservative
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Best Local Similarity 100.
Matches 9; Conservative
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; ORGANISM: Murine
US-09-881-823-6
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; ORGANISM: Mouse
US-09-976-787-29
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Patent No. US20020052311A1
GENERAL INFORMATION:
APPLICANT: SOLOMON, Beka
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US-09-808-037-19
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                                                                                                                                                                       US-09-14-886-88

US-09-144-886-89

Sequence 88, Application US/09144886

Patent No. US-20020155114A1

GENERAL INFORMATION:

APPLICANT: Marks, James B

TITLE OF INVENTION: Therapeutic Monoclonal Antibodies That Neutralize

TITLE OF INVENTION: Detail Nourocoxins

FILE REFERENCE: 2500.1170SO

CURRENT APPLICATION NUMBER: US/09/144,886

CURRENT FILENCE PATE: 1998-08-31

NUMBER OF SEQ ID NOS: 98

SEQ ID NO 88

SEQ ID NO 88

MARCH AND SEC ID NOS: 98

SEQ ID NO 88

MARCH AND SEC ID NOS: 98

SEQ ID NO 88
                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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APPLICANT Marks, James D
APPLICANT Manersdorfer, Peter
TITLE OF INVENTION: Therapeutic Monoclonal Antibodies That Neutralize
TITLE OF INVENTION: Botulinum Neurotoxins
FILE REFERENCE: 2500 117050
CURRENT APPLICATION WIMBER: US/09/144,886
CURRENT FIGING DATE: 1998-08-31
NUMBER OF SEQ ID NOS: 98
SOFTWARE: @tentin Ver. 2.0
SEQ ID NO 8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; OTHER INFORMATION: Description of Artificial Sequence: BONT/a clone; OTHER INFORMATION: 2G5 region VL epitope 2
US-09-144-886 98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; OTHER INFORMATION: Description of Artificial Sequence: BoNT/A clone; OTHER INFORMATION: 3C3 region VL epitope 2
US-09-144-886@89
  DB 10; Length 240; 0.03;
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Pred. No. 0.051;
1; Mismatches 0; Indels
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93.8%; Score 45; DB 9; Length 112;
Best Local Similarity 88.9%; Pred. No. 0.053;
Matches 8; Conservative 1; Mismatches 0; Indels
                                              0; Indels
                                              0; Mismatches
  100.0%; Score 48; 100.0%; Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 13 $ 100-09-144-886#89 US-09-144-886#89 Application US/09144886 Patent No. US20020155114A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: PRT (CORGANISM: Artificial Sequence FEATURE: F
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: PRF ORGANISM ARTIficial Sequence FEATURE:
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88.9%;
Query Match 100.

Best Local Similarity 100.

Matches 97 Conservative
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Best Local (1978)
Matches (1978)
Conservative
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220 QQRSSYPFT 228
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APPLICANT: SOLOMON, Beka
APPLICANT: SOLOMON, Beka
APPLICANT: HANAN, Ellat
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR THE TREATMENT AND/OR DIAGNOSIS OF
TITLE OF INVENTION: METHODGICAL DISEASES AND DISORDERS
FILE REFERENCE: SOLOMON=2D
CURRENT APPLICATION NUMBER: US/09/808,037
CURRENT FILING DATE: 2001-03-15
PRIOR FILING DATE: 2000-07-31
PRIOR PILING DATE: 1999-12-29
PRIOR APPLICATION NUMBER: US 69/473,653
PRIOR FILING DATE: 1999-12-29
PRIOR FILING DATE: 1999-12-29
PRIOR FILING DATE: 1999-12-29
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TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR THE TREATMENT AND/OR DIAGNOSIS OF
TITLE OF INVENTION: NEUROLOGICAL DISEASES AND DISORDERS
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Best Local Similarity 100.0%; Pred. No. 8.9e+04;
Matches 8; Conservative 0; Mismatches 0;
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Best Local Similarity 100.0%; Pred. No. 8.9e+04;
Matches 8; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILE REFERENCE: SOLOMON-2D
CURRENT APPLICATION NUMBER: US/09/808,037
CURRENT FILING DATE: 2001-03-15
PRIOR APPLICATION NUMBER: 09/629,971
PRIOR FILING DATE: 2000-07-31
PRIOR APPLICATION NUMBER: US 09/473,653
PRIOR FILING DATE: 1999-12-29
PRIOR FILING DATE: 1999-12-29
PRIOR FILING DATE: 1999-12-29
SPRIOR FILING DATE: 1999-12-29
NUMBER OF SEQ ID NOS: 33
SOFTWARE: PatentIn version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; OTHER INFORMATION: synthetic peptide US-09-808-037-17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; OTHER INFORMATION: synthetic peptide US-09-808-037-19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 19, Application US/09808037
                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQ ID NOS: 33
SOFTWARE: Patentin version 3.0
SEQ ID NO 17
LENGTH: 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: PRT ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2 QRSSYPFT
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Search completed: December 23, 2002, 07:58:19 Job time : 0.837209 secs

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4 . 2 / Q80923 human papil Q2522 leishmania P54639 dictyostell Q9w552 drosophila O43868 homo sapien P75338 mycoplasma P3804 emericella P52496 candida alb P09436 saccharomyc P53585 caenorhabdi P53094 saccharomyc P53094 saccharomyc

VE2_HPV48
IF4A_LEIBR
CYS4_DICDI
VP26_DROME
CNT2_HUMAN
YE40_MYCPN
FLUG_EMENI
DNLI_CANAL
SYIC_YEAST
ACLY_CABEL
MDS3_YEAST
NCO2_XENLA

396 403 442 478 658 726 865 928 1107 1106

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December 23, 2002, 07:16:17; Search time 0.889535 Seconds (without alignments) 419.643 Million cell updates/sec
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Copyright (c) 1993 - 2002 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 2000000000
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48
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Perfect score:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

ALIGNMENTS

	Description	P10676 drosophila	P04430 homo sapien	P01618 canis famil	-		_			P42251 bacillus su	Q09512 caenorhabd1	P91809 strongyloce		Q9np56 homo sapien		P49015 cricetulus			Q9x9k2 vibrio para				043524 homo sapien				Q04276 saccharomyc	Q57609 methanococc	P52525 human herpe	_	P14693 saccharomyc	P04989 dictyosteli		P13962 bacillus su
SUMMARIES	QI	NINC_DROME	KV1V_HUMAN	KV1_CANFA	CHR1_VIBCH	HEAD_LAMBD	CYS1_DICDI	KV1L_HUMAN	YDE9_SCHPO	PPBD_BACSU	YLN9_CAEEL	TF2D_STRPU	CN7B_MOUSE	CN7B_HUMAN	SCD5_YEAST	AT7A_CRIGR	KV4A_MOUSE	CHER_VIBAN	CHER_VIBPA	CHLI_MESVI	KYE1_KLULA	CMC2_CAEEL	FXO3_HUMAN	PTP2_YEAST	MAZ3_SCHCO	DP3A_BACSU	YMX2_YEAST	Y145_METJA	VU47_HSV7J	YRC3_CAEEL	YHO3_YEAST	CYS2_DICDI	CYB_HUMAN	REPA_BACSU
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đ	Query Match	77.1	72.9	70.8	70.8	70.8	70.8	68.8	68.8	68.8	68.8	66.7	66.7	66.7	66.7	66.7	9.49	9.49	64.6	9.49	9. 49	9. 49	9. 49	64.6	64.6	9. 49	62.5	62.5	62.5	62.5	62.5	62.5	62.5	62.5
	Score	37	35	34		34	34	33	33	33	33	32	32	32	32	32	31	31	31	31	31	31	31	31	31	31	30	30	30	30	30	30	30	30
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InterPro; IPRO00048;
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modified and this statement is not removed. Usage by and for commercentials requires a license agreement (See http://www.isb-sib.ch/announcor send an email to license agreement (See http://www.isb-sib.ch/announcor send an email to license (sisb-sib.ch). EMBL: 03131; AAA28719.1;
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the European Bioinformatics Institute. There are no restrictions on use by non-profit institutions as long as its content is in no modified and this statement is not removed. Usage by and for commerce entities requires a license agreement (See http://www.isb-sib.ch/annour or send an email to license@isb-sib.ch). EMEL: J03131; AAA28718.1;
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herween the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on use by non-profit institutions as long as its content is in no modified and this statement is not removed. Usage by and for commercentities requires a license agreement (See http://www.isb-sib.ch/annour.or send an email to license@isb.sib.ch). EMBL; J03131; AAA28718.1;
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SUFERRAMILY: CONTAINS 1 10 DOMAIN. 11. SIMILARRITY: CONTAINS 1 10 DOMAIN. This SWISS-PROT entry is copyright. It is produced through a collaborate between the Swiss Institute of Bioinformatics and the ERBL outstatic the European Bioinformatics Institute. There are no restrictions on use by non-profit institutions as long as its content is in no modified and this statement is not removed. Usage by and for commerce entities requires a license agreement (See http://www.isb-sib.ch/announ or send an email to license@isb-sib.ch). EMBL: J03131; AAA28718.1;
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MODICALI C., KUDIN G.M.; "The Drosophila ninac locus encodes two photoreceptor cell specific proteins with domains homologous to protein kinases and the myosin head."; Cell 52:757-772(1988). -!- FUNCTION: REQUIRED FOR PHOTORECEPTOR CELL FUNCTION. THE NINAC PROTEINS JOIN PUTATIVE SERINE/THREONINE-PROTEIN KINASE AND MYOSIN ACTIVITIES!- CATALYTICA ACTIVITY: ATP + a protein - ADP + a phosphoprotein!- SUBCELLUIAR LOCATION: CYTOSRELETON!- SUBCELLUIAR LOCATION: CYTOSRELETON!- ALTERNATIVE PRODUCTS: 2 isoforms; a long form (shown here) and a short form; are produced by alternative splicing!- SIMILARITY: IN THE N-TERMINAL SECTION; BELONGS TO THE MYOSIN SUPERANITY OF PROTEIN KINASES!- SIMILARITY: IN THE C-TERMINAL SECTION; BELONGS TO THE MYOSIN SUPERFAMILY!- SIMILARITY: ONTAINS 1 IQ DOMAIN!- SIMILARITY: CONTAINS 1 IQ DOMAIN!- SIMILARITY: CONTAINS 1 IQ DOMAIN!- SIMILARITY: CONTAINS 1 IQ DOMAIN!- SHALLS AND STATEMENT IS STATEMENT
Montell C., Rubin G. M.; "The Drosophila ninac locus encodes two photoreceptor cell specific proteins with domains homologous to protein kinases and the myosin head." Cell 52:757-772(198).
Montell C., Rubin G.M.; Montell C., Rubin G.M.; "The Drosophila ninac locus encodes two photoreceptor cell specific proteins with domains homologous to protein Kinases and the myosin head."; Cell 53.757-772(198).
Montell C., Rublin G.M.; "The Drosophila ninae locus encodes two photoreceptor cell specific proteins with domains homologous to protein Kinases and the myosin heavy chain head."; Cell 52:75-772(1988).
Mortell C., Rubin G.M.; "The Drosophila ninac locus encodes two photoreceptor cell specific proteins with domains homologous to protein kinases and the myosin heavy chain head."; Cell 52:757-772(1988)
Montell C., Rubin G.M.; The Drosophila ninac locus encodes two photoreceptor cell specific proteins with domains homologous to protein kinases and the myosin heavy chain head.; PEROTEINS with domains homologous to protein kinases and the myosin heavy chain head.; Cell 22:157-72(1988).
MEDLINE-BRIJO167; Nubsid-2449973; MODITELL C., Rubin G.M.; "The Drosophila ninaC locus encodes two photoreceptor cell specific proteins with domains homologous to protein kinases and the myosin head,"; Cell 52:757-772(1988).
MEDLINE-88151067; PubMed=2449973; Montell C., Rubin G.M.; The Drosophila ning locus encodes two photoreceptor cell specific proteins with domains homologous to protein Kinases and the myosin head, "; Cell 52:757-772(1988).
MEDLINE=88151067; PubMed=2449973; Montell C. Rubin G.M.; The Drosophila ninacl locus encodes two photoreceptor cell specific proteins with domains homologous to protein kinases and the myosin heavy chain head." Cell 52:757-772(1988)
MEDLINE-88151067; PubMed-2449973; Montell C., Rubin G.M.; Mandtell C., Rubin G.M.; Proteins with domains homologous to protein kinases and the myosin cell 52:757-772(1988). 1- FUNCTION: REQUIRED FOR PHOTORECEPTOR CELL FUNCTION. THE NINAC PROTEINS JOIN PUTATIVE SERINE/THREONINE-PROTEIN KINASE AND MYOSIN ACTIVITIES. 1- CATALITIC ACTIVITY: ATP + a protein - ADP + a phosphoprotein. 1- SUBCELLULAR LOCATION: CYTOSKELETON. 1- ALTERMATIVE PRODUCTS: 2 isoforms; a long form (shown here) and a short form; are produced by alternative splicing. 1- ALTERMATIVE PRODUCTS: 2 isoforms; a long form (shown here) and a short form; are produced by alternative splicing. 1- SIMILARITY: IN THE C-TERMINAL SECTION; BELONGS TO THE MYOSIN SUBCREAMILY. 1- SIMILARITY: COWTAINS 1 IQ DOMAIN. 1- SIMILARITY: COWTAINS 1 IQ DOMAIN. 1- SIMILARITY: COMPAINS 1 IQ
MEDLINE=88151067; PubMe=1209. MEDLINE=88151067; PubMe=1209. MEDLINE=88151067; PubMe=1209. MEDLINE=88151067; PubMe=1209. Proteins with domains homologous to protein kinases and the myosin head. "The Drosophila ninac locus encodes two photoreceptor cell specific proteins with domains homologous to protein kinases and the myosin head."; Cell 52:757-772(1988).
MEDLINE=88151067; PubMed-1209 DECEMBER TOWN NAT. MEDLINE=88151067; PubMed-1249973; MORTELL C., Rubin G.M.; MEDLINE=88151067; PubMed-1249973; MORTELL C., Rubin G.M.; MORTELL C., Rubin G.M.; Proteins with domains homologous to protein kinases and the myosin head.
SECURNCE FROM N.A. FUNCTION, AND ALTERNATIVE SPLICING. MEDLINE-88151667; PubMed-2449973; Montell C., Rubin G.M.; Proposphila ninac locus encodes two photoreceptor cell specific proteins with domains homologous to protein kinases and the myosin heavy chain head. 152:777-772(1988). 1- FUNCTION: REQUIRED FOR PHOTORECEPTOR CELL FUNCTION. THE NINAC ACTIVITIES. 1- CATALYTIC ACTIVITY: ATP + a protein - ADP + a phosphoprotein. 1- SUBCELLUIAR LOCATION: CYTOSKELETON. 1- ALTERNATIVE PRODUCTS: 2 isoforms; a long form (shown here) and a short form; are produced by alternative splicing. 1- SIMILARITY: IN THE N-TERNINAL SECTION; BELONGS TO THE MYOSIN SUPERFAMILY. 1- SIMILARITY: IN THE N-TERNINAL SECTION; BELONGS TO THE MYOSIN SUPERFAMILY. 1- SIMILARITY: IN THE C-TERMINAL SECTION; BELONGS TO THE MYOSIN SUPERFAMILY. 1- SIMILARITY: IN THE N-TERMINAL SECTION; BELONGS TO THE MYOSIN SUPERFAMILY. 1- SIMILARITY: IN THE C-TERMINAL SECTION; BELONGS TO THE MYOSIN SUPERFAMILY. 1- SIMILARITY: IN THE C-TERMINAL SECTION; BELONGS TO THE MYOSIN DELWEEN THE SWISS-PROT entry is copyright. It is produced through a collaborate between the Swiss Institute of Bloinformatics Institute. There are no restrictions on use by non-profit institutions as long as its content is in non-profit institutions as long as its content is not removed. Usage by and for commerce on titles requires a license agreement (See http://www.isb-sib.ch/announ.or send an email to license@isb-sib.ch). ERBEL: J03131; AAA28719.1; - ERBEL: M20230; AAA28720.1; - ERBEL: M20230; AAA28720.1; - ERBEL: M20330; AAA28720.1; - ERBEL:
SEQUENCE FROM N.A., FUNCTION, AND ALTERNATIVE SPLICING. MEDLINE=88151067; PubMed=244993; MODICIL C., Rubin G.M.; Problement of the myosin head. The Drosophila ninac locus encodes two photoreceptor cell specific proteins with domains homologous to protein kinases and the myosin heavy chain head. The Drosophila ninac locus encodes two photoreceptor cell specific proteins with domains homologous to protein kinases and the myosin heavy chain head. The STATIST CATALYTIC ACTIVITY: ATP + a protein - ADP + a phosphoprotein. THE SUBCELLIAR CATIVITY: ATP + a protein - ADP + a phosphoprotein. THE SUBJECTION: REQUIRED FOR PHOTORECEPTON. THE SUBJECTION: ALTORICATION: CYTOSRELETON. THE SUBJECTION: ALTORICATION: CYTOSRELETON. THE STMILARITY: IN THE C-TEMBINAL SECTION; BELONGS TO THE MYOSIN SIMPLEARITY: IN THE C-TEMBINAL SECTION; BELONGS TO THE MYOSIN SUPERFAMIX. THE STMILARITY: IN THE C-TEMBINAL SECTION; BELONGS TO THE MYOSIN SUPERFAMIX. THIS SWIESPENDY: CONTAINS 1 IQ DOMAIN. THIS SWIESPENDY: CONTAINS 1 IQ DOMAIN. THIS SWIESPENDY: CHITY is copylight. There are no restrictions on use by non-profit institute of Bloinformatics and the Embl. on the connect on titles requires a license agreement (See http://www.isb-sib.ch/announ or send an email to license@isb-sib.ch). EMBL: M20230; AAA28719.1; - EMBL: M20230; AAA28719.1; - EMBL: M20230; AAA28719.1; - EMBL: M20230; AAA28720.1; - EMBL: M20230; AAA287
SEDURNCE FROM N.A., FUNCTION, AND ALTERNATIVE SPLICING. MEDLINE-88151067; PubMed-2449973; MODICAL C., RUBIN G.M.; "The Drosophila ninac locus encodes two photoreceptor cell specific proteins with domains homologous to protein kinases and the myosin heavy chain head." 1
SEQUENCE FROM N.A., FUNCTION, AND ALTERNATIVE SPLICING. MEDLINE-88151067; bubmed-2449973; Montell C., Rubin G.M.; "The Drosophila ninaC locus encodes two photoreceptor cell specific proteins with domains homologous to protein kinases and the myosin heavy chain head."; Cell 52:772(1988).
SEQUENCE FROM N.A., FUNCTION, AND ALTERNATIVE SPLICING. MEDLINE-BRISIOGY; PubMed=2449973; Montell C., Rubin G.M.; "The Drosophila ninac locus encodes two photoreceptor cell specific proteins with domains homologous to protein kinases and the myosin heavy chain head."; Cell 52:77-772(1988). - FUNCTION: REQUIRED FOR PHOTORECEPTOR CELL FUNCTION. THE NINAC PROTEINS JOIN PUTATIVE SERINE/THREONINE-PROTEIN KINASE AND MYOSIN ACTIVITIES. CATALITIES CATALITIE ACCATION: CYTOSRELETON ALTERNATIVE PRODUCTS: 2 isoforms, a long form (shown here) and a short form; are produced by alternative splicing SIMILARITY: IN THE N-TERMINAL SECTION; BELONGS TO THE MYOSIN Short form; are produced by alternative splicing SIMILARITY: IN THE N-TERMINAL SECTION; BELONGS TO THE MYOSIN SIMILARITY: CONTAINS 11 Q DOMAIN SIMILARITY: CONTAINS 11 Q DOMAIN SIMILARITY: CONTAINS 11 Q DOMAIN SIMILARITY: CONTAINS 11 COPAING THE ACTION and the EMBL outstatic the European Bioinformatics Institute. There are no restrictions on use by non-profit institutions as long as its content is in no modified and this statement is not removed. Usage by and for commerce entities requires a license agreement (See http://www.isb-sib.ch/annour or send an email to license agreement (See http://www.isb-sib.ch/annour or send an email to license agreement (See http://www.isb-sib.ch/annour or send an email to license agreement (See http://www.isb-sib.ch/annour or send an email to license agreement (See http://www.isb-sib.ch/annour or send an email to license agreement (See http://www.isb-sib.ch/annour or send an email to license agreement (See http://www.isb-sib.ch/annour or send an email to license agreement (See http://www.isb-sib.ch/annour or send an email to license agreement (See http://www.isb-sib.ch/annour or send an email to license agreement (See http://www.isb-sib.ch/annour or send an email to license agreement (See http://www.isb-sib.ch/annour or send an email to license agreement (See http://www.isb-sib.ch/annour or send an email to
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SEQUENCE FROM N.A., FUNCTION, AND ALTERNATIVE SPLICING. MEDLINE=88151067; PubMed=2449973; MORDELLC., RUDIO G.M.; MORDELLC., RUDIO G.M.; MORDELLC., RUDIO G.M.; MORDELLC., RUDIO G.M.; MORDELLOSOPHILA ninac locus encodes two photoreceptor cell specific proteins with domains homologous to protein kinases and the myosin cell 52:757-772(1988). 1- FUNCTION: REQUIRED FOR PHOTORECEPTOR CELL FUNCTION. THE NINAC PROTEINS JOIN PUTATIVE SERINE/THREONINE-PROTEIN KINASE AND MYOSIN ACTIVITIES. 1- CATALITIC ACTIVITY: ATP + a protein - ADP + a phosphoprotein. 1- SUBCELLULAR LOCATION: CYTOSKELETON. 1- SUBCELLULAR LOCATION: CYTOSKELETON. 1- SUBCELLULAR LOCATION: TO THE MINAL SECTION; BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES. 1- SIMILARITY: IN THE C-TERMINAL SECTION; BELONGS TO THE MYOSIN SUPERFAMILY: 1- SIMILARITY: COWTAINS 1 IQ DOMAIN. 1- SIMILARITY: COWTAINS 1 IQ DOMAIN. 1- SIMILARITY: COMPAINS
SEQUENCE FROM N.A., FUNCTION, AND ALTERNATIVE SPLICING. MEDLINE=88151067; PubMed=2449973; Montell C., Rubin G.M.; Montell C., Rubin B. Montell C.,

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Score 35;
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InterPro; IPR003596; Ig_v.
Pfam; PR00047; 1g, 1.
SMART; SM00406; IGv; 1.
Immunoglobulin V region.
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75.0%;
72.98;
66.78;
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                                                 SMART; SMUNLJ; LV.
PROSITE: BSSO006; IQ. 1.
PROSITE: BSSO0107: PROTEIN_KINASE_ATP; FALSE_NEG.
PROSITE: PSSO0109; PROTEIN_KINASE_TYR; 1.
PROSITE: PSSO011; PROTEIN_KINASE_DOM; 1.
Cytoskeleţon; Actin-binding; ATP-binding; Myosin; Transferase; Vision; Scrine/threonine-protein kinase; Alternative splicing.
                                                                                                                                                                                                                BY SIMILARITY.
ACTIN-BINDING (BY SIMILARITY).
AFRGFRDPVRLPPLVNEKSGQLNENTADFIRPFAKKWREKS
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EAEEMFLEARMDEALAAVRIAKIEQASAEE (IN SHORT
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K -> Q (IN REF. 1; AAA28720/AAA28721).

P -> R (IN REF. 1; AAA28721).
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NON ALPHA-HELICAL, C-TERMINAL DOMAIN.
ATP (BY SIMILARITY).
ATP (BY SIMILARITY).
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Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_raxib=9606;
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MEDILINE; 86174817; PubMed=3083240;

Dwulet [S.E., O'Connor T.P., Benson M.D.;

Dwulet [S.E., O'Connor T.P., Benson M.D.;

Mol. Immunol. 23:73-78(1986).

Mol. Immunol. 23:73-78(1986).

HSSP: P804878; KIHUBN.

HSSP: P804878; KIHUBN.

InterPro. IPR0033066; Ig_MRC.

InterPro. IPR003566; Ig_V.

SMARY; $SM00406; IGy. 1.

SMARY; $SM00406; IGy. 1.

Immuno@lobulin V region; Amyloid.
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COMPLEMENTARITY-DETERMINING-1.
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                      ProDom; P0000001; Euk_pkinase; 1.
ProDom; P0000355; myosin_head; 1.
SMART; SM0015; IQ; 2.
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Pfam; PF00069; pkinase; 1.
Pfam; PF00612; IQ; 2.
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"The amino acid sequence of the light chain variable region of a canine myeloma immunoglobulin: evidence that the VK subgroups predated mammalian speciation.";
Immunochemistry 15:303-305(1978).
-i- MISCELLANEOUS: PEPTIDES WERE ALIGNED BY HOMOLOGY WITH HUMAN KAPPA
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-1- MISCELLANBOUS: THE SEQUENCE OF THE V REGION OF THE HEAVY CHAIN OF THIS MYELOMA PROTEIN HAS ALSO BEEN DETERMINED.
PIR; A01907; K2DGGM.
HSSP; P01607; 1REI.
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Bacteria; Proteobacteria; gamma subdivision; Vibrionaceae; Vibrio.
NCBI_TaxID=666;
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Mammalia, Butheria, Carnivora, Fissipedia, Canidae, Canis.
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COMPLEMENTARITY-DETERMINING-1.
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COMPLEMENTARITY-DETERMINING-2.
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COMPLEMENTARITY-DETERMINING-3.
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09KO06: 09XCL5;
15-JUN-2002 (Rel. 41, Created)
15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
15-JUN-2002 (Rel. 41, Last annotation update)
Chem
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 34; DB 1;
Pred. No. 3.2;
DB 1;
                                                                                                                                                                                                                                                                                                                             21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
                                                                                                                                                                                                                                                                                108 AA
                                               2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   BY SIMILARITY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mismatches
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                       Pred. No.
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NCBI_TaxID=10710;
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                                                                                                                                                                                                                                                                                                     Coat
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                                                                                                                                                                                                                                                                                                                                                                                                                                 modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
         STRAIN=E1 Tor N16961 / Serotype 01;
MEDLINE=20406833; PubMed=10952301;
Heidelberg J.F. Eisen J.A. Nelson W.C., Clayton R.A., Gwinn M.L.,
Dodson R.J., Haft D.H., Hickey E.K., Peterson J.D., Umayam L.A.,
Gill S.R., Nelson K.E., Read T.D., Tettelin H., Richardson D.,
Ermolaeva M.D., Vamathevan J., Bass S., Qin H., Dragol I., Sellers P.,
McDonald L., Utterback T., Fleischmann R.D., Nierman W.C., White O.,
Salzberg S.L., Smith H.O., Colwell R.R., Mekalanos J.J., Venter J.C.,
                                                                                                                                                                                                                                            "The chemotactic response of Vibrio anguillarum to fish intestinal mucus is mediated by a combination of multiple mucus components.";
J. Bacteriol. 181:4308-4317(1999).
-!-FUNCTION: METHILATION OF THE MEBRANE-BOUND METHYL-ACCEPTING CHEMOTAXIS PROTEINS (MCP) TO FORM GAMMA-GLUTAMYL METHYL ESTER RESIDUES IN MCP (BY SIMILARITY).
-!-CATALYTIC ACTIVITY: S-adenosyl-L-methionine + protein L-glutamate = S-adenosyl-L-homocysteine + protein L-glutamate methyl ester.
-!-SIMILARITY: CONTAINS 1 CHER-TYPE METHYLTRANSFERASE DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                   O'Toole R., Lundberg S., Fredriksson S.A., Jansson A., Nilsson B., Wolf-Watz H.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bacteriophage lambda.
Viruses; dsDNA viruses, no RNA stage; Caudovirales; Siphoviridae;
Lambda-like viruses.
                                                                                                                            DNA sequence of both chromosomes of the cholera pathogen Vibrio
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 275;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Iransferase; Methyltransferase; Complete proteome.
DOMAIN
1 275 CHER-TYPE METHYLTRANSFERASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           30871 MW; F008ADCBFA46A921 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
01-JUN-1994 (Rel. 29, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Major head protein (GPE) (Major coat protein)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 34; DB :
Pred. No. 8.8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0; Mismatches
                                                                                                                                                                                                      MEDLINE-99328977; PubMed-10400589;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      InterPro; IPR000780; CheR_Metranf.
InterPro; IPR001601; Methyltransf.
Jeam; PF01739; CheR; 1.
Pfam; PF03705; CheR, 1.
PRNINTS; PR00996; CHERMIFRASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; AE004291; AAF95346.1; -. EMBL; AF139167; AAD45254.1; -. HSSP; P07801; IAF7.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   70.8%;
85.7%;
                                                                                                                                                                                SEQUENCE OF 10-266 FROM N.A.
                                                                                                                                                      Nature 406:477-483(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SMART; SM00138; MeTrc; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PROSITE; PS50123; CHER;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE 275 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       | ||||||||
82 RDSYPFT 88
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                                                                                                                  Fraser C.M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 HEAD_LAMBD
P03713;
                                                                                                                                            cholerae.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DOMAIN
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HEAD_LAMBD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches
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J. Biol. Chem. 271:10897-10903(1996)
-:-FUNCTION: CYSTEINE PROTEINSES I AND 2 ARE BELIEVED TO PARTICIPATE IN THE BREAKCHOWN OF PROTEIN DURING DIFFERENTIATION OF DICTYOSTELIUM AS A RESPONSE TO STARVATION.
                             MEDLINE-83189071; PubMed-6221115; Sanger F., Coulson A.R., Hong G.F., Hill D.F., Petersen G.B.; Sanger F., Coulson A.R., Hong G.F., Hill D.F., Petersen G.B.; Sanger F., Coulson A.R., 1902 G.F., 1902 G.F., Mol. Biol. 162:729-773 (1982).

-I- FUNCTION: GENE E PROTEIN IS A MAJOR COMPONENT OF THE PHAGE HEAD. THERE ARE ABOUT 420 COPIES OF PROTEIN E PER MATURE PHAGE. SOME OF THE E PROTEIN IS COVALENTLY LINKED MITH AN EQUIMOLAR AMOUNT OF PROTEIN C AND CLEAVED TO YIELD MINOR CAPSID PROTEINS X1 AND X2.

-I- SIMILARITY: STRONG, TO MAJOR HEAD PROTEIN OF PHI-80 AND P21.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -!- PTM: PHOSPHOGLYCOSYLATED, CONTAINS GLCNAC-ALPHA-1-P-SER RESIDUES.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRUCTURE OF CARBOHYDRATES.
MEDLINE-96210028; PubMed-8631906;
Mehta D.P., Ichikawa M., Salimath P.V., Etchison J.R., Haak R.,
Manzi A., Freeze H.H.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ;
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Pred. No. 11;
0; Mismatches 1; Indels
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NCBI_TaxID=44689;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           13-AUG-1987 (Rel. 05, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Cysteine proteinase 1 precursor (EC 3.4.22.-)
CPRA OR CPI.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -!- SUBCELLULAR LOCATION: Lysosomal
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MEDLINE-85257519; PubMed-2990918;
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13-AUG-1987 (Rel. 05, Last seq
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85.7%;
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Matches 6; Conserv
SEQUENCE FROM N.A.
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29 RESYPFT 35
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P04988;
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YDE9_SCHPO
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eulitz-M., Kley H.-P., Zeitler H.-J.;
"The primary structure of the Bence-Jones protein Kue. The amino acid sequence of the variable part of a human L-chain of the kappa-type.";
HOPPE-SEYLEY'S Z. Physiol. Chem. 360:725-734(1979).
-!- MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE INV (3) MARKER. PIR: A01870; KHUKU.
HSPP: PO1607; IREI.
InterPro: IPRO03006; Ig_MHC.
InterPro: IPRO03596; Ig_V.
SMART: SW00406; IGV: 1.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Thiol protease; Lysosome; Zymogen; Glycoprotein; ttion; Signal.
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FRAMEWORK-1.
COMPLEMENTARITY-DETERMINING-1.
FRAMEWORK-2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 34; DB 1; Length 343;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2; Indels
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71804C15F2B361E2 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ACTIVATION PEPTIDE.
CYSTEINE PROTEINASE 1.
BY SIMILARITY.
BY SIMILARITY.
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BY SIMILARITY.
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21-JUL-1986 (Rel. 01, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
18 Appha chain V-I region Kue.
Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 108 AA
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PRODOM: PROBLE:
PROSTE: PSO00139; THIOL_PROTEASE_CYS; 1.
PROSITE: PS00639; THIOL_PROTEASE_LYS; 1.
PROSITE: PS00640; THIOL_PROTEASE_RS: 1.
PROSITE: PS00640; THIOL_PROTEASE_RS: 1.
                                                                        email to license@isb-sib.ch)
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                                                                                                                                                                                                                                                                        DictyDb; DD02003; cpra.
InterPro; IPR000668; Peptidase_C1.
InterPro; IPR000169; SHprot_acsite.
Pfam; PF00112; Peptidase_C1; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              38495 MW;
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66.7%;
                                                                                                                   EMBL, XO2ÅO7; CAA26255.1; -.
PIR; A22827; KHDO.
HSSP; P25779; 1AIM.
MEROPS; CO1.UPA; -.
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DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           343 AA;
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P01604;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches
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RKA MEDLINE-21848401; PubMed=11859360;

RA MEDLINE-21848401; PubMed=11859360;

RA Godoros V., Gwilliam R., Rajandream M.A., Lyne M., Lyne R., Stewart A., Squoros J., Peat N., Hayles J., Basham D., Bowman S.,

Brooks K., Brown D., Brown S., Chillingworth T., Churcher C.M.,

Brooks K., Brown D., Brown S., Chillingworth T., Churcher C.M.,

RA Gollins M., Connor R., Cronin A., Davis P., Feltwell T., Fraser A.,

Gollins M., Connor R., Cronin N., Harris D., Hidalgo J., Hodson G.,

RA Gones P., Moule S., Munghy E., Hurtle E.J., Hunt S., Jagels K.,

RA Holroyd S., Hornsby T., Howarth S., Huckle E.J., Hunt S., Jagels K.,

RA Holroyd S., Hornsby T., Howarth S., Huckle E.J., Hunt S., Jagels K.,

RA Holroyd S., Woules M., Squares R., McDonald S., McLean J.,

RA Holroyd S., Saunders D., Quail M.A., Rabbinowitsch E.,

RA Oliver K., O'Neil S., Pearson D., Quail M.A., Rabbinowitsch E.,

RA Skelton J., Simmonds M., Squares R., Squares S., Stevens K.,

RA Taylor K., Taylor R.G., Tivey A., Walsh S.V., Warren T., Whitehead S.,

RA Gabel C., Fuchs M., Fritzc C., Holzer E., Moestl D., Hilbert H.,

RA Gabel C., Fuchs M., Fritzc C., Holzer E., Moestl D., Hilbert H.,

RA Galbert F., Aves S.J., Xiang Z., Hunt C., Moore K., Hurst S.M.,

Lucas M., Rochet M., Gaillardin C., Tallada V.A., Garzon A., Thode G.,

RA Galibert F., Aves S.J., Xiang Z., Hunt C., Moore K., Hurst S.M.,

Lucas M., Rochet M., Gaillardin C., Tallada V.A., Garzon A., Thode G.,

RA Galibert F., Aves S.J., Xiang Z., Hunt C., Moore K., Hurst S.M.,

Lucas M., Rochet M., Gaillardin C., Tallada V.A., Garzon A., Thode G.,

RA Dominguez A., Revuelta J.L., McCombie W.R., Paulsen I., Potashkin J.,

RA Shawayoski G.V., Ussery D., Barrell B.G., Nurse P.;

RA Daga R.R., Charlout B., McCompie W.R., Paulsen I., Potashkin J.,

RA Shapakovski G.V., Ussery D., Barrell B.G., Nurse P.;

RA Hure Genome Sequence of Schizosaccharomyces pombe.";

RA Hure L. Inder L. Lowe I., McCharle M., Revielle M., Inder M., Inde
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profilt institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@ib.sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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-!- DOMAIN: COMPOSED OF THREE HOWOLOGOUS DOMAINS.
-!- SIMILARITY: BELONGS TO THE MITOCHONDRIAL CARRIER FAMILY
COMPLEMENTARITY - DETERMINING - 2.
                                         FRAMEWORK - 3 .
COMPLEMENTARITY - DETERMINING - 3 .
                                                                                                                                                                                                                                                                                                                    Length 108;
                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                 12127 MW; 906679A5D90E4E98 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota, Fungi, Ascomycota; Schizósaccharomycetes;
Schizosaccharomycetales; Schizosaccharomycetaceae;
                                                                                                                                                                                                                                                                                                               Score 33; DB 1;
Pred. No. 5.2;
1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-OCT-1996 (Rel. 34, Created)
01-OCT-1996 (Rel. 34, Last sequence update)
115-UNN-2002 (Rel. 41, Last annotation update)
Putative mitochondrial carrier C12B10.09.
                                                                                                                                                       BY SIMILARITY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Schizosaccharomyces pombe (Fission yeast).
                                                                                                                  FRAMEWORK-4
                                                                                                                                                                                                                                                                                                               68.8%;
66.7%;
                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STANDARD;
56
88
97
107
88
108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Schizosaccharomyces.
50
57
89
98
23
108
108 AA;
                                                                                                                                                                                                                                                                                                                                                Best Local Similarity
Matches 6; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          89 QOYSRYPYT 97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 QQRSSYPFT 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=4896;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SPAC12B10.09.
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EMBL; U49060; AAB47803.1; -.
EMBL; D30808; BAA06483.1; -.
EMBL; Z99105; CAB12056.1; -.
SubtiList; BG11174; phoD.
Hydrolase; Signal; Complete proteome.
SIGNAL 1 56
                                                                                                                                                                             62829 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        662 T' 76750 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 68.8%;
55.6%;
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PROSITE; PS50280; SET; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        5; Conservative
                                                                                                                                                                                                                                                          6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Caenorhabditis elegans.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Hypothetical protein
DOMAIN 209 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          662 AA;
                                                                                                                                                                           556 AA;
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Best Local Similarity
                                                                                                                                                                                                                                    Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN-Bristol N2;
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EDRSAYPFS 11
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                                                                                                                                  57
59
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                                                                                                                                                                                                                   Query Match
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VARIANT
                                                                                                                                                                                                                                                                                                                                                                                            RESULT 10
YLN9_CAEEL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eder S., Shi L., Jensen K., Yamane K., Hulett F.M.;
"A Bacillus subtilis secreted phosphodiesterase/alkaline phosphatase
is the product of a Pho regulon gene, phoD.";
Microbiology 142:2041-2047(1996).
                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-NOV-1995 (Rel. 32, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Alkaline phosphatase D precursor (EC 3.1.3.1) (APASED) (RAN1) (BC6).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Yamane K., Marto, Santa Control of Attracellular soluble and "Purification and characterization of extracellular soluble and membrane-bound insoluble alkaline phosphatases possessing phosphodiesterase activities in Bacillus subtilis.";
J. Bacteriol. 134:100-107(1978)
J. CATALYTIC ACTIVITY: An orthophosphoric monoester + H(2)O = an alcohol + phosphate STARVATION.
                                                                                                                                                                                                                                                                                                                                                        ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ogawa K.-I., Akagawa E., Nakamura K., Yamane K.; "Determination of a 21548 bp nucleotide sequence around the 24 degrees region of the Bacillus subtilis chromosome."; Microbiology 141:269-275(1995).
                                    InterPro; IPR001993; Mitoch_carrier.
Pfam; PF00153; mito_carr; 3.
PROSTIE; PS00215; MITOCH_CARRIER; 2.
Hypothetical protein; Mitochondrion; Inner membrane; Repeat;
                                                                                                                                                                                                                                                                                                             Score 33; DB 1; Length 345;
Pred. No. 18;
0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus NCBI_TaxID=1423;
                                                                                                                                                                                                                                                                          39081A6AAC984B2C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   556 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A., AND SEQUENCE OF 57-76
                                                                                                                                                                                                               POTENTIAL. POTENTIAL.
                                                                                                                                                        POTENTIAL. POTENTIAL.
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                                                                                                                                    POTENTIAL
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MEDLINE=96349109; PubMed=8760916;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN=168;
MEDLINE=95219079; Pubmed=7704254;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRAIN=6060-BC6;
MEDLINE=78171419; PubMed=25878;
                                                                                                                                                                                                                                                                        38451 MW;
                                                                                                                                                                                                                                                                                                               68.8%;
77.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE OF 95-556 FROM N.A.
                  Z70721; CAA94699.1;
                                                                                                                                                                                                                                                                                                                                                      7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STANDARD;
                                                                                                                Transport
                                                                                                                                      21
103
148
240
282
339
                                                                                                                                                                                         220
262
296
319
345 AA;
                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                 111 || ||
290 QQRLSYVFT 298
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bacillus subtilis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CHARACTERIZATION.
                                                                                                                                                                                                                                                                                                                                                                                          1 CORSSYPFT 9
                                                                                                                Transmembrane;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PPBD_BACSU
P42251;
                                                                                                                                                                                           TRANSMEM
TRANSMEM
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TRANSMEM
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TRANSMEM
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                                                                                                                                                                                                                                                                                                                                                    Matches
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                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
Rhabditidae; Peloderinae; Caenorhabditis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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                                                                                                                                                                                ó
                                                                                                       bB.8%; Score 33; DB 1; Length 556; 100.0%; Pred. No. 30; O; Indels.ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 33; DB 1; Length 662;
Pred. No. 36;
3; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mortimore B., Matthews P.;
Submitted (DEC-1998) to the EMBL/GenBank/DDBJ databases.
-!- SIMILARITY: CONTAINS 1 SET DOMAIN.
-!- SIMILARITY: CONTAINS 1 TIL DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                         009512.

30-MAY-2000 (Rel. 39, Created)

30-MAY-2000 (Rel. 39, Last sequence update)

15-JUN-2002 (Rel. 41, Last annotation update)

Hypothetical 76.7 kDa protein D2013.9 in chromosome II.

D2013.9.
                                  N -> K.
125F7FDDA08817E3 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          5044C76422145698 CRC64;
ALKALINE PHOSPHATASE D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL, 247808; CAA87778.1; -.
EMBL, 247809; CAA87778.1; JOINED.
EMBL, 247809; CAA87783.1; -.
EMBL, 247809; CAA87783.1; -.
MOTIMPEP, 247809; CAA87783.1; JOINED.
WOTIMPEP, 1978013.9; CE01535.
InterPro; IPR004344; Tub_tyr_lygase.
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410
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Best Local Similarity
Matches 5; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    41 ERRGSYPF 48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Hydrolase; cAMP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 QORSSYPF 8
                                                                                                                                                                                                                                                                                                                                                                                                                                             SM0047
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           IISSUE-Brain
                                                                                                                                                                                                                                        FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CN7B_HUMAN
Q9NP56;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                               PRINTS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CN7B_HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    [2]
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                                                                                                                                                                                                                                                                                           This SWISS-PROT entry is copyright. It is produced through a collaboration between the SWISS institute of Bioinformatics and the EMBL outstation the European Bloinformatics Institute. There are no restrictions on its by inon-profit institutions as long as its content is in no way modified, and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                             SEQUENCE EROM N.A.

RYDACAL IF, Childs G.;
Submitted# (FEB-1997) to the EMBL/GenBank/DDBJ databases.

-!- FUNCTION: GENERAL FACTOR THAT PLAYS A MAJOR ROLE IN THE ACTIVATION OF EUKARYOTIC GENES TRANSCRIBED BY RNA POLYMERASE II. TFIID BINDS SPECIFICALLY TO THE TAM BOX PROMOTER ELEMENT WHICH LIES CLOSE TO THE FOSTION OF TRANSCRIPTION INITIATION.
-!- SUBMIT: BINDS DAM AS A MONOMER.
-!- SUBMIT: BINDS DAM AS A MONOMER.
-!- SUBCELLULAR LOCATION: UNLClear.
-!- SIMILARITY: BELONGS TO THE TBP FAMILY.
                            15-JUL-1998 (Rel. 36, Created)
15-JUL-1998 (Rel. 36, Last sequence update)
15-JUL-1998 (Rel. 40, Last annotation update)
Transcription initiation factor TFIID (TATA-box factor)
(TATA sequence-binding protein) (TBP).
Strongylogentrotus purpuratus (Purple sea urchin).
Eukaryota: Metazoa: Echinodermata: Eleutherozoa: Echinozoa:
Strongylogentrotus.
Strongylogentrotus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mus mušculus (Mouse).
Eukaryota Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Manmalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBL_TāxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                Interprof. IPRO00814; TFIID.
PFAN, PRO0352; TBP; 2.
PRINTS; PRO0565; TFATORIID.
PROSITE, PS00331; TFIID; 2.
Transcription regulation; DNA-binding; Nuclear protein; Repeat.
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16-0CT-2001 (Rel. 40, Created)
16-0CT-2001 (Rel. 40, Last sequence update)
15-UNN*2002 (Rel. 41, Last annotation update)
CAMP-specific 3',5'-cyclic phosphodiesterase 7B (EC 3.1.4.17).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 1; Length 265;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
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HetmantJ.M., Soderling S.H., Glavas N.A., Beavo J.A.;
"Cloning and characterization of PDE7B, a cAMP-specific
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    29107 MW; 53AED314D2D98926 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Natl. Acad. Sci. U.S.A. 97:472-476(2000)
          265 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 32;
Pred. No. 2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          66.7%;
85.7%;
                                                                                                                                                                                                                                                                                                                                                                                         EMBL; U86586; AAB47272.1; -.
HSSP; P20226; 1TGH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STANDARD;
          STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           167
258
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    265 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       phosphodiesterase."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 QORSSYP 7
|||||| ||
23 QORSHYP 29
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        STRPU
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                                                                                                                Gaps
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"Identification of human PDE7B, a cAMP-specific phosphodiesterase.";
Biochem. Biophys. Res. Commun. 271:575-583(2000).
                  Gardner C.E., Robas N.M., Cawkill D., Fidock M.D.; "Cloning and characterisation of the human and mouse PDE7B, a novel cAMP-specific nucleotide phosphofasterase."; Blochem. Blophys. Res. Commun. 272:186-192(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
CAMP-specific 3',5'-cyclic phosphodiesterase 7B (EC 3.1.4.17).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 446;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CATALYTIC (BY SIMILARITY).
7C052664B693A5A8 CRC64;
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38;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MGD; MGI:1352752; Pde7b.
InterPro; IPR003607; ME_Pplase_HDc.
InterPro; IPR002073; PDEase.
MEDLINE=20329226; PubMed=10872825;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE-20275458; PubMed-10814504;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; AF190639; AAF25195.1; -. EMBL; AJ251859; CAB92530.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PROSITE; PS00126; PDEASE_I; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     66.7%;
62.5%;
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                                                                                                                                                                                                                                                                                 .! • FUNCTION: Involved in vesicular transport at a late stage of the
                                                                                                                                                                                                                                                                                               secretory pathway.
                                                                                                                                                                         SEQUENCE FROM N.A.
MEDLINE-97051586; PubMed-8896263;
Parle-Mcdermott A.G., Hand N.J., Goulding S.G., Wolfe K.H.;
Sequence 0f 29 kb around the PDR10 locus on the right arm of
Saccharomyces cerevisiae chromosome XV: similarity to part of
                                                       Wang W., Zheng L., Chan C.;
Submitted (NOV-1993) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                 Song J.M., Cheung E., Rabinowitz J.C.;
Submitted (JAN-1996) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Repeat.
                                                                                                                                                                                                                                                                                                                         -1- SUBCELLULAR LOCATION: Membrane-associated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRT; 1476 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Membrane;
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1.
Biol. Cell 7:245-260(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                transport;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     97305 MW;
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55.68;
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                                                                                                                                                                                                                                                    chromosome I.";
Yeast 12:999-1004(1996)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Transport; Protein
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                              SEQUENCE FROM N.A.
                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 QORSSYPFT 9
                                             STRAIN-S288C;
                                                                                                                    STRAIN=GRF88
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (Fragment).
ATP7A.
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P49015;
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                                                                                 EDIOCHMIN. BLOPHYS. Res. COMMUN. 272:186-192(2000).

- I- FUNCTION: MAY BE INVOLVED IN THE CONTROL OF CAMP-MEDIATED NEURAL ACTIVITY AND CAMP METABOLISM IN THE CONTROL OF CAMP-MEDIATED NEURAL OF CATALYTIC ACTIVITY: Adenosine 3',5'-cyclic phosphate + H(2)0 = adenosine 5'-phosphate 3',5'-cyclic phosphate + H(2)0 = copector: Regulated Divalent Cations (BY SIMILARITY).

- I- COFACTOR: REGULATION: INHIBITED BY DIPYRIDAMOLE, IBMX AND SCH51866.

- I- ENZYME REGULATION: INHIBITED BY DIPYRIDAMOLE, IBMX AND SCH51866.

- I- PATHWAY: Cyclic nucleotide metabolism.

- I- PATHWAY: Cyclic nucleotide metabolism.

- I- STATEN SKELETAL MUSCLE AND PANCREAS.

- I- DOMAIN: COMPOSED OF A C-TERMINAL CATALYTIC DOMAIN CONTAINING TWO PUTATIVE DIVALENT METAL SITES AND AN N-TERMINAL REGULATORY DOMAIN.

- I- SIMILARITY: BELONGS TO THE CYCLIC NUCLEOTIDE PHOSPHODIESTERASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Nelson K.K., Holmer M., Lemmon S.K.;
"SCD5, a suppressor of clathrin deficiency, encodes a novel protein
with a late secretory function in yeast.";
             TISSUE-Fetal brain;
BEDIINE-20139225; Pubmed-10872825;
Gardner C.E., Robas N.M., Cawkill D., Fidock M.D.;
"Cloning and characterisation of the human and mouse PDE7B, a novel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Saccharomyces cerevisiae (Baker's yeast).
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Saccharomyces.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 32; DB 1; Length 450;
Pred. No. 38;
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51835 MW; EC142BF3E28D0028 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-FFB-1994 (Rel. 28, Created)
01-FEB-1994 (Rel. 28, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
                                                                         cAMP-specific nucleotide phosphodiesterase."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                872 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 InterPro; IPR003607; ME_Pplase_HDc.
InterPro; IPR002073; PDEase.
                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; AB038040; BAA96537.1; -. EMBL; AJ251860; CAB92441.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pfam; PF00233; PDEase; 1.
PRINTS; PR00387; PDIESTERASE1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SMART; SM00471; HDc; 1.
PROSITE; PS00126; PDEASE_I; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 62.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     protein (FTB1 protein).
OR FTB1 OR YOR329C.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    450 AA;
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Best Local Similarity
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41 ERRGSYPF 48
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ID SCD5_YEAST
AC P34758;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MIM; 604645;
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20 AA APPROXIMATE REPEATS
                                                                                            AA APPROXIMATE REPEATS
                                                                                                                                                                                                                                                                                                                                                                                     Score 32; DB 1; Length 872;
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01-FEB-1996 (Rel. 33, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Copper-transporting ATPase 1 (EC 3.6.3.4) (Copper pump 1)
                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                      C60F5BE8808E1D31 CRC64;
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                                                                                                                                                                                                                                                                                                                            Hum. Mol. Genet. 4:2117-2123(1995).

-i- FUNCATION: MAY FUNCTION IN THE EXPORT OF COPPER FROM THE CYTOPLASM
TO AM INTRACELLULAR ORGANELLE. IT MAY SERVE AS WELL FOR THE EXPORT
OF OTHER METALS.

-i- CATALYTIC ACTIVITY: ATP + H(2)O + Cu(2+)(In) = ADP + phosphate +
                                                                                                                                                                                                   Camakarishu, Petris M.J., Balley L., Shen P., Lockhart P., Glover T.W., Barcroft C., Patton J., Mercer J.F.; "Gene amplification of the Menkes (MNK; ATP7A) P-type ATPase gene of CHO cells is associated with copper resistance and enhanced copper efflux."
Cricetulus griseus (Chinese hamster).
Bukaryota Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Cricetinae;
Cricetulus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (POTENTIAL).
(POTENTIAL).
(POTENTIAL).
(POTENTIAL).
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                                                                                                                                                                                                                                                                                                                                                                                                                                               Cu(2½)(Out).
SUBUNIT: MONOMER.
SUBUNIT: MONOMER.
SUBCELLULAR LOCATION: Integral membrane protein.
TISSÜE SPECIFICITY: FOUNDS IN MOST TISSUES EXCEPT LIVER.
SIMIÉMRITY: BELONGS TO THE CATION TRANSPORT ATPASES FAMILY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PHOSPHORYLATION (PROBABLE)
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POTENTIAL.
HWA 1.
HWA 2.
HWA 3.
HWA 4.
HWA 5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (E1-E2 ATPASES).
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                                                                                                                                                                                                 MEDLINE-90154683; Pubmed-8589689;
Camakaris J., Petris M.J., Bailey
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; U29946; AAB39918.1; -.
HSSP; QQ4656; IAWO.
                                                                                                                                                     ROM N.A.
                                                                                                           NCBI_TaxID-10029;
                                                                                                                                                     SEQUENCE EN
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Gaps
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                          Length 1476;
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160335 MW; 6B36F5A2AC358C0B CRC64;
                          Score 32; DB 1; I
Pred. No. 1.4e+02;
0; Mismatches 1;
                                                                                                                                                  Search completed: December 23, 2002, 07:26:10 Job time: 2.88953 secs
                        66.7%;
nilarity 85.7%;
Conservative 0,
 1476 AA;
                                     Best Local Similarity
Matches 6; Conserv
                                                                                                    111 | 11
267 QORPSYP 273
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 SEQUENCE
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Run on:

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09787.2 3-1-2 3-1-2 3-1-2 3-1-2 3-1-2 3-1-2 3-1-2 3-1-2 3-1-2 3-1-2 3-1-2 3-1-2 3-1-2 3-1-2 3-1-2 3-1-2 3-1-2 3-1-2 3-1-2 3-1-2 3-1-2 3-1-2 3-1-2 3-1-2 3-1-2 3-1-2 3-1-2 3-1-2 3-1-2 3-1-2 3-1-2 3-1-2 3-1-2 3-1-2 3-1-2 3-1-2 3-1-2 3-1-2 3-1-2 3-1-2 3-1-2 3-1-2 3-1-2 3-1-2 3-1-2 3-1-2 3-1-2 3-1-2 3-1-2 3-1-2 3-1-2 3-1-2 3-1-2 3-1-2 3-1-2 3-1-2 3-1-2 3-1-2 3-1-2 3-1-2 3-1-2 3-1-2 3-1-2 3-1-2 3-1-2 3-1-2 3-1-2 3-1-2 3-1-2 3-1-2 3-1-2 3-1-2 3-1-2 3-1-2 3-1-2 3-1-2 3-1-2 3-1-2 3-1-2 3-1-2 3-1-2 3-1-2 3-1-2 3-1-2 3-1-2 3-1-2 3-1-2 3-1-2 3-1-2 3-1-2 3-1-2 3-1-2 3-1-2 3-1-2 3-1-2 3-1-2 3-1-2 3-1-2 3-1-2 3-1-2 3-1-2 3-1-2 3-1-2 3-1-2 3-1-2 3-1-2 3-1-2 3-1-2 3-1-2 3-1-2 3-1-2 3-1-2 3-1-2 3-1-2 3-1-2 3-1-2 3-1-2 3-1-2 3-1-2 3-1-2 3-1-2 3-1-2 3-1-2 3-1-2 3-1-2 3-1-2 3-1-2 3-1-2 3-1-2 3-1-2 3-1-2 3-1-2 3-1-2 3-1-2 3-1-2 3-1-2 3-1-2 3-1-2 3-1-2 3-1-2 3-1-2 3-1-2 3-1-2 3-1-2 3-1-2 3-1-2 3-1-2 3-1-2 3-1-2 3-1-2 3-1-2 3-1-2 3-1-2 3-1-2 3-1-2 3-1-2 3-1-2 3-1-2 3-1-2 3-1-2 3-1-2 3-1-2 3-1-2 3-1-2 3-1-2 3-1-2 3-1-2 3-1-2 3-1-2 3-1-2 3-1-2 3-1-2 3-1-2 3-1-2 3-1-2 3-1-2 3-1-2 3-1-2 3-1-2 3-1-2 3-1-2 3-1-2 3-1-2 3-1-2 3-1-2 3-1-2 3-1-2 3-1-2 3-1-2 3-1-2 3-1-2 3-1-2 3-1-2 3-1-2 3-1-2 3-1-2 3-1-2 3-1-2 3-1-2 3-1-2 3-1-2 3-1-2 3-1-2 3-1-2 3-1-2 3-1-2 3-1-2 3-1-2 3-1-2 3-1-2 3-1-2 3-1-2 3-1-2 3-1-2 3-1-2 3-1-2 3-1-2 3-1-2 3-1-2 3-1-2 3-1-2 3-1-2 3-1-2 3-1-2 3-1-2 3-1-2 3-1-2 3-1-2 3-1-2 3-1-2 3-1-2 3-1-2 3-1-2 3-1-2 3-1-2 3-1-2 3-1-2 3-1-2 3-1-2 3-1-2 3-1-2 3-1-2 3-1-2 3-1-2 3-1-2 3-1-2 3-1-2 3-1-2 3-1-2 3-1-2 3-1-2 3-1-2 3-1-2 3-1-2 3-1-2 3-1-2 3-1-2 3-1-2 3-1-2 3-1-2 3-1-2 3-1-2 3-1-2 3-1-2 3-1-2 3-1-2 3-1-2 3-1-2 3-1-2 3-1-2 3-1-2 3-1-2 3-1-2 3-1-2 3-1-2 3-1-2 3-1-2 3-1-2 3-1-2 3-1-2 3-1-2 3-1-2 3-1-2 3-1-2 3-1-2 3-1-2 3-1-2 3-1-2 3-1-2 3-1-2 3-1-2 3-1-2 3-1-2 3-1-2 3-1-2 3-1-2 3-1-2 3-1-2 3-1-2 3-1-2 3-1-2 3-1-2 3-1-2 3-1-2 3-1-2 3-1-2 3-1-2 3-1-2 3-1-2 3-1-2 3-1-2 3-1-2 3-1-2 3-1-2 3-1-2 3-1-2 3-1-2 3-1-2 3-1-2 3-1-2 3-1-2 3-1-2 3-1-2 3-1-2 3-1-2 3-1-2 3-1-2 3-1-2 3-1-2 3-1-2 3-1-2 3-1-2 3-1-2 3-1-2 3-1-2 3-1-2 3-1-2 3-1-2 3-1-2 3-1-
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                                  Q9vsi2 drosophila
Q8svy7 encephalito
Q8r062 mus musculu
Q9w6e5 gallus gall
            097357 trypanosoma
092kb6 rhizobium m
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01-MAR-2002 (TEBMELrel. 20, Created)
01-MAR-2002 (TEBMELrel. 20, Last sequence update)
01-JUN-2002 (TEBMELrel. 21, Last annotation update)
anti-MOG Z12 variable light chain (Fragment).
ANTI-MOG KAPPA.
MUS musculus (Mouse).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Musculus zaxiD-10090;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "Targeting T cells to the CNS.";
Submitted (JAN-2002) to the EMBL/GenBank/DDBJ databases.
BMBL, AJ416311. CAC94866.1; -.
InterPro; IPR003599; Ig.
InterPro; IPR003599; Ig.
InterPro; IPR003596; Ig_V.
Pfam; PPF0047; Ig; 1.
SMART; SM00409; IG; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Chernajovsky Y.;
Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 134 AA; 14525 MW; CFDF8E2236E2D0CF CRC64;
                                                                                                                                                                                                                                                                                                                                                                            ALIGNMENTS
PRT;
                                                                                                                                 Best Local Similarity 87.5
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                    PRELIMINARY;
 134
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SEQUENCE FROM N.A.
STRAIN=BALB/C;
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2 QRSSYPFT 9
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SEQUENCE
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 08VDD0
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Q1852 caenorhabdi
Q8uuz5 brachydanio
Q9kr72 bacillus ha
Q8vij0 mus musculu
Q12744 saccharomyc
Q8x6y8 escherichia
Q8x6y8 escherichia
Q8x6y8 escherichia
Q9x07 glycine max
Q4424 phaseolus v
Q4448 glycine max
O96635 trypanosoma
O35007 bacillus su
Q9k6q6 bacillus ha
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                                                                            December 23, 2002, 07:17:27; Search time 3.73256 Seconds (without alignments) 496.824 Million cell updates/sec
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Description
            GenCore version 5.1.3
Copyright (c) 1993 - 2002 Compugen Ltd.
                                                                                                                                                                                                                                       Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                  671580 seqs, 206047115 residues
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Maximum Match 1008
Listing first 45 summaries
                                                          OM protein - protein search, using sw model
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035007
09K6Q6
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Q12171
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Q9U410
Q18582
Q8UUZ5
Q9KC72
Q8VIJ0
Q12744
Q8SWC7
Q9SWC7
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sp_unclassified:*
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sp_mammal:*
sp_mhc:*
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sp_phage:*
sp_plant:*
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sp_bacteriap:*
sp_archeap:*
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Maximum DB seq length: 2000000000
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Match Length DB
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48
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sp_human:*
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Perfect score:
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Result

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090410

RESULT 2 090410

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"Direct Submission.";
Submitted (JUN-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; U56966; AAA98721.2; -.
Hypothetical Protein:
SEQUENCE 269 AA; 30847 MW; 32D2B7A1C0102F93 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRT;
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                                                                                                                                                                             Query Match
Best Local Similarity 66./v,
6. Conservative
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Matches 7; Conservative
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225 QRRENYPFT 233
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                                                                                                                                                                                                                                                                                                                                    1 QQRSSYPFT 9
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      Waterston R.;
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Q9KC72
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   RA
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DR
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                                                                                                                                                                                                                               01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
Monoclonal anti-idiotypic antibody NP30 immunoglobulin light chain variable region (Fragment).
Schistosoma Japonicum (Blood fluke).
Eukaryota: Metazoa; Platyhelminthes; Trematoda; Digenea; Strigeidida; Schistosomatoidea; Schistosomatidae; Schistosoma.
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Rhabditidae; Peloderinae; Caenorhabditis.
NCBI_TaxID=6239;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

SONG X.T., Feng Z.Q., Qiu Z.N., Li Y.Q., Huang H.L., Guan X.H.;

"Amplification, cloning and sequence analysis of the light chain
variable region gene of monoclonal anti-idiotypic antibody NP30 of
Schistosoma japonicum.";

Submitted (NOV-1999) to the EMBL/GenBank/DDBJ databases.

EMBL; AF207620; AAF19431.1;

HSSP; P01679; ZFBJ.

InterPro; IPR003596; Ig_MHC.

InterPro; IPR003596; Ig_V.
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investigating biology. The C. elegans Sequencing Consortium.";
Science 282:2012-2018(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 77.1%; Score 37; DB 5; Length 106; Best Local Similarity 77.8%; Pred. No. 4; Matches 7; Conservative 1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "The sequence of C. elegans cosmid C42D8.";
Submitted (MAY-1996) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      11478 MW; F20F544426BAE63E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-NOV-1996 (TrEMBLrel. 01, Created)
01-OCT-2001 (TrEMBLrel. 18, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
Hypothetical 30.8 kDa protein.
                                                                                                                                                                                   106 AA.
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STRAIN-BRISTOL N2;
MEDLINE-99069613; Pubmed-9851916;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRELIMINARY;
                                                                                                                                                                                   PRELIMINARY:
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SMART; SM00406; IGv; 1.
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88 QQWTSYPFT 96
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=6182;
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NON_TER
SEQUENCE
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Q18582 Q18582;

RESULT 3 Q18582

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Gamse J.T., Liang J.O., Shen Y.-C., Raymond P., Thisse B., Thisse C., Halpern M.E., "Otx5 requiates genes that show circadian expression in the zebrafish pineal complex.";
                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                  01-MAR-2002 (TrEMBLrel. 20, Created)
01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
01-MON-2002 (TrEMBLrel. 21, Last annotation update)
01-MON-2002 (TrEMBLrel. 21, Last annotation update)
01-Modenticle-related homeobox 5.
Brachydanio rerio (Zebrafish) (Zebra danio).
Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes; Cyprinidae; Danio.
NCBI_TaxID=7955;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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Q9KC72;
01-0C7-2000 (TrEMBLrel. 15, Created)
01-0C7-2000 (TrEMBLrel. 15, Last sequence update)
01-0C7-2000 (TrEMBLrel. 21, Last annotation update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Penicillin-binding proteins 1A/1B.
PowA ob BH1702.
Bacillus halodurans.
Bacillus halodurans.
Bacteria; Firmicutes; Bacillus/Clostridium group; Bacillales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 289;
77.1%; Score 37; DB 5; Length 269; 66.7%; Pred. No. 10;
                                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homeobox; DNA-binding; Nuclear protein.
SEQUENCE 289 AA; 31422 MW; 542FA0F69AE90DAC CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                77.1%; Score 37; DB 13;
87.5%; Pred. No. 11;
Live 0; Mismatches 1
                                                                                                                                                                                                                                                                                                                                                 289 AA.
                                                                2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Nat. Genet. 30:117-121(2002).

BMBL: AY036005; AAK62029.1; -

InterPro: IPR001356; Homeobox.

InterPro: IPR0013025; Otx.TF.

Pfam; PF00046; homeobox; 1.

Pfam; PF00046; homeobox; 1.

PRINTS; PR00024; HOMEOBOX.

PRINTS; PR00024; HOMEOBOX.

PRINTS; PR00013; HTHREPRESS.

PRINTS; PR00013; HTHREPRESS.

PRINTS; PR0001010; HOMEOBOX.

PROSITE; PS000101; HOMEOBOX. 1.

PROSITE; PS00017; HOMEOBOX. 2; 1.

PROSITE; PS00017; HOMEOBOX. 2; 1.
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region A22726

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Melss Wa., Friedberg E.C.

"Welss Wa., Friedberg E.C.

"Molecular cloning and characterization of the yeast RAD10 gene and expression of RAD10 protein in E. coli.";

EMBC J. 4:1575-1582(1987).

EMBL; Z46660; CAA86643.1; -.

EMBL; X20591; CAA26432.1; -.

SGD; S0004561; YRL0956-A.

InterPro; IPR002016; Peroxidase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-WAR-2002 (TrEMBLrel. 20, Last sequence update)
01-WAR-2002 (TrEMBLrel. 20, Last annotation update)
Putative capsid protein of prophage CP-933X (Putative major capsid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN-0157:H7, EDL933 / ATCC 700927;
MEDLINE-21074935; PubMed-11206551;
MEDLINE-21074935; PubMed-11206551;
MEDLINE-21074935; PubMed-11206551;
Medla N.T., Plunkett G. III, Burland V., Mau B., Glasner J.D.,
Rose D.J., Mayhew G.E., Evans P.S., Gregor J., Kirkpatrick H.A.,
Posfal G., Hackett J., Klink S., Boutin A., Shao Y., Miller L.,
Grotbeck E.J., Davis N.W., Lim A., Dimalanta E.T., Potamousis K.,
Apodaca J., Anantharaman T.S., Lin J., Yen G., Schwartz D.C.,
Welch R.A., Blattner F.R.;
"Genome sequence of enterchaemorrhagic Escherichia coli 0157:H7.";
Nature 409:529-533(2001).
                                                                                                                                                            Saccharomyces cerevisiae (Baker's yeast).
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Saccharomyces.
NCBI_TaxID=4932;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
                                                                                                                                                                                                                                                                                                   Gentles S., Bowman S.;
Submitted (NOV-1994) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                            Barrell B., Rajandream M.A.;
Submitted (NOV-1994) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PROSITE; PS00435; PEROXIDASE_1; UNKNOWN_1.
SEQUENCE 133 AA; 15007 MW; B930075888867456 CRC64;
                                                                                           01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Hypothetical ORF IDENTICAL to ORF NOTED in RAD10 5'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 35; DB 3;
Pred. No. 13;
                                       133 AA.
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01-MAR-2002 (TrEMBLrel. 20, Last seq
01-MAR-2002 (TrEMBLrel. 20, Last ann
                                                                            Created)
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                                       PRT;
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SEQUENCE OF 2-133 FROM N.A.
MEDLINE-85284950; PubMed=3896774;
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77.8%;
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                                                                            (TrEMBLrel. 01,
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Best Local Similarity 77.0
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21888 OR ECS2174 OR ECS1(
Escherichia coli 0157:H7
                                       PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                        [2]
SEQUENCE FROM N.A.
STRAIN=AB972;
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                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
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01-NOV-1996
01-JUN-2002
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                                   Q12744
Q12744;
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Q8X6Y8
ID Q8X61
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                                                                                                                                          The complete genome sequence of the alkaliphilic bacterium Bacillus
Thalodurans and genomic sequence comparison with Bacillus subtilis.";
In Mucleic Acids Res. 28:43174331(2000).
REMBL, AP001512; BAB05421.1.
RINGTPRO; IPR001364; FN_III.
RINGTPRO; IPR001264; GT_51.
RINGTPRO; IPR001466; Transpeptidse.
R Pfam; PF00912; Transpeptidse.
R Pfam; PF00912; Transpeptidase; 1.
R Pfam; PF00915; Transpeptidase; 1.
R Probom; P001895; GT_51; 1.
R Probom; P001895; GT_51; 1.
R SMART; SM00060; FN3; 1.
R Hydrolase; Complete proteome.
O SEQUENCE 886 AA; 99280 MW; 0662807F75148534 CRC64;
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EMBL, U59155; ABA02917.1; -..
InterPro; IPR003599; Ig. InterPro; IPR003596; Ig.MC.
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBL_raxID=10090;
                                                                                       Takami H., Nakasone K., Takaki Y., Maeno G., Sasaki R., Masui N.,
Fuji F., Hirama C., Nakamura Y., Ogasawara N., Kuhara S.,
Horikoshi K.;
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                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 886;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         08VIJO;
01-MAR-2002 (TrEMBIrel. 20, Created)
01-MAR-2002 (TrEMBIrel. 20, Last sequence update)
01-JUN-2002 (TrEMBIrel. 21, Last annotation update)
Anti-DNA 11ght chain (Fragment)
                                                                                                                                                                                                                                                                                                                                                                                                                                Score 36; DB 16;
Pred. No. 56;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1; Mismatches
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                                                                        MEDLINE-20512582; PubMed=11058132;
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STRAIN-C3H/HEJ-LPR/LPR;
MEDLINE-96409289; Pubmed-8814271;
                                                                                                                                                                                                                                                                                                                                                                                                                              75.0%;
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                         SEQUENCE FROM N.A.
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SMART; SM00409; IG; 1.
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108 AA;
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Best Local Similarity
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282 QERESYPF 289
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NCBI_TaxID=86665;
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9
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SEQUENCE
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Matches
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Gaps

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Length 133; Indels

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SEQUENCE FROM N.A.
STRAIN=CV. FISKEBY V; TISSUE=COTYLEDON;
MEDLINE=95260869; PubMed=7742372;
Nong V., Becker C., Muentz K.;
"CDNA cloning for a putative cysteine proteinase from developing seeds of soybean:";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-UDN-2002 (TrEMBLrel. 21, Last annotation update)
Cysteine proteinase precursor.
Glycine max (Soybean).
Eukaryota: Viridiplantae; Streptophyta: Embryophyta: Tracheophyta: Spermatophyta; Magnoliophyta; edicotyledons; core eudicots; Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae; Glycine.
NCBI_TaxID=3847;
01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
01-MR-2002 (TrEMBLrel. 20, Last annotation update)
Cysteine proteinase precursor.
Phaseolus vulgaris (Kidney bean) (French bean).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnollophyta; eudicotyledons; core eudicots; Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae; Ph
                                                                                                                                                                                                                      SEQUENCE FROM N.A.
STRAIN-CV. MOLDAVIAN; TISSUE-COTYLEDON;
Senyuk V., Becker C., Muentz K.;
Senyuk V., Bocker C., Muentz K.;
"Isolation of cDNA clone encoding cysteine proteinase (CP4) from a cotyledon-specific cDNA library of germinating kidney bean seeds.";
Submitted (OCT-1997) to the EMBL/GenBank/DDBJ databases.
EMBL; 299555; CABI1707.1; -.
HSSP; P25779; IAIM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        70.8%; Score 34; DB 10; Length 377; 55.6%; Pred. No. 61;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          6576DEF3F1B26DA9 CRC64;
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Pfan: PF00112; Peptidase_C1; 1.
PRINTS; PR00705; PAPAIN.
PRODOM; PD000158; Peptidase_C1; 1.
PROSITE; PS00640; THIOL_PROTEASE_ASN; 1.
PROSITE; PS00639; THIOL_PROTEASE_CYS; 1.
Hydrolase; Signal; Thiol_Protease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Biochim. Biophys. Acta 1261:435-438(1995)
EMBL, 232795; CAA83673.1; -.
HSSP; P25779; 1AIM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRINTS; PRO0705; PAPAIN.
ProDom; PD000158; Peptidase_C1; 1.
PROSITE; PS00640; THIOL_PROTEASE_ASN; 1.
PROSITE; PS00139; THIOL_PROTEASE_CS; 1.
Hydrolase; Signal; Thiol protease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          POTENTIAL.
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                                                                                                                                                                                                                                                                                                                                                                                                                     InterPro; IPR000668; Peptidase_Cl.
InterPro; IPR000169; SHprot_acsite.
Pfam; PF00112; Peptidase_Cl; 1.
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Matches 5; Conservative
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138
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                                                                                                Hayashi T. Makino K., Ohnishi M., Kurokawa K., Ishii K., Yokoyama K., Han C.-G., Ohtsubo E., Nakayama K., Murata T., Tanaka M., Tobe T., Lida T., Takami H., Honda T., Sasakawa C., Ogasawara N., Yasunaga T., Kuhara S., Shiba T., Hattori M., Shinagawa H.;
Completel genomic equence of enterohemorrhagic Escherichia coli O157:H7 and genomic comparison with a laboratory strain K-12.";
DNA Res. E.11-22(2001).
EMBL; AR005357; BAB35591;
EMBL; AP005557; BAB355971;
EMBL; AP005555; BAB355981;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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eurosidd*1; Fabales; Fabaceae; Papilionoideae; Phaseoleae; Glycine.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Glycine max (Soybean).
Eukaryotą: Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
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                                                                                                                                                                                                                                                                                                                                                                                                                          16; Length 341;
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SEQUENCE § 341 AA; 38123 MW; C0310C4DE97C0037 CRC64;
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Last annotation update)
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Pred. No. 55;
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01-JAN-1998 (TrEMBLrel. 05, Created)
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GMPM33.
                                                     STRAIN-015 H7 / RIMD 0509952;
MEDLINE-21056231; PubMed-11258796;
Hayashi T. Makino K., Ohnishi M.,
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85.7%;
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Best Local Similarity
Matches 66 Conserv
     [2]
SEQUENCE FROM N.A.
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213 EEESSYPYT 221
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397 AA;
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288 OSSNYPFT 295
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BH3672.
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"The short interspersed repetitive element of Trypanasoma cruzi, SIRE, is associated to VIPER, a novel and unusual retroelement related to LTR-retrotransposons.";
                                                                                                                                                                                                              Trypanosoma cruzi.
Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae; Trypanosoma.
NCBI_TaxID=5693;
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                                 Gaps
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          DB 10; Length 380;
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SEQUENCE 393 Aa; 44188 MW; A728125DDA5CA282 CRC64;
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Last annotation update)
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Last annotation update)
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EMBL; AF096926; AAC72969.1; -.
                                                                                                                                   393 AA
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                               3; Mismatches
         Score 34;
Pred. No. 6
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01-MAY-1999 (TrEMBLrel. 10, Last sequenc
01-DEC-2001 (TrEMBLrel. 19, Last annotat
Lysosomal alpha mannosidase (Fragment).
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01-JAN-1998 (TrEMBLrel. 05, Last seq
01-MAR-2002 (TrEMBLrel. 20, Last anno
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MEDLINE-20160916; PubMed=10688909;
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MEDLINE=98044033; PubMed=9384377;
         70.8%;
55.6%;
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                   Best_Local Similarity 55.6
Matches 5; Conservative
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Bacteria; Firmicutes;
Bacillaceae; Bacillus.
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230 EEESSYPYT 238
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Nobayashi Y., Koetter P., Koningstein G., Krogh S., Kumen C.,
Kurita K., Lapidus A., Lardinois S., Lauber J., Lazarevic V.,
Lee S.M., Levine A., Liu H., Masuda S., Lauber J., Lazarevic V.,
Lee S.M., Levine A., Liu H., Masuda S., Mauel C., Medigue C.,
Medina N., Melladd R.P., Mizuno M., Moestl D., Mekai S., Noback M.,
Noone D., O'Reilly M., Ogawa K., Ogiwara A., Oudega B., Park S.H.,
Parco V., Pohl T.M., Portecelle D., Porvollik S., Prescott A.M.,
Presecan E., Pulic P., Purnelle D., Porvollik S., Prescott A.M.,
Rieger M., Rivolta C., Rocha E., Roche B., Ros M., Sadaie Y.,
Sato T., Scanlan E., Schleich S., Schroeter R., Scoffone F.,
Schiguchi J., Sakowska A., Seroz S.J., Serror P., Shin B.S., Soldo B.,
Sorokin A., Tacconi E., Tarkagi T., Tarkamashi H., Takemaru K.,
Takeuchi M., Tamakoshi A., Tanaka T., Terpstra P., Tognoni A.,
Tosato V., Uchiyama S., Vandenbol M., Vannier F., Vassarotti A.,
Viari A., Mambutt R., Wedler E., Wedler H., Waitzenegger T.,
Winters P., Wipat A., Yamamoto H., Yaname K., Yasumoto K., Yata K.,
Yoshida K., Yoshikawa H.F., Zumstein E., Yoshikawa H., Danchin A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "The complete genome sequence of the gram-positive bacterium Bacillus subtilis.",
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Harwood D.R.;
Submitted (OCT-1995) to the EMBL/GenBank/DDBJ databases.
EMBL; 299120; CAB15319.1; -.
EMBL; 299121; CAB15334.1; -.
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Rose M., Entian K.;
Submitted (FEB-1998) to the EMBL/GenBank/DDBJ databases.
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Submitted (NOV-1997) to the EMBL/GenBank/DDBJ databases.
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Last annotation update)
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1; Mismatches
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01-0CT-2000 (TrEMBLrel. 15, Created)
01-0CT-2000 (TrEMBLrel. 15, Last seq
01-0CT-2000 (TrEMBLrel. 15, Last and
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STRAIN-C-125 / JCM 9153;
MEDLINE-20512582; Pubmed-11058132;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 70.8%;
75.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Nature 390:249-256(1997).
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Bacillaceae; Bacillus.
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NCBI_TaxID=31286;
Takami H., Nakasone K., Takaki Y., Maeno G., Sasaki R., Masui N., Fuji F., Hirama C., Nakamura Y., Ogasawara N., Kuhara S., Horthoshi K., "Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans and genomic sequence comparison with Bacillus subtilis."; Nucleic Acids Res. 28.4317-4331(2000).
EMBL; APO01519; BAB07391.1; -. Complete proteome.
SEQUENCE 399 AA; 45051 MW; 4FA5D772A8D3960C CRC64;
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MEDLINE-29081299; PubMed-9865701;

Xong H.V., Vanhamme L., Chamekh M., Chimfwembe E.C.,

Van den Abbeele J., Pays A., van Meirvenne N., Hamers R.,

Van den Abbeelle T., Pays E.;

A VG expression site-associated gene confers resistance to human
serum in Trypanosoma rhodesiens.";

Cell 95:3819-846(1998).

EMBL; AJ010094; CAAO9000.1; -

SEQUENCE 478 AA; 52703 MW; 3CC5004781E5B97F CRC64;
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                                                                                                                                                                          Query Match 70.8%; Score 34; DB 16; Length 399; Best Local Similarity 75.0%; Pred. No. 64; Matches 6; Conservative 1; Mismatches 1; Indels
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01-MAY-1999 (TrEMBLrel. 10, Created)
01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
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Best Local Similarity
Matches 7; Conserv
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287 QSSNYPFT 294
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ESAG5.
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Search completed: December 23, 2002, 07:29:54 Job time : 5.73256 secs

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us-09-865-198-7.rai

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TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 38:
US-08-983-035A-38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LENGTH: 535 amino acids TYPE: amino acid
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Best Local Similarity
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Sequence 6, Appl
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163.250 Million cell updates/sec
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                                                                                                                                 December 23, 2002, 07:20:23 ; Search time 21.0872 Seconds
                                                                                                                                                                                                                                                                        1 QVKLQQSGAELVGSGASVKL.....AYYGDYEGYWGQGTTVTVSS 117
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/cgn2_6/ptodata/1/iaa/5B_COMB.pep:*
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/cgn2_6/ptodata/1/iaa/6B_COMB.pep:*
/cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
/cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
GenCore version 5.1.3
Copyright (c) 1993 - 2002 Compugen Ltd.
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PCT-US96-09448-18
                                                                                                                                                                                                                                                                                                                                                                                                                                    Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-08-767-128-22
US-08-652-507-2
US-08-017-570-6
US-08-471-426-6
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US-08-661-052-16
US-09-188-082-16
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US-09-102-716-16
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US-09-423-439-26
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US-09-171-945-19
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US-09-171-945-11
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Maximum Match 100%
Listing first 45 summaries
                                                                                        - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 2000000000
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Match Length DB
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2, Appli
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Sequence 13
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Sequence 7
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Sequence 38, Application US/08983035A
Batent No. 6326464
GENERAL INFORMATION:
APPLICANT: CONSEILLER, EMMANUEL
BRACCO, LAURENT
TITLE OF INVENTION: P53 PROTEIN VARIANTS AND THERAPEUTICAL
USES THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRITY APPLICATION DATA:
APPLICATION NUMBER: US/08/983,035A
FILING DATE: 20-Feb-1998
CLASSIFICATION: CUNKNOWN>
PRIOR APPLICATION: CUNKNOWN>
FILING DATE: 17-UL-1996
FILING DATE: 19-UUL-1995
                                                                                                                                                                                                                                                                                                                                                                                                                   ADDRESSEE: FINNEGAN, HENDERSON, FARABOW, GARRETT
US-08-646-265A-29
US-08-32-081B-38
US-08-561-521-9
PCT-US95-01219-9
US-08-822-830B-13
US-08-822-830B-2
US-08-950-660-2
PCT-US93-00030-2
PCT-US93-00030-2
PCT-US93-00030-2
PCT-US95-0121-4
PCT-US95-01219-4
US-08-951-521-4
US-08-951-521-4
US-08-951-521-4
US-08-951-521-4
US-08-951-521-4
US-08-95-01219-4
US-08-95-01219-4
US-08-9792-824-7
US-08-792-824-7
                                                                                                                                                                                  US-08-792-824-13
US-08-871-488A-15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: Strauss, William L.
REGISTRATION NUMBER: 47,114
REFERENCE/DOCKET NUMBER: 03804.0142
                                                                                                                                                                                                          US-08-207-169A-2
                                                                                                                                                                                                                                               ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                             DUNNER, LLP
30 I Street, NW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-408-4000
TELEFAX: 202-408-4400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             INFORMATION FOR SEO ID NO: 38
                                                                                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQUENCES: 59
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                       CITY: Washington STATE: DC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COUNTRY: USA
ZIP: 20005-3315
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Length 535;

Score 554.5; DB 4; Pred. No. 5.1e-48;

87.9%; 88.9%;

Length 118;

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TELEPHONE:
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      Query Match
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3100 No. 6111079west Center, 90 South Seventh St
Minneapolis
      Indels
                                                                                                                                                                                                                                                  APPLICANT: WYLIE, DWANE E.
APPLICANT: WOREZ, OSYALDO
APPLICANT: GOREZ, OSYALDO
APPLICANT: GOREEL, PETER
TITLE OF INVENTION: LEAD BINDING POLYPEPTIDES AND
TITLE OF INVENTION: NUCLEOTIDES CODING THEREFORE
CORRESPONDENCE ADDRESS:
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9
      6; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CLASS FETCATION: 424
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE: 04-DEC-1996
CLASS FETCATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US96/09258
FILING DATE: 05-JUN-1996
FILING DATE: 10-CCT-1995
FILING DATE: 10-CCT-1995
FILING DATE: 10-CCT-1995
APPLICATION DATA:
FILING DATE: 10-CCT-1995
FILING DATE: 05-JUN-1995
ATTORNEY, AGENT INFORMATION:
NAME: CATLER: CATLES G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         8648.49USF1
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/767,128
FILING DATE:
                                                                                                                                                                                                      Sequence 22, Application US/08767128 Patent No. 611079 GENERAL INFORMATION: APPLICANT, WYLIE, DWANE E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          35,093
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REFERENCE/DOCKET NUMBER: 86
TELECOMPUNICATION INFORMATION
TELERENGE: 612/371-5278
TELERERAX: 612/332-9081
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     22:
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SEQUENCE CHARACTERISTICS:
LENGTH: 118 amino acids
TYPE; amino acids
STRANDEDNESS: single
    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDIUM TYPE: Diskette
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MOLECUÜE TYPE: protein
HYPOTHËTICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
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ORIGINAL SOURCE:
US-08-767-128-22
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STREET[ 31
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Matches 104
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                                                                                   1 QVKLQQSGAELVGSGASVKLSCTTSGFNIKDFYMHWVKQRPEQGLEWIGWIDPENGDSGY 60
                                                                                                      Gaps
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                                                                                                                                                                                          61 DPKFQGKATMTADTSSNIAYLQLSSLTSEDTAVYYCNPYGYDDAMDYMGQGTSVTVSS 118
                                                                                                                                                                  61 APKFQGKATMTADSSSNTAYLQLSSLTSEDTAVYYCNAY-YGDYEGYWGQGTTVTVSS 117
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                                                                                                                                                                                                                                                                                                                                                                                        TITLE OF INVENTION: ANTIBODY AGAINST CARCINOEMBRYONIC ANTIGEN TITLE OF INVENTION:
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 270;
                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/652,507
FILLING DATE: 02-Jul-1996
CLASSIFICATION: 530
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADDRESSEE: Nixon & Vanderhye, P.C.
STREET: 1100 No. 5876691th Glebe Road, 8th Floor
Score 532.5; DB 3;
Pred. No. 1.4e-46;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 81.4%; Score 513.5; DB 2; Best Local Similarity 81.3%; Pred. No. 3e-44; Matches 100; Conservative 4; Mismatches 10;
                                        6; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 2, Application US/08652507 Patent No. 5876691 GENERAL INFORMATION:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; Sequence 6, Application US/08017570
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ATTORNEY/AGENT INFORMATION:
NAME: Arthur R. Crawford
REGISTRATION NUMBER: 25,327
REFERENCE/DOCKET NUMBER: 117
TELECOMMUNICATION INFORMATION:
  84.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             703-816-4000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                270 amino acids
                       Best Local Similarity 85.6
Matches 101; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              703-816-4100
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CITY: Arlington STATE: Virginia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-08-017-570-6
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/017,570
FILING DATE: 16-FEB-1993
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                              NAME: ULMER, DUANE C
REGISTRATION NUMBER: 34,941
REPERENCE/DOCKET NUMBER: C-38
TELECOMMUICATION INFORMATION:
TELEPHONE: (517) 636-8104
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LENGIH: 124 amino acids
TYPE: amino acid
                                  COUNTRY: US
ZIP: 48641-1967
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; MOLECULE TYPE: protein US-08-471-426-6
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| 118 TTVTVSS 124
Midland
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PCT-US94-01709-6
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STATE: M.
COUNTRY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 124;
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APPLICANT: RIXON, MARK W
APPLICANT: MEZES, PETER S
APPLICANT: KAPLAN, DONALD A
APPLICANT: SCHLOM, JEFREY
TITLE OF INVENTION: A NOVEL FAMILY OF ANTI-CARCINOEMBRYONIC
TITLE OF INVENTION: ANTIGEN CHIMERIC ANTIBODIES
        GENERAL INCOLAGOS

APPLICANT: GOURLIE, BRIAN B

APPLICANT: RIXON, MARK W

APPLICANT: REZES, PETER S

APPLICANT: KAPLAN, DONALD A

APPLICANT: KAPLAN, DONALD A

APPLICANT: SCHLOM, JEFFREY

TITLE OF INVENTION: A NOVEL FAMILY OF ANTI-CARCINOEMBRYONIC

TITLE OF INVENTION: ANTIGEN CHIMERIC ANTIBODIES

NUMBER OF SEQUENCE: 24

CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE: PatentIn Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
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77.2%; Pred. No. 4.8e-44;
iive 8; Mismatches 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: US/08/017,570 FILLING DATE: 19930216 CLASSIFICATION: 424
                                                                                                                                                                                                                                                                                                                                                  MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: ULMER, DUANE C
REGISTRATION NUMBER: 34,941
REFERENCE/DOCKET NUMBER: C-38
TELECOMMUNICATION INFORMATION:
TELEPHONE: (517) 636-8104
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 6, Application US/08471426 Patent No. 5808033 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESS:
ADDRESSEE: Duane C. Ulmer
STREET: P.O. BOX 1967
                                                                                                                                                                                                            ADDRESSEE: Duane C. Ulmer
STREET: P.O. Box 1967
CITY: Midland .
STATE: MI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LENGTH: 124 amino acids TYPE: AMINO ACID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best Local Similarity 77.2
Matches 98; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; MOLECULE TYPE: protein US-08-017-570-6
                                                                                                                                                                                                                                                                                                           ZIP: 48641-1967
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         111 TTVTVSS 117
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                                                                                                                                                                                                                                                                                             COUNTRY:
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61 APKFQGKATMTADSSSNTAYLQLSSLTSEDTAVYYCNA-----YYGDYEGYWGQG 110
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 80.4%; Score 507.5; DB 1; Length 124; Best Local Similarity 77.2%; Pred. No. 4.8e-44; Matches 98; Conservative 8; Mismatches 8; Indels 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 6, Application PC/TUS9401709
GENERAL INFORMATION:
APPLICANT: THE DOW CHEMICAL COMPANY
APPLICANT: THE DOW CHEMICAL COMPANY
APPLICANT: TU.S.A. DEPT. OF HEALTH AND HUMAN SERVICES
TITLE OF INVENTION: A NOVEL FAMILY OF ANTI-CARCINOEMBRYONIC
TITLE OF INVENTION: A NATIGEN CHIMERIC ANTIBODIES
NUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESS:
ADDRESSEE: Duane C. Ulmer
STREET: P.O. Box 1967
CITY: Midland
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
FILING DATE: 06-JUN-1995
CLASSIFICATION: 536
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ZIP: 48641-1967
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFWARRE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/01709
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278 IKLQQSGAELVRSGTSVKLSCTASGFNIKDSYMHWLRQGPEQGLEWIGWIDPENGDTEYA 337
                                                                                                                                                                                               PKFQGKATMTADSSSNTAYLQLSSLTSEDTAVYYCN-----AYYGDYEGYWGQGTTVTV 115
                                                                                                                                                                                                                  62 PKFQGKATMTADSSSNTAYLQLSSLTSEDTAVYYCN-----AYYGDYEGYWGQGTTVTV 115
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                                                                                                                 2 VKLQQSGAELVGSGASVKLSCTTSGFNIKDFYMHWVKQRPEQGLEWIGWIDPENGDSGYA 61
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                                                                            6
                                         Length 553;
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                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TITLE OF INVENTION: THERAPEUTIC COMPOUNDS COMPRISED TITLE OF INVENTION: OF ANTI-FC RECEPTOR ANTIBODIES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ZIP: 02109-1875
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: DEM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/188,082
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 4;
                                     Score 507.5; DB 2
Pred. No. 2.8e-43;
5; Mismatches 10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               80.4%; Score 507.5;
80.3%; Pred. No. 2.8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       E: LAHIVE & COCKFIELD
60 State Street, Suite 510
                                                                                                                                                                                                                                                                                                                                                                            RESULT 8
US-09-188-082-16
'Sequence 16, Application US/09188082
'Patent No. 6270765
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION DATA: APPLICATION NUMBER: 08/661,052
                                                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
APPLICANT: Yashwant M. Deo
APPLICANT: Joel Goldstein
APPLICANT: Robert Graziano
APPLICANT: Chezian Somasundaram
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME: Arnold, Beth E.
REGISTRATION NUMBER: 35,430
REFERENCE/DOCKET NUMBER: MXI
TELECOMMUNICATION:
TELEPHONE: (617)227-7400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEFAX: (617)227-5941 INFORMATION FOR SEQ ID NO: 16:
                                   80.4%;
ilarity 80.3%;
Conservative
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ATTORNEY/AGENT INFORMATION:
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amino acid
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CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CITY: Boston
STATE: Massachusetts
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MOLECULE TYPE: protein
                                Query Match
Best Local Similarity
Matches 98; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
Matches 98; Conserv
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                                                                                                                                                                                                                                                                                                  11
SS 396
US-08-661-052-16
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                                                                                                                                                                                                                                                     Length 124;
                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 16% Application US/08661052
Patent No. 5837243
GENERAL INFORMATION
APPLICANT: Vashwant M. Deo
APPLICANT: Robert Graziano
TITLE OFFINVENTION: THERAPEUTIC COMPOUNDS COMPRISED
TITLE OFFINVENTION: OF ANTI-FC RECEPTOR ANTIBODIES
NUMBER OF SEQUENCES: 16
CORRESPONDENTS: ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD
STREET: 60 State Street, Suite 510
                                                                                                                                                                                                                                                       80.4%; Score 507.5; DB 5; ilarity 77.2%; Pred. No. 4.8e-44; Conservative 8; Mismatches 8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PatentIn Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ATTORNEY ALENT INFORMATION:

NAME: ARIOID BELF.

REGISTRATION NUMBER: 35,430

REFERENCE/DOCKET NUMBER: MXI-043CP

TELECOMÜNUICATION INFORMATION:

TELEPHONE: (617)227-7400

TELEFAX: (617)227-5941

INFORMATION FOR SEQ ID NO: 16:

SEQUENCE CHARACTER.STICS:

LENGTH: 553 amino acids

TYPE: amino acids

TYPE: amino acids

TYPE: Innear

MOLECULÉ TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PETOR APPLICATION DATA:
PROLIGATION NUMBER: US 08/484,172
FILING DATE: 07-JUNE-1995
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWÄRE: Patentin Release #1.0, CURRENTÄRPELICATION DATA:
APPLICATION NUMBER: US/08/661,052 FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LIF: WALLY LOOP COMPUTER READABLE FORM:
MEDITUR TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
            REGISTRATION NUMBER: 34,941
REFERENČE/DOCKET NUMBER: 38,7
TELECOMMUNICATION INFORMATION:
TELEPHONE: (51) 636-8104
INPORMATION FOR SEQ ID NO: 6:
SEQUENCE GHARACTERISTICS:
                                                                                                                                   124 amino acids
mino acid
                                                                                                                                                                      TOPOLOG姿: linear
MOLECULE 群YPE: protein
ULMER, DUANE C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Massachusetts
                                                                                                                                                                                                                                                                         Best Local Similarity
Matches 98; Conserv
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STATE: Massacl
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             111 TTVTVSS 117
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                                                                                                                                     LENGTH:
                                                                                                                                                                                                                                                         Query Match
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NO. 6395272
AL INFORMATION:
   Patent No.
GENERAL
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62 PKFQGKAIMTADSSSNTAYLQLSSLTSEDTAVYYCN-----AYYGDYEGYWGQGTTVTV 115
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                                                                                                                                                                                                                APPLICANT: Yashwant M. Deo, et al.
TITLE OF INVENTION: THERAPEUTIC COMPOUNDS COMPRISED
TITLE OF INVENTION: OF ANTI-FC RECEPTOR ANTIBODIES
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD, LLP
STREET: 28 State Street, 24th Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: PATENTEN PC-DOS/MS-DOS SOFTWARE: PATENTIN Release #1.0, Version #1.25 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/09/364,088 FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 80.4%; Score 507.5; DB 4;
80.3%; Pred. No. 2.8e-43;
Five 5: Mismatches 10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: US 08/484,172
FILING DATE: 07-UNE-1995
ATTORNEY/AGENT INFORMATION:
NAME: REMILIARG, Jane E.
REGISTRATION NUMBER: 38,872
REFERENCE/DOCKET NUMBER: MXI-043CP2
TELECHUNE: (617)227-740
TELECHUNE: (617)227-740
INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: US 09/188,082 FILING DATE: 07-JUNE-1996 PRIOR APPLICATION DATA:
                                                                                                                                                                   Sequence 16, Application US/09364088 Patent No. 6365161 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; Sequence 16, Application US/09102716
                                                                                                                                                                                                                                                                                                                                                                                ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 80.35
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                   CITY: Boston
STATE: Massachusetts
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           amino acid
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                                                                                                                                                                                                                                                                                                                                                                     USA
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SS 396
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US-09-102-716-16
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62 PKFQGKATMTADSSSNTAYLQLSSLTSEDTAVYYCN-----AYYGDYEGYWGQGTTVTV 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2 VKLQQSGAELVGSGASVKLSCTTSGFNIKDFYMHWVKQRPEQGLEWIGWIDPENGDSGYA 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 553;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A NOVEL FAMILY OF ANTI-CARCINOEMBRYONIC ANTIGEN CHIMERIC ANTIBODIES
                                                                   Chezian Somasundaram
TITLE OF INVENTION: THERAPEUTIC COMPOUNDS COMPRISED
OF ANTI-FC RECEPTOR ANTIBODIES
                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: PatentIn Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          80.4%; Score 507.5; DB 4;
80.3%; Pred. No. 2.8e-43;
11ve 5; Mismatches 10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                  CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/102,716
FILING DATE: 22-Jun-1998
PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/661,052
FILING DATE: CUNROWN>
ATTORNEY/AGENT INFORMATION:

NAME: AFOLD BLL E.

REGISTRATION NUMBER: 35,430
REFERENCE/DOCKET NUMBER: MXI-043CP
TELECOMMUNICATION INFORMATION:

TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                            ADDRESSEE: LAHIVE & COCKFIELD
STREET: 60 State Street, Suite 510
                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY: linear MOLECULE TYPE: protein SEQUENCE DESCRIPTION: SEQ ID NO: 16: US-09-102-716-16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 4, Application US/08017570

Patent No. 5472693

GENERAL INFORMATION:
APPLICANT: GOURLIE, BRIAN B
APPLICANT: RIXON, MARK W
APPLICANT: RAPLAN, DONALD A
APPLICANT: KAPLAN, DONALD A
APPLICANT: KAPLAN, JEFFRES
TITLE OF INVENTION: A NOVEL FAMILY
TITLE OF INVENTION: ANTIGEN CHIMER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE CHARACTERISTICS:
LENGTH: 553 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEPHONE: (617)227-74(
TELEFAX: (617)227-5941
INFORMATION FOR SEQ ID NO: 16:
APPLICANT: Yashwant M. Deo
                                               Robert Graziano
                                                                                                                                                                                                                                                             STATE: Massachusetts
COUNTRY: USA
ZIP: 02109-1875
                                                                                                                                                                   CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best_Local Similarity 80.3
Matches 98; Conservative
                                                                                                                                               NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                              CITY: Boston
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQUENCES:
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US-08-017-570-4
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ZIP: 48641-1967
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURREMY APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/01709
                                                                                                                                                                                                                                                                                                                                                                                                           Score 502.5; DB 1;
Pred. No. 1.5e-43;
8; Mismatches 9;
APPLICATION NUMBER: US/08/471,426 FILING DATE: 06-JUN-1995 CLASSIFICATION: 536
                             CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/017,570
FILLING DATE: 16-FEB-1993
ATTORNEY/AGENT INFORMATION:
NAME: ULMER, DUANE C
REGISSTRATION NUMBER: 34,941
REFERENCE/DOCKET NUMBER: C-38,777
TELECOMMUNICATION INFORMATION:
TELECHONE: (517) 636-8104
INFORMATION FOR SEQ ID NO: 4:
                                                                                                                                                                                   C-38,777
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: ULAER, DUANE
REGISTRATION NUMBER: 34,941
REFERENCE/DOCKET NUMBER: 38,77
TELECOMUNICATION INFORMATION:
TELEPHONE: (517) 636-8104
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADDRESSEE: Duane C. Ulmer
STREET: P.O. Box 1967
CITY: Midland
STATE: MI
                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 79.6%;
Best Local Similarity 76.4%;
Matches 97; Conservative
                                                                                                                                                                                                                                                                                      LENGTH: 124 amino acids
TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LENGTH: 124 amino acids TYPE: amino acid
                                                                                                                                                                                                                                                                   SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                            ; MOLECULE TYPE: protein US-08-471-426-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         111 TTVTVSS 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   118 TTVAVSS 124
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 13
PCT-US94-01709-4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 QVKLOSGAELVGSGASVKLSCTTSGFNIKDFYMHWVKQRPEQGLEWIGWIDPENGDSGY 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 1; Length 124;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: GOURLIE, BRIAN B
APPLICANT: RIXON, MARK W
APPLICANT: RIXON, MARK W
APPLICANT: ASLOW
APPLICANT: SCHLOM, DONALD A
APPLICANT: SCHLOM, DEFEREY
TITLE OF INVENTION: A NOVEL FAMILY OF ANTI-CARCINOEMBRYONIC
TITLE OF INVENTION: ANTIGEN CHIMERIC ANTIBODIES
NUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESS:
ADDRESSE: Duane C. Ulmer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                 COMPUTEN WEALPABLE FORD,
MEDIUM TYPE: Floppy disk
COMPUTEN: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURREWT MEPPLICATION DATA:
APPLICATION NUMBER: US/08/017,570
FILING BATE: 19930216
CLASSIFICATION: 424
ATTORNEY AGENT INFORMATION:
NAME: ULMER, DUANE C
REGISTRATION NUMBER: 34,941
REFERENCE/DOCKET NUMBER: C-38,777
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION SEQ ID NO: 4:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWÄRE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             19.6%; Score 502.5; DB 1; ilarity 76.4%; Pred. No. 1.5e-43; Conservative 8; Mismatches 9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-08-471-426-4
; Sequence 4, Application US/08471426
; Patent No. $5808033
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE CHARACTERISTICS:
LENGTH 124 amino acids
TYPE: AMINO ACID
                  ADDRESSEE: Duane C. UIN
STREET: P.O. Box 1967
CITY: Midland
STATE: MI
COUNTRY: US
ZIP: 48641-1967
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADDREŠSEE: Duane C. UJ
STREET: P.O. BOX 1967
CITY: Midland
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: protein
CORRESPONDENCE ADDRESS:
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STATE: ML
COUNTRY: US
THE FORM THE F
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Best Local Similarity
Matches 97; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      linear
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US-08-017-570
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1 QVKLQQSGAELVGSGASVKLSCTTSGFNIKDFYMHWVKQRPEQGLEWIGWIDPENGDSGY 60
                                                                                                             Indels 13;
Length 124;
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GENERAL INFORMATION:
APPLICANT: THE DOW CHEMICAL COMPANY
APPLICANT: U.S.A. DEPT. OF HEALTH AND HUMAN SERVICES
TITLE OF INVENTION: A NOVEL FAMILY OF ANTI-CARCINOEMBRYONIC
TITLE OF INVENTION: ANTIGEN CHIMERIC ANTIBODIES
NUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESS:
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ORGANISM: Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           111 TTVTVSS 117
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Tempest, Philip R.
APPLICANT: Tempest, Philip R.
APPLICANT: Tempest, Philip R.
APPLICANT: Tempest, Philip R.
APPLICANT: Harris, William J.
APPLICANT: Harris, William J.
APPLICANT: Armour, Kathryn
TITLE OF INVENTION: High Affinity Humanized Anti-CEA Monoclonal Antibodies
FILE REFERENCE:
CURRENT APPLICATION NUMBER: US/09/672,609
FRICR PRIOR APPLICATION NUMBER: 09/025,403
PRIOR FILING DATE: 1998-02-18
NUMBER OF SEQ ID NOS: 50
SOFTWARE: Microsoft Word 97 SR-2
SEQ ID NO: LENGTH: 124
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    61 APKFQGKATMTADSSSNTAYLQLSSLTSEDTAVYYCNA-----YYGDYEGYWGQG 110
                                                                                                                                                                                                             61 APKFQGKATMTADSSSNTAYLQLSSLTSEDTAVYYCNA------YYGDYEGYWGQG 110
                                                                                                                                                                                                                                61 APKFQGKAIMTIDISSNIAYLQLSSLISEDIAVYYCNIRGLSIMITIRWFFD---VWGAG 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 QVKLQQSGAELVGSGASVKLSCTTSGFNIKDFYMHWVKQRPEQGLEWIGWIDPENGDSGY 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels 13; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 QVKLQQSGAELVGSGASVKLSCTTSGFNIKDFYMHWVKQRPEQGLEWIGWIDPENGDSGY 60
                                                                                                   Indels 13; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 499.5; DB 4; Length 124;
Pred. No. 3e-43;
7; Mismatches 10; Indels 13
                                                                 Length 124;
                                                             Score 502.5; DB 5;
Pred. No. 1.5e-43;
8; Mismatches 9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 1, Application US/09025403A Patent No. 6417337
                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 1, Application US/09672609
Patent No. 6333405
GENERAL INFORMATION:
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APPLICANT: Anderson, W.H. Kerr
APPLICANT: Tempest, Philip R.
APPLICANT: Carr, Frank J.
APPLICANT: Harris, William J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      79.28;
                                                             Query Match 79.6%;
Best Local Similarity 76.4%;
Matches 97; Conservative
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Best Local Similarity 76.48
Matches 97; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ) NAME/KEY: Murine Col-1 VH
; LOCATION: 1..124
US-09-672-609-1
; MOLECULE TYPE: protein PCT-US94-01709-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ORGANISM: Mus musculus
                                                                                                                                                                                                                                                                                    111 TTVTVSS 117
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                                                                                                                                                                                                                                                                                                                       118 TTVAVSS 124
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US-09-025-403A-1
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GenCore version 5.1.3
Copyright (c) 1993 - 2002 Compugen Ltd.
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OM protein - protein search, using sw model
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December 23, 2002, 07:30:08; Search time 10.8837 Seconds Run on:

(without alignments) 180.208 Million cell updates/sec

US-09-865-198-7

631 1 QVKLQQSGAELVGSGASVKL.....AYYGDYEGYWGQGTTVTVSS 117 Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

106657 segs, 16763532 residues Searched:

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

Published_Applications_AA:*

1: /cgn2_6/ptodata/2/pubpaa/USOB_NEW_PUB.pep:*
2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep:*
3: /cgn2_6/ptodata/2/pubpaa/USO6_NEW_PUB.pep:*
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7: /cgn2_6/ptodata/2/pubpaa/USO3_NEW_PUB.pep:*
8: /cgn2_6/ptodata/2/pubpaa/USO3_PUBCOMB.pep:*
9: /cgn2_6/ptodata/2/pubpaa/USO3_PUBCOMB.pep:*
10: /cgn2_6/ptodata/2/pubpaa/USO3_PUBCOMB.pep:*
11: /cgn2_6/ptodata/2/pubpaa/USO3_PUBCOMB.pep:*
12: /cgn2_6/ptodata/2/pubpaa/USO3_PUBCOMB.pep:*
13: /cgn2_6/ptodata/2/pubpaa/USO3_PUBCOMB.pep:*
13: /cgn2_6/ptodata/2/pubpaa/USO3_PUBCOMB.pep:*
14: /cgn2_6/ptodata/2/pubpaa/USO3_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Description	Sequence 7. Appli	, ,	28,	Sequence 27, Appl	Sequence 23, Appl	Sequence 22, Appl	29,	28,	Ä		٦	19,	11,	11,	Sequence 11, Appl	11,	Sequence 11, Appl	18,	Sequence 17, Appl
	ID	US-09-976-787-7	US-09-865-198-7	US-09-976-787-28	US-09-865-198-27	US-09-976-787-23	US-09-865-198-22	US-09-976-787-29	US-09-865-198-28	US-09-974-052-1	US-09-974-051-1	US-09-910-059-11	US-09-910-059-19	US-09-564-329A-11	US-09-855-153-11	US-09-854-811-11	US-09-934-773-11	US-09-963-620-11	US-09-158-120A-18	US-09-158-120A-17
	Query Match Length DB	117 10	117 10	240 10	240 10	117 10	117 10	238 10	238 10	124 9	124 9	120 10	255 10	136 10	136 10	136 10	136 10	136 10	117 10	117 10
ф	Query Match Le	100.0	100.0	100.0	100.0	6.86	6.86	6.86	98.9	79.2	79.2	79.0	79.0	8.92	8.92	76.8	8.94	8.92	75.8	67.8
	Score	631	631	631	631	624	624	624	624	499.5	499.5	498.5	498.5	484.5	484.5	484.5	484.5	484.5	478	428
	Result No.		7	٣	4	5	9	7	œ	6	10	11	12	13	14	15	16	17	18	19

Sequence 5, Appli	Sequence 1, Appli	Sequence 9, Appli	Sequence 12, Appl	Sequence 9, Appli	Sequence 12, Appl	Sequence 8, Appli	Sequence 8, Appli	Sequence 89, Appl	Sequence 7, Appli	Sequence 79, Appl		Sequence 85, Appl	Sequence 28, Appl	Sequence 4, Appli	Sequence 81, Appl	Sequence 2, Appli	Sequence 7, Appli	Sequence 7, Appli	78,	Sequence 55, Appl	Sequence 57, Appl	Sequence 93, Appl	Sequence 95, Appl	Sequence 113, App	Sequence 125, App
10 US-09-809-739-5	10 US-09-940-391-1	9 US-09-974-052-9	9 US-09-974-052-12	9 US-09-974-051-9	9 US-09-974-051-12	9 US-09-974-052-8	9 US-09-974-051-8	10 US-09-910-059-89		10 US-09-910-059-79	10 US-09-910-059-91	10 US-09-910-059-85	1 US-08-779-784-28	10 US-09-861-294-4	10 US-09-910-059-81	12 US-10-025-687-2	9 US-09-974-052-7	9 US-09-974-051-7	10 US-09-753-436-78	10 US-09-910-059-55	_	_	10 US-09-910-059-95	10 US-09-910-059-113	10 US-09-910-059-125
139	244	124	124	124	124	124	124	120	127	120	120	120	122	153	120	120	124	124	138	120	255	260	306	613	716
67.7	8.99	65.5	65.5	65.5	65.5	64.9	64.9	64.7	64.4	64.1	63.8	63.3	63.3	63.3	63.2	63.0	63.0	63.0	62.9	62.7	62.7	62.7	62.7	62.7	62.7
427.5	421.5	413.5	413.5	413.5	413.5	409.5	409.5	408.5	406.5	404.5	402.5	399.5	399.5	399.5	398.5	397.5	397.5	397.5	397	395.5	395.5	395.5	395.5	395.5	395.5
20	21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

ALIGNMENTS

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Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 OVKLQOSGAELVGSGASVKLSCTTSGFNIKDFYMHWVKQRPEQGLEWIGWIDPENGDSGY 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 7, Application US/09976787

Sequence 10. US20020064528A1

GENERAL INFORMATION:

APPLICANT: Zhu, Zhenping

APPLICANT: Witte, Larry

TUTLE OF INVENTION: Antibodies Specific to KDR and Uses Thereof

FILE REFERENCE: 11245,46505

CURRENT APPLICATION NUMBER: US/09/976,787

CURRENT FILING DATE: 2000-10-12

PRIOR APPLICATION NUMBER: US 60/117,726

PRIOR APPLICATION NUMBER: US 60/117,726

PRIOR PILING DATE: 1999-01-29

NUMBER OF SEC ID NOS: 40

SOFTWARE: WordPerfect 8.0 for Windows
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 2
US-09-865-198-7
; Sequence 7, Application US/09865198
; Patent No. US20020103345A1
; GENERAL INPORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 100.(
Matches 117; Conservative
                                                                                                                                                                                                                                                                                                                                                                                             ; ORGANISM: Mus musculus US-09-976-787-7
                                                                                                                                                                                                                                                                                                                                  SEQ ID NO 7
LENGTH: 117
7-181-976-90-SU
                                                                                                                                                                                                                                                                                                                                                                              TYPE: PRT
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Gaps

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Indels

Length 240;

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APPLICANT: Zhu, Zhenping
TITLE OF INVENTION: Bispecific Immunoglobulin-Like Antigen Binding Proteins and Me
TITLE OF INVENTION: Production
FILE REFERENCE: 11245/4710A
CURRENT APPLICATION NUMBER: US/09/865,198
CURRENT FILING DATE: 2001-05-24
PRIOR APPLICATION NUMBER: US 60/206,749
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 QVKLQQSGAELVGSGASVKLSCTTSGFNIKDFYMHWVKQRPEQGLEWIGWIDPENGDSGY 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 QVKLQQSGAELVGSGASVKLSCTTSGFNIKDFYMHWVKQRPEQGLEWIGWIDPENGDSDY 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    61 APKFQGKATMTADSSSNTAYLQLSSLTSEDTAVYYCNAYYGDYEGYWGQGTTVTVSS 117
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Zhu, Zhenping
APPLICANT: Zhu, Zhenping
APPLICANT: Witte, Larry
TITLE OF INVENTION: Antibodies Specific to KDR and Uses Thereof
FILE REFERENCE: 11245/46505
CURRENT APPLICATION NUMBER: US/09/976,787
CURRENT APPLICATION NUMBER: US 09/493,539
PRIOR APPLICATION NUMBER: US 60/117,726
PRIOR APPLICATION NUMBER: US 60/117,726
PRIOR FILING DATE: 1999-01-29
NUMBER OF SEQ ID NOS: 40
SOFTWARE: WORDPEFECT 8.0 for Windows
                                                                                                                                                                                                                                                                                                                                                              Score 631; DB 10;
Pred. No. 1.1e-41;
Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 624; DB 10;
Pred. No. 2.1e-41;
0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                      100.0%; Scor.
100.0%; Pred. No. 1...
0; Mismatches
CURRENT APPLICATION NUMBER: US/09/865,198
CURRENT FILING DATE: 2001-05-24
PRIOR APPLICATION NUMBER: US 60/206,749
PRIOR FILING DATE: 2000-05-24
                                                                                                                  NUMBER OF SEQ ID NOS: 34
SOFWARE: WordPerfect 8.0 for Windows
SEQ ID NO 27
LENGTH: 240
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Patent No. US20020103345A1
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99.1%;
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Best Local Similarity 100.(
Matches 117; Conservative
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Best Local Similarity 99.15
Matches 116; Conservative
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US-09-865-198-27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; ORGANISM: Mouse US-09-976-787-23
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                                                                                                                                                                                                                                            TYPE: PRT
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Patent No. US20020103345A1

GRNERAL INFORMATION:
APPLICAMI: Zhu, Zhenping

TITLE OF INVENTION: Bispecific Immunoglobulin-Like Antigen Binding Proteins and Methor TITLE OF INVENTION: Production
FILE REFERENCE: 11245/47102
TITLE OF INVENTION: Bispecific Immunoglobulin-Like Antigen Binding Proteins and Methd
TITLE OF INVENTION: Production
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 QVKIGOSGAELVGSGASVKLSCTTSGFNIKDFYMHWVKQRPEQGLEWIGWIDPENGDSGY 60
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GENERAL INFORMATION:
APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
FILE REPRENEUE: 11245/46505
FILE REPRENEUE: 11245/46505
FILE REPRENEUE: 1245/46505
FILE REPRENEUE: 1245/46505
FILE REPRENEUE: 1201-10-12
FRIOR APPLICATION NUMBER: US 09/493,539
FRIOR APPLICATION NUMBER: US 60/117,726
FRIOR FILENG DATE: 1999-01-28
FRIOR FILENG DATE: 1999-01-29
NUMBER OFFER ON NOW OFFER OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 117;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 240;
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100.0%; Pred. No. 6e-42;
tive 0; Mismatches (
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                                           FILE REFERENCE: 11245/47102
CURRENT APPLICATION NUMBER: US/09/865,198
CURRENT FILING DATE: 2001-05-24
PRIOR APPLICATION NUMBER: US 60/206,749
PRIOR FILING DATE: 2000-05-24
NUMBER OF SEO ID NOS: 34
SEO ID NO 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 28th Application US/09976787 Patent No. US20020064528A1
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Best Local Similarity
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Matches 117 Conserv
                                                                                                                                                                                                                                                                                                                            TYPE: PRT ORGANISM: Mouse US-09-865-198-7
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US-09-976-787-28
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TYPE: PRE
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Gaps

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Indels

Length 117;

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GENERAL INFORMATION:

APPLICANT: Anderson, W.H. Kerr

APPLICANT: Tempest, Philip R.

APPLICANT: Tempest, Philip R.

APPLICANT: Garr, Frank J.

APPLICANT: Armour, Kathryn

TITLE OF INVENTION: High Affinity Humanized Anti-CEA Monoclonal Antibodies

FILE REPERENCE:

CURRENT APPLICATION NUMBER: US/09/974,052

CURRENT APPLICATION NUMBER: US/09/974,052

CURRENT PILING DATE: 1998-02-18

PRIOR FILING DATE: 1998-02-18

PRIOR FILING DATE: 1997-10-30

PRIOR FILING DATE: 1997-10-30

PRIOR FILING DATE: 1996-10-31

NUMBER OF SEQ ID NOS: 50

SOFTWARE: Microsoft Word 97 SR-2

FENDINE DATE: 100 NOS: 50

SOFTWARE: Microsoft Word 97 SR-2
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                                                                                                                                                                      Gaps
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                                                                                                                           Score 624; DB 10;
Pred. No. 3.8e-41;
0; Mismatches 1;
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; Publication No. US20020183495A1
; GENERAL INFORMATION:
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; Patent No. US20020165387A1
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Best Local Similarity 99.1%;
Matches 116; Conservative
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; LOCATION: 1..124
US-09-974-052-1
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Matches 97; Conserv
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                                                             ; ORGANISM: Mouse US-09-865-198-28
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US-09-974-052-1
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                   LENGTH: 238
TYPE: PRT
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Sequence 28, Application US/09865198
Patent NO. US20020103345A1
GENERAL INFORMATION:
APPLICANT: Zhu, Zhenping
TITLE OF INVENTION: Bispecific Immunoglobulin-Like Antigen Binding Proteins and Methor IITLE OF INVENTION: Production
FILE REFERENCE: 11245/4102
CURRENT APPLICATION NUMBER: US/09/865,198
CURRENT FILING DATE: 2001-05-24
PRIOR APPLICATION NUMBER: US 60/206,749
PRIOR FILING DATE: 2000-05-24
NUMBER OF SEQ ID NOS: 34
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APPLICANT: Zhu, Zhenping
APPLICANT: Witte, Larry
TITLE OF INVENTION:
FILE REFERENCE: 11245/46505
CURRENT FILING DATE: 2001-10-12
PRIOR PAPLICATION NUMBER: US 09/493,539
PRIOR PELICATION NUMBER: US 60/117,726
PRIOR PELICATION NUMBER: US 60/117,726
PRIOR FILING DATE: 1999-01-29
NUMBER OF SEQ ID NOS: 40
SOFTHARR: WORDPEFFECT 8.0 for Windows
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Pred. No. 2.1e-41;
0; Mismatches 1; Indels (
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Pred. No. 3.8e-41;
0; Mismatches 1;
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SOFTWARE: WordPerfect 8.0 for Windows
               NUMBER OF SEQ ID NOS: 34
SOFTWARE: WordPerfect 8.0 for Windows
SEQ ID NO 22
ENGTH: 117
TYPE: PRT
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                                                                                                                                                                                      Query Match 98.9%;
Best Local Similarity 99.1%;
Matches 116; Conservative (
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Best Local Similarity 99.1%;
Matches 116; Conservative
PRIOR FILING DATE: 2000-05-24
                                                                                                                           ; ORGANISM: Mouse US-09-865-198-22
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LENGTH: 238
TYPE: PRT
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US-09-865-198-28
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Squence 19, Application US/09910059

Patent No. US20020142359A1

GENERAL INCORPARTION:

APPLICANT: Edge, Michael Derek

APPLICANT: Edge, Michael Derek

APPLICANT: Edge, Michael Derek

TILE OF INVENTION: Monoclonal Antibody to CEA, Conjugates Comprising Said Antibod

TILE OF INVENTION: Their Therapeutic use in an Adept System

FILE REFRERENCE: 1991-209

CURRENT APPLICATION NUMBER: US 09/171,945

PRIOR APPLICATION NUMBER: US 09/171,945

PRIOR APPLICATION NUMBER: PCT/GB97/01165

PRIOR PLILNG DATE: 1997-02-14

PRIOR FILING DATE: 1997-02-14

PRIOR FILING DATE: 1997-02-14

PRIOR FILING DATE: 1997-02-14

PRIOR FILING DATE: 1996-05-04

NUMBER OF SEQ ID NOS: 131

SOSTWARE: PatentIn version 3.1
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APPLICANT: Witte, Owen N.
APPLICANT: Witte, Owen N.
APPLICANT: Witte, Owen N.
APPLICANT: Saffran, Douglas C.
TITLE OF INVENTION: PSCA: PROSTATE STEM CELL ANTIGEN AND USES THEREOF
FILE REFERENCE: 30435.540S14
CURRENT APPLICATION NUMBER: U5/09/564,329A
CURRENT FILING DATE: 1990-03-03
PRIOR PILING DATE: 1990-03-10
PRIOR PILING DATE: 1997-03-10
PRIOR FILING DATE: 1997-03-10
PRIOR FILING DATE: 1997-03-10
PRIOR FILING DATE: 1997-03-10
PRIOR FILING DATE: 1998-01-12
PRIOR FILING DATE: 1998-01-12
PRIOR PLING DATE: 1998-01-12
                                                                                                                                                     61 APKFRGKATLTADSSSNTAYLHLSSLTSEDTAVYYCHVLIYAGYLAMDYWGQGTSVAVSS 120
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US-09-910-059-19
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ORGANISM: Artificial Sequence
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US-09-910-059-19
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APPLICANT Copley, Clive G
APPLICANT Copley, Clive G
APPLICANT Copley, Clive G
APPLICANT Edew, Michael Derek
APPLICANT Edew, Michael Derek
APPLICANT Edew, Michael Derek
APPLICANT Edew, Michael Derek
TITLE OF INVENTION: Wonoclonal Antibody to CEA, Conjugates Comprising Said Antibody,
TITLE OF INVENTION: Their Therapeutic use in an Adept System
FILE REFERENCE: 1991-209
CURRENT APPLICATION NUMBER: US/09/910,059
CURRENT APPLICATION NUMBER: US 09/171,945
PRIOR PIÈTNG DATE: 1998-10-29
PRIOR FIÈTNG DATE: 1998-10-29
PRIOR FIÈTNG DATE: 1997-02-14
PRIOR FIÈTNG DATE: 1997-02-14
PRIOR FIÈTNG DATE: 1996-05-04
PRIOR FIÈTNG DATE: 1996-05-04
SETOR FIÈTNG DATE: 1996-05-04
SOFTWARE PALENTION NUMBER: GB9609405.7
FRIOR FIÈTNG DATE: 1996-05-04
SOFTWARE PALENTION NUMBER: GB9609405.7
FRIOR FIÈTNG DATE: 1996-05-04
SOFTWARE PALENTIN VERSION 3.1
SEQ ID NO, 131
SEQ ID NO, 131
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3;
                                    APPLICANT: #Armour, Kathryn
TITLE OF INVENTION: High Affinity Humanized Anti-CEA Monoclonal
TITLE OF INVENTION: Antibodies
FILE REFERENCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 120
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                                                                                                                                                                     CURRENT APPLICATION NUMBER: US/09/974,051
CURRENT FILING DATE: 2001-10-09
PRIOR APPLICATION NUMBER: 09/025,403
PRIOR FILING DATE: 1998-02-18
PRIOR APPLICATION NUMBER: US 60/029,694
PRIOR FILING DATE: 1996-10-31
NUMBER OF SEO ID NOS: 50
SOFTWARE: MACROSOft Word 97 SR-2
SEO ID NO 124
LENGTH: 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 11, Application US/09910059 Patent No. 10520020142359A1
                          Carr, Frank J.
Harris, William J.
Tempest, Philip R.
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Best Local Similarity 76.4
Matches 97; Conservative
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; LOCATION: 1..124
US-09-974-051#1
                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: PRT ORGANISM: Mus musculus
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ORGANISM: Mus musculus
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US-09-910-059-11
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APPLICANT:
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Gaps

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Length 136;

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RESULT 15
US-09-854-811-11
| Sequence 11, Application US/09854811
| Patent No. US20020119157A1
| GENERAL INFORMATION:
| APPLICANT: Relier, Robert E. APPLICANT: Rather, Wown N. APPLICANT: Saffran, Douglas C. TITLE OF INVENTION: PROSTATE STEM CELL ANTIGEN AND USES THEREOF FILE REFERENCE: 30435.540514
| CURRENT APPLICATION NUMBER: US/09/854,811
| CURRENT FILING DATE: 2001-05-14
| PRIOR FILING DATE: 2000-05-03
| PRIOR FILING DATE: 1999-07-20
| RIGHT FILING DATE: 1999-07-20
| NUMBER: OF SEQ ID NOS: 27
| SOFTWARE: PatentIn Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                     14 EVQLQOSGAELVRSGASVKLSCTASGENIKDYXIHWVNQRPDQGLEWIGWIDPENGDTEF 73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 QVKLQQSGAELVGSGASVKLSCTTSGFNIKDFYMHWVKQRPEQGLEWIGWIDPENGDSGY 60
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SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 11
LENGTH: 136
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Matches 91; Conserv
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Best Local Similarity
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                                                                                                TYPE: PRT
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TITLE OF INVENTION: PSCA: PROSTATE STEM CELL ANTIGEN AND USES THEREOF
FILE REFERENCE: 30435.540S14
FILE REFERENCE: 3001-05-14
FILE REPERENCE: 3001-05-14
FRIOR APPLICATION NUMBER: 09/564,329
FRIOR APPLICATION NUMBER: 09/564,329
FRIOR APPLICATION NUMBER: 09/564,329
FRIOR APPLICATION NUMBER: 06/071,141
FRIOR APPLICATION NUMBER: 60/071,141
FRIOR APPLICATION NUMBER: 60/071,141
FRIOR APPLICATION NUMBER: 60/113,230
FRIOR PILING DATE: 1998-02-13
FRIOR PELING DATE: 1998-02-13
FRIOR APPLICATION NUMBER: 60/113,230
FRIOR FILING DATE: 1998-02-17
FRIOR APPLICATION NUMBER: 60/1124,588
FRIOR FILING DATE: 1998-02-17
FRIOR APPLICATION NUMBER: 09/203,939
FRIOR FILING DATE: 1998-03-16
FRIOR APPLICATION NUMBER: 09/203,939
FRIOR FILING DATE: 1998-02-17
FRIOR APPLICATION NUMBER: 09/203,939
FRIOR FILING DATE: 1998-02-17
FRIOR APPLICATION NUMBER: 09/203,939
FRIOR FILING DATE: 1998-02-17
FRIOR APPLICATION NUMBER: 09/203,51835
FRIOR APPLICATION NUMBER: 09/203,51835
FRIOR APPLICATION NUMBER: 09/203,51835
FRIOR APPLICATION NUMBER: 09/203,939
FRIOR FILING DATE: 1998-02-17
FRIOR APPLICATION NUMBER: 09/203,51835
FRIOR FILING DATE: 1999-02-17
FRIOR APPLICATION NUMBER: 09/203,503
FRIOR FILING DATE: 1999-02-17
FRIOR APPLICATION NUMBER: 09/203,503
FRIOR FILING DATE: 1999-02-17
FRIOR APPLICATION NUMBER: 09/203,503
FRIOR FILING DATE: 1999-02-27
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Pred. No. 9.3e-31;
9; Mismatches 12; Indels 5;
                     PRIOR APPLICATION NUMBER: 60/13,230
PRIOR FILING DATE: 1938-12-21
PRIOR FILING DATE: 1998-12-21
PRIOR FILING DATE: 1998-02-17
PRIOR PILING DATE: 1999-02-17
PRIOR APPLICATION NUMBER: 60/124,658
PRIOR APPLICATION NUMBER: 09/038,261
PRIOR FILING DATE: 1999-03-10
PRIOR FILING DATE: 1998-12-02
PRIOR FILING DATE: 1998-12-02
PRIOR PELLING DATE: 1999-02-17
PRIOR PLILING DATE: 1999-02-17
PRIOR PLILING DATE: 1999-02-17
PRIOR PLILING DATE: 1999-02-17
PRIOR PLILING DATE: 1999-02-17
PRIOR PLING DATE: 1999-02-17
SOFTWARE PLING DATE: 1999-02-15
NUMBER OF SEQ ID NOS: 27
SOFTWARE: PALENTIN VET: 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 11, Application US/09855153 Patent No. US20020102666A1
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Local Similarity 77.8%;
hes 91; Conservative
      PRIOR FILING DATE: 1998-02-13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; ORGANISM: SCID Mice US-09-564-329A-11
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Matches
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Length 136;

Indels

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(without alignments)
486.327 Million cell updates/sec
                                                                                                                             December 23, 2002, 07:17:57 ; Search time 23.1279 Seconds
                                                                                                                                                                                                                                        631
1 QVKLQQSGAELVGSGASVKL.....AXYGDYBGYWGQGTTVTVSS 117
GenCore version 5.1.3
Copyright (c) 1993 - 2002 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries
                                                                                 OM protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 200000000
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                                                                                                                                                                                                                                          Perfect score:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

pir_73:*
: pirl:*
: pir2:*
: pir3:*

Database :

SUMMARIES

		Description	Iq heavy chain pre	heavy chain	heavy			heavy	Ig gamma-1 chain -		Ig gamma chain (WM		nitrophenyl phosph	neavy cha		heavy	specific si	Ig heavy chain Vr	single chain Fv an	Ig heavy chain V r	Iq heavy chain pre	neavy chain	Ig heavy chain V r	Iq heavy chain V r	Ig gamma chain - m	Ig gamma-2a chain	Ig heavy chain V r	antibody Fab Jel 1			
		ΙD	804576	A56446	S15672	S25174	S52445	S17586	S49220	S03471	S29594	S24289	A47271	S06823	S03484	S03482	JC5322	PH1012	S41374	PL0246	PH1403	PH1013	G37267	PS0024	A54378	S21810	B22769	838950	S40295	A27646	S53751
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		Length	136	268	116	118	137	117	221	120	178	116	114	122	120	115	233	108	249	115	123	107	118	139	115	138	120	246	446	107	116
æ	Query	Match	80.7	78.8	78.4	77.2		75.9	75.8	75.3	74.4		73.6		71.9		71.6				68.0				64.9	4.	4	64.2	4	63.9	63.8
		Score	509	497.5	494.5	487	481.5	479	478	475	469.5	466	464.5	460.5	454	453	452	434	432	429.5	429	24	419.5	412.5	409.5	409	405.5	405	405	403.5	402.5
	Result	No.	1	7	3	4	S	9	7	80	თ	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	56	27	28	29

Ig heavy chain pre pelB leader/Ig hea	Ig heavy chain V r	Ig heavy chain pre Ig heavy chain V r	Ig heavy chain pre	Ig heavy chain v r	Ig heavy chain pre	Ig heavy chain pre	Ig gamma-2a chain	Ig heavy chain V r	Ig heavy chain pre	Ig heavy chain pre	Ig heavy chain V r	Ig heavy chain V r	* It abada micod of
HMS18 C4402	341394	PC1155	PL0208	030562	JL0077	110076	37483	55542	27472	124672	128195	37262	03000
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139 1 M 287 4 P	120 2	~ ~	136 2	119 2	136 2	~	~	7	7	7	7	2	
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139 1 N 287 4 I	63.5	63.2 133 2 1 62.8 120 2 1	62.8	62.6	62.4	62.4 141 2	62.4 469 2	62.3 116 2 8	62.3 131 2 1	62.2 119 2 1	62.2 120 2 (62.0 99 2 1	

ALIGNMENTS

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Cypeavy chain V region (3H-3H scFv) - mouse (strain BALB/C)
Cypecies: Mus musculus (house mouse)
Cybacies: Mus musculus (house mouse)
Cybace: 19-Jan-1996 #sequence_revision 19-Jan-1996 #text_change 16-Aug-1996
Cyacession: A5646
RyTang, P.M.; Foltz, L.A.; Mahoney, W.C.; Schueler, P.A.
A. High affinity digoxin-binding protein displayed on M13 is functionally id.
A. Reference number: A56446; MUD:95229583; PMID:7713873
A. Accession: A56446; MUD:95229583; PMID:7713873
A. Molecule type: mRNA
A. Residues: 1-268 <-TAN>
A. Residues: 1-268 <-TAN>
A. Residues: 1-268 <-TAN>
A. Residues: 1-268 <-TAN>
Cybross references: GB:U20617
C. Keywords: heterotetramer; immunoglobulin
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               20 EVQLQQSGAELVRPGASVKLSCTASGFNIKDDYMHWVKQRPEQGLEWIGWIDPENGDTQY 79
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                                                                                                                                                                                                                                                                                                                                                                                    Length 136;
                                                                                                                                                                                                                                                                                                                                                                                   Query Match 80.7%; Score 509; DB 2; Length 13
Best Local Similarity 82.9%; Pred. No. 1.4e-38;
Matches 97; Conservative 5; Mismatches 15; Indels
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83.1%;
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Best Local Similarity
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R;Mylvaganam, S.E.; Paterson, Y.; Kaiser, K.; Bowdish, K.; Getzoff, E.D.
J. Mol. Biol. 221, 455-462, 1991
A;Title: Biochemical implications from the variable gene sequences of an anti-cytochr
                                                                                                                                                                                                                                                                                                                                                                                 C,Accession: $52445
R;Berdoz, J.; Kraehenbuhl, J.P.
submitted to the EMBL Data Library, November 1994
A;Description: Specific amplification by the polymerase chain reaction of rearranged
                                                                                                                                                                                                                                                                                      Ig heavy chain V region precursor - mouse
C;Species: Mus musculus (house mouse)
C;Date: 08-May-1995 #sequence_revision 21-Jul-1995 #text_change 21-Jan-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ig heavy chain V region (E8) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 22-Nov-1993 *sequence_revision 26-May-1995 #text_change 21-Jan-2000
C;Accession: S17586
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Molecule type: DNA
A;Residues: 1-137 <BER>
A;Cross-references: EMBL:X82690; NID:g673439; PIDN:CAA58011.1; PID:g673440
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            20 EVQLQQSGAELVRPGALVKLSCKASGFNIKDYYMYWKQRPEQGLEWIGWIDPENGNTVY 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       QVKLQQSGAELVGSGASVKLSCTTSGFNIKDFYMHWVKQRPEQGLEWIGWIDPENGDSGY 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PID:951821
      1 EIQLQQSGAELVXXGASVKLSCTASGFNIKDDYLHWVKQRPEQGLEWIGWIDPENGDTEY
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C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;15-98/Domain: immunoglobulin homology <IMM>
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A;Accession: S17586
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; Pred. No. 4e-36;
11; Mismatches 12;
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C;Keywords: heterotetramer; immunoglobulin
F;34-115/Domain: immunoglobulin homology <IMM>
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Best Local Similarity 78.2%;
Matches 93; Conservative 1
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Best Local Similarity 78.88
Matches 93; Conservative
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A; Accession: S52445
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A; Residues: 1-117 <MYL>
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                                                                                                                                                                                                                              RESULT 5
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                                                                                                                                                                                                                                                                                                                                                                                                        Ig heavy chain V region - mouse (fragment)
C; Species: Mus musculus (house mouse)
C; Species: Mus musculus (state)
S; Species: Musculus (state)
S; Tempest, P.R.; Bremner, P.; Lambert, M.; Taylor, G.; Furze, J.M.; Carr, F.J.; Harris, B; Tempest, P.R.; Bremner, P.; Lambert, M.; Taylor, G.; Furze, J.M.; Carr, F.J.; Harris, A; Title: Reshaping a human monoclonal antibody to inhibit human respiratory syncytial via A; Reference number: S15672; MUID:91337412; PMID:1367535
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C'Species: Wiss musculus (house mouse)
C'Spaces 2017-1995 #sequence_revision 20-Feb-1995 #text_change 21-Jan-2000
C'Accession: S25174, S31313
R'Monestier, M.; Rasy, T.M.; Losman, M.J.; Novick, K.E.; Muller, S.
Submitted to the EMBL Data Library, July 1992
A; Description: Structure and binding properties of monoclonal antibodies to A; Reference number: S25174
A; Reference number: S25174
A; Status: preliminary
A; Residues F: 1-118 < MON>
   Gaps
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                                                                                              Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Cross-references: EMBL:X67622; NID:951854; PIDN:CAA47880.1; PID:9938259
Superfamily: immunoglobulin V region; immunoglobulin homology
Keywords; heterotetramer; immunoglobulin
                                                                                                                                                                                       61 APKEOGRATMTADSSSNTAYLOLSSLTSEDTAVYYCNAYY-GDYEGYWGQGTTVTVSS 117
                                                                                                                                                                                                                           A;Cross-references: EMBL:X58835; NID:q51978; PIDN:CAA41644.1; PID:g51979 C;Superfamily: immunoglobulin V region; immunoglobulin homology C;Keywords: heterotetramer; immunoglobulin F:15-98/Domain: immunoglobulin homology <IMM>
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      Indels
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   14;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          78.4%; Score 494.5; DB 2 79.3%; Pred. No. 2.3e-37;
   Mismatches
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Conservative
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Best Local Similarity
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A; Residues: 1-118 <MO2>
8
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Matches
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Gyamma chain V region (JS34/32) - mouse
C;Species: Mus musculus (house mouse)
C;Species: Mus musculus (house mouse)
C;Species: Nus musculus (house mouse)
C;Species: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 20-Jun-2000
C;Accession: S24289
R;Moncharmont, B.
Submitted to the EMBL Data Library, September 1991
A;Description: Cloning and sequencing of the cDNA coding for the variable regions of A;Reference number: S24287
A;Reference number: S24289
A;Rolecule type: mRNA
A;Residues: 1-116 <MON>
A;Cross-references: EMBL:X62705; NID:951690; PIDN:CAA44584.1; PID:g1333963
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Superfamily: immunoglobulin homology <IMM>
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Proc. Natl. Acad. Sci. U.S.A. 90, 1160-1165, 1993
A;Title: A genetic approach to the generation of antibodies with enhanced catalytic
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                     G;Species: Mus musculus (house mouse)
C;Species: Mus musculus (house mouse)
C;Species: Mus musculus (house mouse)
C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 05-Nov-1999
C;Accession: S29594
R;Seymour, R.
Submitted to the EMBL Data Library, February 1991
A;Reference number: S29593
A;Accession: S29594
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               61 APKFQGKATMTADSSSNTAYLQLSSLTSEDTAVYYC---NAYYGDYEGYWGQGTTVTVSS 117
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                                                                                                                                                                                                                                                                    A;Status: preliminary
A;Molecule type: mRNA
A;Molecule type: mRNA
A;Residues: 1-178 <SEY>
A;Cross-references: EMBL:X57857; NID:952590; PIDN:CAA40992.1; PID:952591
C;Keywords: immunoglobulin
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76.7%; Pred. No. 8.1e-35;
ive 12; Mismatches 15; Indels
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Pred. No. 6.1e-35;
8; Mismatches 13
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Best Local Similarity 76.7%
Matches 89; Conservative
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Best Local 9
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S24289
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A; Residues: 7-120 <ROCI>
A; Residues: 7-120 <ROCI>
A; Residues: 7-120 <ROCI>
A; Cross-references: EMBL:X01820; NID:951833; PIDN:CAA25962.1; PID:91333983
A; Note: this sequence was determined from the differentiated gene
A; Note: this sequence was determined from the differentiated gene
A; Note: this sequence was determined from the differentiated gene
A; Note: 1, Mazie, J.C.; Moinier, D.; Leclercq, L.; Somme, G.; Theze, J.; Fougere
A; Immunol. 129, 2554-2558, J.; Fougere
A; Title: The limited diversity of the mouse gamma-chains anti-GAT repertoire does not se
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                                                                                                                                                submitted to the EMBL Data Library, September 1994
A;Description: Cloning and expression of a recombinant mouse Fab-fragment recognizing
A;Reference number: S49220
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ig heavy chain V-D-J region (hybridoma G5 Bb 2.2) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Species: 07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change 20-Jun-2000
C;Accession: S03471; S07453
R;Rocca-Serra, J.; Matthes, H.W.; Kaartinen, M.; Milstein, C.; Theze, J.; Fougereau, EMBO J. 2, 867-872, 1983
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                                                 C:Date: 19-Mar-1997 #sequence_revision 01-Aug-1997 #text_change 21-Jan-2000 C;Accession: S49220 R;Kipp, B.; Becker, W.P.; Schlaak, M.M.
                                                                                                                                                                                                                                                                                                                        A)Cross-references: EMBL:237502; NID:9541778; PIDN:CAA85732.1; PID:9541779
A)Experimental source: strain Balb/c
C)Superfamily: immunoglobulin C region; immunoglobulin homology
C; Keywords: immunoglobulin C region; francology
F):1-120/Domain: V region #status predicted <VRG>F):1-120/Domain: C region #status predicted <CRG>F):139-203/Domain: immunoglobulin homology <IMM>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          61 APKFQGKATMTADSSSNTAYLQLSSLTSEDTAVYYC -- NAYYGDYEGYWGQGTTVTVSS 117
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A;Residues: 1-43 <ROC2>
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: htetroterramer; immunoglobulin
F;15-98/Domain: immunoglobulin homology <IMM>
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Best Local Similarity 79.0%; Pred. No. 1.3e-35;
Matches 94; Conservative 8; Mismatches 15;
g gamma-1 chain - mouse (fragment)
Species: Mus musculus (house mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local Similarity 79.0 nes 94; Conservative
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A; Residues: 1-221 <KIP>
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A.Moue: this sequence was determined from the differentiated gene
R;Rocca-Serra, J.; Maaie, J.C.; Moinier, D.; Leclercq, L.; Somme, G.; Theze, J.; Foug
J. Immunol. 129, 2554-2558, 1982
A;Title: The limited diversity of the mouse gamma-chains anti-GAT repertoire does not
A;Reference number: S07453; MUID:83058021; PMID:6815271
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A;Title: The limited diversity of the mouse gamma-chains anti-GAT repertoire does not A;Reference number: S07453; MUID:83058021; PMID:6815271
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ig heavy chain V-D-J region (hybridoma G8 Ad 3.8) - mouse (fragment)
C:Species: Mus musculus (house mouse)
A;Variety: strain BALB/C
C;Date: 26-Feb-1998 #sequence_revision 26-Feb-1998 #text_change 21-Jan-2000
C;Accession: S03482; S07453
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C;Species: Homo sapiens (man)
C;Date: 15-May-1997 #sequence_revision 15-May-1997 #text_change 18-Jul-1997
C;Accession: JC5322
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 QVKLQQSGAELVGSGASVKLSCTTSGFNIKDFYMHWVKQRPEQGLEWIGWIDPENGDSGY 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 QVKLQQSGAELVGSGASVKLSCTTSGFNIKDFYMHWVKQRPEQGLEWIGWIDPENGDSGY 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     61 APKFQGKATMTADSSSNTAYLQLSSLTSEDTAVYYCNA--YYGDYEGYWGQGTTVTVSS 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 EVQLQQSGAELVKPGASVKLSCTASGFNIKDTYMHWVKQRPEQGLEWIGRIDPAKGNTKY
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A; Molecule type: protein
A; Readles: 1-43 <ROC2>
C; Superfamily: immunoglobulin V region; immunoglobulin homology
F;15-98/Domain: immunoglobulin homology <IMM>
                                                                                                                                                                                                                                                                                                                                 C;Superfamily: immunoglobulin V region; immunoglobulin homology F;15-98/Domain: immunoglobulin homology <IMM>
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1.2e-33;
thes 20; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      R;Rocca-Serra, J.; Matthes, H.W.; Kaartinen, M.; Milstein, EMBO J. 2, 867-872, 1983
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               hypervariable regions.
A;Reference number: S03471; MUID:84057768; PMID:6416834
A;Accession: S03482
                                                                                                                                                                                                                                                                                                                                                                                                                      Score 454; DB 2; I
Pred. No. 9.9e-34;
8; Mismatches 19;
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Fred. No. 1.2e-3
7; Mismatches
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Best Local Similarity 76.5%;
Matches 88; Conservative
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1 Similarity 75.6%;
90; Conservative
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A, Residues: 10-115 <ROC1>
A, Cross-references: EMBL:X03219
                                                                                                                                                                                                                                                              A; Molecule type: protein A; Residues: 1-43 <ROC2>
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Best Local Similarity
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C; Species: Mus musculus (house mouse)
A; Variety: Strain BALBAC
C; Date: 26 Peb-1998 #sequence_revision 26-Feb-1998 #text_change 21-Jan-2000
C; Accession: 803484; 807453
F; Rocca-Segra, J; Matthes, H.W.; Kaartinen, M.; Milstein, C.; Theze, J.; Fougereau, M. Britle: Analysis of antibody diversity: V-D-J mRNA nucleotide sequence of four anti-GAT hypervariable regions.
A; Reference number: 803471; MUID:84057768; PMID:6416834
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                                                                                                        A; Molecule type: DNA; protein
A; Residues: 1.114 <LES>
A; Note: sequence extracted from NCBI backbone (NCBIN:124854, NCBIP:124855)
A; Note: parts of this sequence were determined by protein sequencing
F; 22-96/Disulfile bonds: *status predicted
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                                               A; Reference number: A47271; MUID:93165660; PMID:8094556
                                                                                                                                                                                                                                                                                                                                                             7; Mismatches 16;
                                                                                                                                                                                                                                                                                                    DB 4;
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                                                                                                                                                                                                                                                                                                 Score 464.5; DB 4
Pred. No. 1.1e-34;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 460.5; DB 2
Pred. No. 2.6e-34;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 8; Mismatches
                                                                                                                                                                                                                                                                                              ch: 73.6%;
1 Similarity 77.8%;
91; Conservative
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1 Similarity 77.9%;
95; Conservative
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A Residues 10-120 <ROC1>
A;Cross-references: EMBL:X07144
                                                                                                                                                                                                                                                                                                                                 Best Local Similarity
Matches 91% Conserv
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Preliminary
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A; Accession:
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S03484
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R;Jannot, C.B.; Hynes, N.E.
Biochem. Biophys. Res. Commun. 230, 242-246, 1997
A;Title: Characterization of scFv-421, a single-chain antibody targeted to p53.
A;Reference number: JC5322, MUID:97168950; PMID:9016757
A;Accession: JC5322
A;Accession: JC5323 A;Ans.
A;Residues: 1-233 <JAN>
A;Residues: 1-233 <JAN>
A;Experimental source: hydricloma cell
C;Comment: This protein specifically binds the tumor suppressor protein p53. It restores
                                                                                                                                                                                                                                                                                    1;
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                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 71.6%; Score 452; DB 2; Length 233; Best Local Similarity 79.6%; Pred. No. 3e-33; Matches 90; Conservative 5; Mismatches 14; Indels
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GenCore version 5.1.3

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OM protein - protein search, using sw model

Run on: December 23, 2002, 07:16:17; Search time 11.564 Seconds

(without alignments)

419.643 Million cell updates/sec

Title:

US-09-865-198-7

Sequence:

1 US-09-865-198-7

Sequence:

1 UXLQOSGAELVGSGASVKL......AYYGDYECYWGQCTTVTVSS 117

Scoring table: BLOSUM62

Gapop 10.0, Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SwissProt_40:*

Database :

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     3; Gaps
                                                       10 QVQLQQPGAELVKPGASVKLSCKASGYTFTSYWMHWVKQRPGRGLEWIGRIDPNSGGTKY 79
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                                      QVKL/QQSGAELVGSGASVKLSCTTSGFNIKDFYMHWVKQRPEQGLEWIGWIDPENGDSGY
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi;
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
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Mammalia® Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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62.5%; Pred. No. 3.9e-32;
tive 19; Mismatches 22; Indels
   Indels
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   25;
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MEDLINE-38131886, Pubmed-6186498;
Siekevitz M., Gefter M.L., Brodeur P., Riblet R.,
Marshak Rothstein A.;
                                                                                                                                                                                                                                                                              21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
19 heavy chain V region 36-65.
Mus muscúlus (Mouse).
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15-JUL-1999 (Rel. 38, Last annotation update)
19 heavy chain V region S43 precursor.
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   Conservative 13; Mismatches
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MEDLINE-81234548; PubMed-6788376;
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P01755;
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                                                       "Heavy chain variable region contribution to the NPb family of antibodies: somatic mutation evident in a gamma 2a variable region."; cell 24:625-637(1981).
-!- MISCELLANEOUS: THE GAMMA-2A CHAIN MRNA WAS CLONED FROM A HYBRIDOMA MAKING ANTIBODIES TO THE HAPTEN (4-HYDROXY-3-NITROPHENYL)ACETYL
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21-JUL-1986 (Rel. 01, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
15-JUL-1999 (Rel. 38) Tast annotation update)
1g heavy chain V region 93G7 precursor.
Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
Bothwell A.L.M., Paskind M., Reth M., Imanishi-Kari T., Rajewsky
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COMPLEMENTARITY-DETERMINING-1.
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COMPLEMENTARITY-DETERMINING-2.
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Pred. No. 1.3e-31;
12; Mismatches 30;
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D SEGMENT.
JH2 SEGMENT.
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MEDLINE-82152818; PubMed-6801765;
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63.6%;
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or send an email to license@isb-sib.ch).
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 SWISS-PROT entry is copyright. It is produced through a collaboration
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Biochemistry 21:5415-5424(1982).
-i- MISCELLANEOUS: THE SEQUENCE OF THE LIGHT CHAIN OF THIS IGM MYELOMA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              61 APKFQGKATMTADSSSNTAYLQLSSLTSEDTAVYYC--NAYYG---DYEGYWGQGTTVTV 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             6; Gaps
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HSSP; P01810; 2FBJ.
HSCPPO: IPR003006; Ig_MHC.
InterPro: IPR003596; Ig_V.
Pfam: PF00047; Ig; 1.
SMART; SM00406; IGv; 1.
Immunoglobulin V region; Antiarsonate antibody; Hybridoma; Signal.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus
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MEDLINE-83075344; PubMed-6816276;
ERITY M.R., Fuhrman J.S., Schilling J.W., Rogers J., Sibley C.H.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  BY SIMILARITY.
N-LINKED (GLCNAC. . .) (COMPLEX).
                                                                                                                                                                                                                                                                                                                                               Length 140;
                                                                                                                                                                                                                                                                              IG HEAVY CHAIN V REGION 93G7.
                                                                                                                                                                                                                                                                                                                                          60.2%; Score 380; DB 1; Length 14
60.7%; Pred. No. 3.7e-31;
live 21; Mismatches 21; Indels
                                                                                                                                                                                                                                                                                                             15514 MW; 25A4CBBE31DA5CE8 CRC64;
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-!- MISCELLANEOUS: THIS PROTEIN BINDS DEXTRAN.
PIR; A02039; MHMS4E.
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21.JUL-1986 (Rel. 01, Created)
21.JUL-1986 (Rel. 01, Last sequence update)
15.JUN-2002 (Rel. 41, Last annotation update)
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DISULFID 22 96 BY SIMILA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                HSSP, PO1789; INCP.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003006; Ig_V.
Pfam; PF00047; Ig; 1.
SMART; SM00406; IGV; 1.
                                                                                                                              EMBL; J00493; AAA38128.1; -
                                                                                                                                                                                                                                                                                                                                                                           74; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STANDARD;
                                                                                                                                                                                                                                                                                                             140 AA;
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Matches 74; Conserv
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P01756;
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NON_TER
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                             Gaps
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                                                       1 QVKLQQSGAELVGSGASVKLSCTTSGFNIKDFYMHWVKQRPEQGLEWIGWIDPENGDSGY 60
                                                                     Gilliam A.C., Shen A., Richards J.E., Blattner F.R., Mushinski J.F.,
                                                                                                                                                                                                                                                                                                                                                                                                       "Illegitimate recombination generates a class switch from C mu to C delta in an IgD-secreting plasmacytoma.";
Proc. Natl. Acad. Sci. U.S.A. 81:4164-4168(1984).
PIR; A02033; HVMST7.
INTERPO. 1PR003006; Ig_MHC.
InterPro; IPR003006; Ig_W.
Frank, PR0047; ig: 1.
SWART; SM04406; IGv; 1.
                                                                                                           61 APKFQGKATMTADSSSNTAYLQLSSLTSEDTAVYYCNAYYGDYEGYWGQGTTVTVSS 117
                                                                                                                          61 NQKFKGKATLIYUDKSSSTAYMQLNSLTSEDSAVYYCARDYDWYFDVWGAGTTVTVSS 117
                                                                                                                                                                                                                                                                                   Mus musculus (Mouse).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi;
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          IG HEAVY CHAIN V REGION TEPC 1017.
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59.7%; Score 377; DB 1; Length 117; 62.4%; Pred. No. 5.9e-31; live 14; Mismatches 30; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPLEMENTARITY - DETERMINING-1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FRAMEWORK-2.
COMPLEMENTARITY-DETERMINING-2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 138;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               26; Indels
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15576 MW; 748157E4C6907B8E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     59.1%; Score 373; DB 1; 61.7%; Pred. No. 1.8e-30;
                                                                                                                                                                                                                                              (Rel. 38, Last sequence update)
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01, Last sequence update)
38, Last annotation update)
                                                                                                                                                                                                                                                          15-JUL-1999 (Rel. 38, Last annotation update
Ig heavy chain V region TEPC 1017 precursor.
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(Rel. 02, Last seq
                             73; Conservative
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  Query Match
Best Local Similarity
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Best Local Similarity
Matches 74; Conserv
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P01757;
21-JUL-1986 (
21-JUL-1986 (
15-JUL-1999 (
                                                                                                                                                                                                                                                                                                                                                                                              Tucker P.W.;
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23-OCT-1986
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P03980;
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DISULFID
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HV13_MOUSE
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InterPro; IPR003006; Ig_MHC.
                      IPR003596; Ig_v.
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120
120 AA;
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Best Local Similarity
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les 71; Conserv
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| 119 SS 120
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                                                                                                                                               CHAIN
NON_TER
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                        InterPro;
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NON_TER
SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "Simultaneous expression of immunoglobulin mu and delta heavy chains by a cloned B-cell lymphoma: a single copy of the VH gene is shared by two adjacent CH genes.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      61 APKFQGKATMTADSSSNTAYLQLSSLTSEDTAVYYC--NAYYGDYEGYWGQGTTVTVSS 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCÉ FROM N.A.
MEDLINE$8222262; PubMed=6806821;
Knapp M*R. Liu C.-P., Newell N., Ward R.B., Tucker P.W., Strober S.
Blattnes F.R.;
                                                                                                                                                                                    Schilling #8. Clevinger B., Davie J.M., Hood L.;

*Amino ack'd sequence of homogeneous antibodies to dextran and DNA rearrangements in heavy chain V-region gene segments.";

Nature 283:35-40(1980).

**INSCELLANBOUGS: THE SEQUENCES OF 10 HYBRIDOMA PROTEINS THAT ALSO BIND DEXTRAN DIFFER FROM THAT SHOWN AT 1-7 POSITIONS, MANY OF WHICH OCCUR IN THE D AND J SEGMENTS.

-!- MISCELLANBOUGS: THIS PROTEIN BINDS DEXTRAN.

HISSP; PO1789; 1MCP.
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                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; ibutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 117;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ouery Match<sup>†</sup> 58.3%; Score 368; DB 1; Length 11:
Best Local Similarity 61.3%; Pred. No. 4.7e-30;
Matches 73; Conservative 16; Mismatches 26; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                117 AA; 13024 MW; 292E2AF4BE447E41 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           HV15_MOUSE STANDARD; PRT; 136 AA. 21-JUL-1986 (Rel. 01, Created) 21-JUL-1986 (Rel. 01, Last sequence update) 15-JUL-1999 (Rel. 38, Last annotation update) Ig heavy chain V region BCL1 precursor. Mus musculus (Mouse).
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                                                                                                                                                                   078170; PubMed=6765983;
  heavy chain V region J558
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| InterPro; | IPR003596; | Ig_V.
| Pfam; | PF00047; | Ig; | 1.
| SMART; SM00406; | IGv; | 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Immunoglobulin V region.
DISULFID 22 96
NON_TER 117 117
Ig heavy chain V reg
Mus musculus (Mouse)
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MEDLINE-800
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MEDLINE-84182519; PubMed-6201362;
Dildrop R., Bovens J., Slekevitz M., Beyreuther K., Rajewsky K.;
Dildrop R., Bovens J., Slekevitz M., Beyreuther K., Rajewsky K.;
A V region determinant (idiotope) expressed at high frequency in B lymphocytes is encoded by a large set of antibody structural genes.";
EMBO J. 3:517-523(1984).
PIR, A02037; MHMS15.
PISSP, P01810; 2FBJ.
InterPro; IPR003006; Ig_MHC..
InterPro; IPR003006; Ig_MC..
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                                                                                                                                                                                                                                                                                                          1 QVKLQQSGAELVGSGASVKLSCTTSGFNIKDFYMHWVKQRPEQGLEWIGWIDPENGDSGY 60
                                                                                                                                                                                                                                                                                                                                                                                                           61 APKFQGKATMTADSSSNTAYLQLSSLTSEDTAVYYCNAYYGDYEGYWGQGTTVTVSS 117
                                                                                                                                                                                                                                                                                                                                                                                                                                     80 NQKFKGKATMIYUDKSSSTVHMELARLISEDSANLYCARYYGNYFDYWGQGTTLIYVSS 136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ig heavy chain V region AC38 15.3.

Mus musculus (Muse).

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus.
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                                                                                                      IG HEAVY CHAIN V REGION BCL1
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13311 MW; 914453F426F09834 CRC64;
                                                                                                                                                       136 AA; 15078 MW; 6827CFBC6DB3F35E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   57.9%; Score 365.5; DB 1;
llarity 58.2%; Pred. No. 8.6e-30;
Conservative 15; Mismatches 29;
                                                                                                                                                                                                       58.3%; Score 368; DB 1;
59.0%; Pred. No. 5.6e-30;
iive 17; Mismatches 31.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-JAN-1988 (Rel. 06, Created)
01-JAN-1988 (Rel. 06, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
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SEGMENT.
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Pfam; PF00047; 1g; 1.
SMART; SM00406; IGv; 1.
Immunoglobulin V region; Signal.
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SMART; SMO0406; IGv; 1.
Immunoglobulin V region.
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Zakut R., Cohen J., Givol D.;
Zakut R., Cohen J., Givol D.;
Nucleic Acids Res. 8:4839-4840(1980).
-!- MISCELLANEOUS: THIS SEQUENCE WAS TRANSLATED FROM AN MRNA ISOLATED
FROM A WYELOWA THAT SECRETES IGG2B.
PIR; A02027; GYMS11.
HSSP; OP101910; 2FBJ.
InterPro; IPR003596; 1g_MHC.
                                                          MEDLINE-84182519; PubMed-6201362;
Dildrop R., Bovens J., Siekevitz M., Beyreuther K., Rajewsky K.;
"A V region determinant (idiotope) expressed at high frequency in B
lymphocytes is encoded by a large set of antibody structural genes.";
PIR; A02040; MHMS38.
                                                                                                                                                                                                                                                                                                                                                                                                                                 61 NQKFKGKATLTVDKSSSATYMELRSLTSEDSAVYYCARGYG-YDPFDVWGTGTTVTVSS 118
                                                                                                                                                                                                                                                                                                                                                                                                                   1 QVKLQQSGAELVGSGASVKLSCTTSGFNIKDFYMHWVKQRPEQGLEWIGWIDPENGDSGY 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              61 APKFQGKATMTADSSSNTAYLQLSSLTSEDTAVYYCNAYYGDYEGY--WGQGTTVTVSS 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
   Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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MEDLINE-81053741; PubMed-6253904;
Zakut R., Cohen J., Givol D.;
"Cloning and sequence of the CDNA corresponding to the variable region of immunoglobulin heavy chain MPC11.";
Nucleic Acids Res. 8:3591-3601(1980).
                                                                                                                                                                                                                                                                                                                                                     57.4%; Score 362.5; DB 1; Length 118; 59.7%; Pred. No. 1.7e-29;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 121;
                                                                                                                                                                InterPro; IPR003006; Ig_MHC.
InterPro; IPR003006; Ig_V.
InterPro; IPR003006; Ig_V.
SMART; SM00407; Ig; 1.
SMART; SM00406; IGv; 1.
Immunoglobulin V region.
DOMAIN 1 99 104 D SEGMENT.
DOMAIN 105 118 J SEGMENT.
DISULFID 22 96 BY SIMILARITY.
NON_TER 118 118 SEQUENCE 118 AA; 12934 MW; 9479EE4C762A018 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                   28; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 121 AA; 13135 MW; 227AEF3EC56ED0BF CRC64;
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Pred. No. 6.1e-28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
peavy chain V region MPC 11.
Mus musculus (Mouse).
                                                                                                                                                                                                                                                                                                                                                                                     17; Mismatches
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56.2%;
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SMART; SM00406; 1Gv; 1.
Immunoglobulin v region.
NON_TER
SEQUENCE 121 AA; 13135
                                                                                                                                                                                                                                                                                                                                                                                     71; Conservative
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Best Local Similarity
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                                                                                                                                                      HSSP; P01789; 1MCP
                   NCBI_TaxID=10090;
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P01745;
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      Mammalia;
                                               SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              61 APKFQGKATMTADSSSNTAYLQLSSLTSEDTAVYYC---NAYYGDYEGY------WGQ 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              20 QTQLVQSGAEVRKPGASVRVSCKASGYTFIDSYIHWIRQAPGHGLEWVGWINPNSGCTNY 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       11; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 QVKLQQSGAELVGSGASVKLSCTTSGFNIKDFYMHWVKQRPEQGLEWIGWIDPENGDSGY 60
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90330,
01-JAN-1988 (Rel. 06, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
15-JUL-1999 (Rel. 38, Last annotation update)
Mus musculus (Mouse).

Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                       Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                SEQUENCE FROM N.A.
MEDILINE-83065524; PubMed-6815656;
KEDILINE-83065244; PubMed-6815656;
MEDILINE-83065244; PubMed-6815656;
Bell L.O., Gould H.J.;
"Cloning and sequence determination of the gene for the human immunoglobulin epsilon chain expressed in a myeloma cell line.";
Proc. Natl. Acad. Sci. U.S.A. 79:6661-6665(1982).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 57.6%; Score 363.5; DB 1; Length 147; Best Local Similarity 51.6%; Pred. No. 1.7e-29; Matches 66; Conservative 24; Mismatches 27; Indels 11.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     IG HEAVY CHAIN V-I REGION ND PYRROLIDONE CARBOXYLIC ACID.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            16491 MW; 948F9F72A5366C20 CRC64;
                                                          21-JUL-1986 (Rel. 01, Created)
16-CCT-2001 (Rel. 40, Last sequence update)
16-CCT-2001 (Rel. 40, Last annotation update)
16-CCT-2001 (Rel. 40, Last annotation update) .
19 heavy chain V-I region ND precursor (Fragments).
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IH -> HI (IN REF. 2).
VG -> GV (IN REF. 2).
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                                 147 AA
                                 PRT;
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HSSP; P01789; 1MCP.
InterPro; IPR0033006; Ig_MHC.
PrtarPro; IPR003596; Ig_V.
Pfam; PF00047; 19; 1.
SMART; SM00406; IGV; 1.
Immunoglobulin V region; Signal.
                              STANDARD;
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                              HV1C_HUMAN
P01744;
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RESULT 10
HV1C_HUMAN
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Baltimore D.;
Heavy chain variable region contribution to the NPb family of
antibodies: somatic mutation evident in a gamma 2a variable region.";
Cell 24:625-637(1981).

-I- MISCELLANEOUS: THIS GERMLINE GENE BELONGS TO A SET OF CLOSELY
RELATED GENES THAT COULD ENCODE V REGIONS OF NPB ANTIBODIES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 QVKLQQSGAELVGSGASVKLSCTTSGFNIKDFYMHWVKQRPEQGLEWIGWIDPENGDSGY 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           20 QVQLQQPGAELVKPGASVKLSCKASGYTFTSYWMHWVKQRPGRGLEWIGRIDPNSGGTKY 79
                                                                                                                                                                          Bothwell A.L.M., Paskind M., Reth M., Imanishi-Kari T., Rajewsky K.,
                                                                    Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                54.2%; Score 342; DB 1; Length 117; llarity 66.7%; Pred. No. 1.8e-27; Conservative 13; Mismatches 19; Indels
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FRAMEWORK-3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      12890 MW; 16191A088CB17F5A CRC64;
21.JUL-1986 (Rel. 01, Created)
01.JUL-1989 (Rel. 11, Last sequence update)
12.JUL-1999 (Rel. 38, Last annotation update)
19 heavy chain V region 186-1 precursor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          BY SIMILARITY.
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FRAMEWORK-1
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HSSP; P01810; 2FBJ.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_V.
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SMART; SM00406; IGv; 1.
Immunoglobulin V region;
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                                                          Mus musculus (Mouse).
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                                                                                                  NCBI_TaxID=10090
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P01748:
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                                                                                                   61 NDNEKGRATLTADTSSSTAYIQLSSLTSEDSAIYHCARGIYYNSSPYFDSWGQGTTLTVS 120
                                                                                    APKF@GKATMTADSSSNTAYLQLSSLTSEDTAVYYC--NAYYGD--YEGYWGQGTTVTVS 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "Heavy chain variable region contribution to the NPD family of antibodies: somatic mutation evident in a gamma 2a variable region."; Cell 24 1625-637(1981).
 4; Gaps
                                         1 QVKL<u>Ö</u>QSGAELVGSGASVKLSCTTSGFNIKDFYMHWVKQRPEQGLEWIGWIDPENGDSGY 60
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Mammalia∰ Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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MEDLINE—C$7BL/6;
MEDLINE—81234548; PubMed—6788376;
Bothwell A.L.M., Paskind M., Reth M., Imanishi-Kari T., Rajewsky
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -!- MISGELLANEOUS: THIS GERMLINE GENE BELONGS TO A SET OF CLOSELY RELATED GENES THAT COULD ENCODE V REGIONS OF NPB ANTIBODIES.
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COMPLEMENTARITY-DETERMINING-1.
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29; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               54.5%; Score 344; DB 1; Length 11
67.4%; Pred. No. 1.2e-27;
ive 12; Mismatches 19; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  IG HEAVY CHAIN V REGION 102.
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                                                                                                                                                                                                                                                                             21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
12-JUL-1999 (Rel. 38, Last annotation update)
19 heavy#chain V region 102 precursor.
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20; Mismatches
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InterPro. IPR003006; Ig_MHC.
InterPro. IPR003596; Ig_V.
Pfam; Pp00047; ig; I.
SMART; $M00406; IGV.
Immunoglobulin V region; Signal.
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Conservative
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117 1
117 AA;
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P01753; P11271;
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SIGNAL
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"Heavy chain variable region contribution to the NPb family of antibodies: somatic mutation evident in a gamma 2a variable region."; Cell 24:625-637(1981).
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Bothwell A.L.M., Paskind M., Reth M., Imanishi-Kari T., Rajewsky K.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
19 heavy chain V region 23 precursor.
Mus musculus (Mouse).
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Search completed: December 23, 2002, 07:26:11 Job time : 12.564 secs THIS PAGE BLANK (USPTO)

Sequence:

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Copyright (c) 1993 - 2002 Compugen Ltd.
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RX MEDLINE-20448942; PubMed-10992488;
RA MEDLINE-20448942; PubMed-10992488;
RA MAIKIAL S., Liao L., Cunningham M.W., Diamond B.;
RT "T-Cell-dependent antibody response to the dominant epitope of RT "T-Cell-dependent antibody response to the dominant epitope of RT streptocococcal polysaccharide, N-acetyl-glucosamine, is cross-reactive RT with cardiac myosin.";
Infect. Emmun. 68:5803-5808(2000).
DR L. Infect. Emmun. 68:5803-5808(2000).
DR HSSP; Pougla0. ZPBJ.
DR HSSP; Pougla0. ZPBJ.
DR HSPS; Pougla0. IPR003596; Ig_W.
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"Direct Estimation of Relative Affinity by Flow Cytometry Reveals
"Birect Estimation of B Cell Antigen Receptors in Response to (4-
Hydroxy-3-Nitrophenyl)Acetyl (NP).";
Submitted (AuG-2001) to the EMBL/GenBank/DDBJ databases.
EMBL, AB069916; BAB63932.1;
InterPro; IPR003006; Ig_MHC.
                                                                                                                                                                                                                                                                                          (Fragment).
Mus muscollus (Mouse).
Eukaryotdi Metazoa, Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_rax‡b=10090;
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Wakaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutharia, Rodentia, Sciurognathi, Muridae, Murinae; Mus
NCBI_TaxID=10090;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         69 TMMADSSSNTAYLQLSSLTSEDTAVYYCNAYYGDYEGYWGQGTTVTVSS 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                67.7%; Score 427; DB 11; Length 1 ilarity 77.1%; Pred. No. 2e-35; Conservative 5; Mismatches 20; Indels
                                                                                                                                                                                                   01-0cr-2000 (TrEMBLrel. 15, Created)
01-0cr-2000 (TrEMBLrel. 15, Last sequence update)
01-0cr-201 (TrEMBLrel. 19, Last sennotation update)
Anti-myosin immunoglobulin heavy chain variable region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               109 109
109 AA; 11944 MW; DFE615FE6CED4EDE CRC64;
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01-DEC 2001 (TrEMBLrel. 19, Created)
01-DEC 2001 (TrEMBLrel. 19, Last sequence update)
01-DEC 2002 (TrEMBLrel. 20, Last annotation update)
V303-D2-J-C mu protein (Fragment).
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                                                                                                                                                              PRT;
                                                                                                                                                            PRELIMINARY;
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STRAINÆC57BL/6;
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                                                                                                                                                                                   Q9JL85;
                                                                                                                                                            Q9JL85
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Q924P9
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61 APKFQGKATMTADSSSNTAYLQLSSLTSEDTAVYYC-NAYYGD---YEGYWGQGTTVTVS 116
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                                                                                                                                                                   1 QVKLQQSGAELVGSGASVKLSCTTSGFNIKDFYMHWVKQRPEQGLEWIGWIDPENGDSGY 60
                                                                                                                                                                                            1 QVKLQQSGAELVGSGASVKLSCTTSGFNIKDFYMHWVKQRPEQGLEWIGWIDPENGDSGY 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Kozono Y., Kozono H., Azuma T.;
Direct Estimation of Relative Affinity by Flow Cytometry Reveals
Affinity Maturation of B Cell Antigen Receptors in Response to (4-
Hydroxy-3-Nitrophenyl)Acetyl (NP).",
Bydroxy-3-Nitrophenyl)Acetyl (NP).",
EMBL; AB067781; Bab83266.1; -
InterPro; IPR003006; Ig_MHC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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                                                                     DB 11; Length 143;
                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
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                   15704 MW; 43CD8C72D52134F6 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
VH186.2-D-J-C mu protein (Fragment).
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01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
VH186.2-D-0-C mu protein (Fragment).
                                                                ; Score 410.5; DB 11;
; Pred. No. 1.3e-33;
14; Mismatches 24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  64.3%; Score 406; DB 11;
65.3%; Pred. No. 3.6e-33;
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                                                                  65.1%;
66.9%;
                                                                                              Best_Local Similarity 66.9%
Matches 79; Conservative
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143
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143 1
143 AA;
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PRT;
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InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_V.
Pfam; PF00047; Ig; 1.
SMART; SMO0406; IGV; 1.
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                                                                         PRELIMINARY;
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SEQUENCE FROM N.A.
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NON_TER
SEQUENCE
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                                                                      Q9Z1C4
Q9Z1C4;
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Q99L25
   RESULT 7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      61 APKFQGKATMTADSSSNTAYLQLSSLTSEDTAVYYC--NAY-YGDYE-GYWGQGTTVTVS 116
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               4; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 QVKLQQSGAELVGSGASVKLSCTTSGFNIKDFYMHWVKQRPEQGLEWIGWIDPENGDSGY 60
                                                                                                                                     Kozono Y., Kozono H., Azuma T.;
Direct Estimation of Relative Affinity by Flow Cytometry Reveals
Affinity Maturation of B Cell Antigen Receptors in Response to (4-
Hydroxy-3 Nitrophenyl)Acetyl (NR).";
Submitted (AUG-2001) to the EMBL/GenBank/DDBJ databases.
InterPro; IPR003006; Ig_MHC.
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*Direct Estimation of Relative Affinity by Flow Cytometry Reveals
Affinity Maturation of B Cell Antigen Receptors in Response to (4-
Hydroxy-3-Nitrophenyl)Acetyl (NP).";

Bydnitted (ANG-2001) to the EMBL/GenBank/DDBJ databases.

EMBL; AB067797; BAB46232.1;

InterPro; IPR003006; Ig_MHC.

NON_TER 146 146
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Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 11; Length 145;
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63.7%; Score 402; DB 11; Length 146;
Best Local Similarity 66.1%; Pred. No. 9.2e-33;
Matches 80; Conservative 14; Mismatches 23; Indels
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145 Aa; 16141 MW; 55A59A7908B2CD6A CRC64;
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01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DRC-2002 (TrEMBLrel. 20, Last annotation update)
VH186.2-D-3-C mu protein (Fragment).
Mus musculus (Mouse).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      / Match 63.8%; Score 402.5; DB 11;
Local Similarity 65.8%; Pred. No. 8.1e-33;
Les 79; Conservative 13; Mismatches 25;
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NCBI_TaxID=10090;
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                                                                                                       STRAIN-C57BL/6;
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STRAIN-BALB/C;
Mueller J.P., Giannoni M.A., Hartman S.L., Elliott E.A., Squinto S.P.,
Mueller J.P., Giannoni M.A., Hartman S.L., Elliott E.A., Squinto S.P.,
Matis L.M., Evans M.J.;
"Humanized porcine VCAM-specific monoclonal antibodies with chimeric
IgG2/G4 constant regions block human leukocyte binding to porcine
endothelial cells."
Submitted (NOV-1996) to the EMBL/GenBank/DDBJ databases.
EMBL, U78801; AADD0233.1;
HSSP; P01810;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 QVKLQQSGAELVGSGASVKLSCTTSGFNIKDFYMHWVKQRPEQGLEWIGWIDPENGDSGY 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                61 TQKFRGKATLTADKSSTAYMQLSSLASEDSAVYYCARRTVGGYFDYWGQGTTLTVSS 118
01-MAY-1999 (TrEMBLrel. 10, Created)
01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
Anti-porcine VCAM mAb 3F4 heavy chain variable region (Fragment).
Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Strausberg R.,
Strausberg R.,
Strausberg R.,
Submitted (FEB-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; BC003888 R. AAH03888.1; -.
HSSP; P01842; FRAB.
InterPro; IPR003599; Ig.
InterPro; IPR003599; Ig.
InterPro; IPR003500; Ig_like.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003006; Ig_W.
InterPro; IPR003096; Ig_w.
Rohary; SM00409; IG. 2.
SWART; SM00400; IG. 3.
SWART; SM00400; IG.1; 3.
PROSITE; PS00290; IG_MHC; UNKNOWN_1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Match 63.5%; Score 400.5; DB 11; Length Local Similarity 66.1%; Pred. No. 1e-32; les 78; Conservative 13; Mismatches 26; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             118 118 118 118 118 AA; 90EEC559D31EC4FC CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Similar to RIKEN cDNA 1810060009 gene.
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Indels

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QVKLQQSGAELVGSGASVKLSCTTSGFNIKDFYMHWVKQRPEQGLEWIGWIDPENGDSGY 60
                                                                                                                                                                                                          20 QVQLKQSGAELVKPGASVKISCKASGYTFTDYYINWVKQRPGQGLEWIGKIGPGSGSTYY 79
                                                                                                                                                                                61 APKFOGKATMTADSSSNTAYLQLSSLTSEDTAVYYC--NAYYGDYEGYWGQGTTVTVSS 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Kozono Y., Kozono H., Azuma T.;
Kozono Y., Kozono H., Azuma T.;
Kozono Y., Kozono H., Azuma T.;

"Direct Estimation of Relative Affinity by Flow Cytometry Reveals
Affinity Maturation of B Cell Antigen Receptors in Response to (4-
Hydroxy-3 Nitrophenyl) Acetyl (NP).";
Submitted (AUG-2001) to the EMBL/GenBank/DDBJ databases.

InterPro: IPR003598; 19_c2.

InterPro: IPR00306; 19_MHC.

SMART; SM00408; 1Gc.2.

Interpro: IPR0047; 11.

SMART; SM00408; 1Gc.2.

Immunoglobulin domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mus musculus (Mouse).

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                          Last sequence update)
Last annotation update)
Pred. No. 7.9e-32;
3: Mismatches 22;
                                                                                                                                                                                                                                                                                                                                                                                                             01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last seq
01-MAR-2002 (TrEMBLrel. 20, Last ann
VH186.2-D-J-C mu protein (Fragment).
                                                                                                                                                                                                                                                                                                                                                                PRT;
                          18;
     64.78;
     Best Local Similarity 64.7%
Matches 77; Conservative
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Matches 77; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                    80 NEKEKGKATLTADKSSSTAYMQLNSLTSEDSAVCFCSRGGSIYYGYGLYYFDYWGQGTTI 139
                                                                                                                                                                                                                                                            GKATMTADSSSNTAYLQLSSLTSEDTAVYYC --- NAYYG --- DYEGYWGQGTTV 113
                                                                                                         Gaps
                                                                                                                                                      Eukaryotā; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammaliaf Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_Taxip=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Hayashigaki Y.;
"Functional annotation of a full-length mouse cDNA collection.";
                                                         Length 473;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 473;
                                                                                                         Indels
     52449 MW; BE9889B7986DA155 CRC64;
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MW; 9DED57A514475FBB CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Last sequence update)
Last annotation update)
                                                    63.3%; Score 399.5; DB 11;
63.7%; Pred. No. 7e-32;
iive 16; Mismatches 22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 11;
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SMART: SM00409; 1G; 2.
SMART: SM00407; IGc1; 3.
SMART: SM004007; IGc1; 3.
SMART: SM004000; IG 11ke; 1.
PROSITE: PS00290; IG_MHC; UNKNOW SEQUENCE 473 AA; 51699 MW; 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MGD; MGI:96443; Igh-1.
InterPic: IPR003599; Ig.
InterPic: IPR003599; Ig.cl.
InterPic: IPR003600; Ig_like.
InterPic: IPR003006; Ig_NHC.
InterPic: IPR003596; Ig_NHC.
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EMBL: AK007918; BAB25349.1; -.
HSSP; P01842; 7FAB.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-JUN-2001 (TrEMBLrel, 17, 01-JUN-2001 (TrEMBLrel, 17, 01-DEC-2001 (TrEMBLrel, 19, 18100600981k protein.
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                                                                                                      Conservative
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     473 AA;
                                                                            Local Sûmilarity
es 79% Conserv
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     SEQUENCE
                                                       Query Match
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                                                                                                      Matches
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RESULT 9 Q9D8L4

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                                                                                                                                                                                              1 QVKLQQSGAELVGSGASVKLSCTTSGFNIKDFYMHWVKQRPEQGLEWIGWIDPENGDSGY 60
                                                                                                                                                                                                                                                                                                   Kozono Y., Kozono H., Azuma T.;
"Direct Estimation of Relative Affinity by Flow Cytometry Reveals
Affinity Maturation of B Cell Antigen Receptors in Response to (4-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                             ;
                                                                                            DB 11; Length 143;
                                                                                                                                                Indels
01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
                                                                                       63.0%; Score 397.5; DB 11;
65.3%; Pred. No. 2.5e-32;
tive 14; Mismatches 26;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          143 AA.
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Mus musculus (Mouse).
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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Best Local Similarity 65.0%
Matches 76; Conservative
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                                                                                                                                       Pfam; PF00047; ig; 1.
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          NCBI_TaxID=10090;
                                                STRAIN-C57BL/6;
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SEQUENCE
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Q924R4;
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0924R1
ID 0924R
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                                                                                                                                                        1 QVKLQQSGAELVGSGASVKLSCTTSGFNIKDFYMHWVKQRPEQGLEWIGWIDPENGDSGY 60
                                                                                                                                                                                                        61 APKFQGKATMTADSSSNTAYLQLSSLTSEDTAVYYCNAYYGDYEGY--WGQGTTVTVSS 117
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Kozono Y., Kozono H., Azuma T.;
"Direct Estimation of Relative Affinity by Flow Cytometry Reveals
"Direct Estimation of B Cell Antigen Receptors in Response to (4-
Hydroxy-3-Nitrophenyl)Acetyl (NP).";
Submitted (AUG-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AB067788; BAB63273.1;
InterPro; IPR003006; Ig_MHC.
Pfam; PF00047; ig; 1.
NON_TER 140 140
                                                                                                                                                                                                                                                                                                                                                  VH186.2-D-J-C mu protein (Fragment).
Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                V23-D-J-C mu protein (Fragment).
V23-D-J-C MU.
Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                          DB 11; Length 143;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                62.9%; Score 397; DB 11; Length 140; 66.1%; Pred. No. 2.8e-32; Live 13; Mismatches 23; Indels
                                                                                                      63.0%; Score 397.5; DB 11; Length
65.5%; Pred. No. 2.5e-32;
tive 14; Mismatches 24; Indels
          Submitted (AUG-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AB067795; BAB63280.1; -.
InterPro; IFR003006; Ig_MHC.
Pfam; PF00047; ig; l.
                                                                    143 143
143 AA; 15908 MW; 55A2372870F0D568 CRC64;
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01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-WAR-2002 (TrEMBLrel. 20, Last annotation update)
                                                                                                                                                                                                                                                                                                                              Last sequence update)
Last annotation update)
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Hydroxy-3-Nitrophenyl)Acetyl (NP).";
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                                                                                                       Query Match 63.0%
Best Local Similarity 65.5%
Matches 78; Conservative
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Matches 78; Conservative
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                                                       NON_TER
NON_TER
SEQUENCE
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61 APKFQGKATMTADSSSNTAYLQLSSLTSEDTAVYYCNAYYGDYE---GYWGQGTTVTVSS 117
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRAIN=C57BL/6;
Kozono Y., Kozono H., Azuma T.;
"Direct Estimation of Relative Affinity by Flow Cytometry Reveals Affinity Maturation of B Cell Antigen Receptors in Response to (4-
Kozono Y., Kozono H., Azuma T.;
"Direct Estimation of Relative Affinity by Flow Cytometry Reveals Affinity Maturation of B Call Antigen Receptors in Response to (4-Hydroxy-3-Nitrophenyl)Acetyl (NP).";
Submitted (AUG-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AB069913; BAB63929.1;
InterProcessor
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 QVKLQQSGAELVGSGASVKLSCTTSGFNIKDFYMHWVKQRPEQGLEWIGWIDPENGDSGY
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                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
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Submitted (AUG-2001) to the EMBL/GenBank/DDBJ databases
EMBL; AB067785; BAB63270.1;
Interpro: IPR003006; Ig_MHC.
Pfam; PF00047; Ig; Il
                                                                                                                                                                                                                                                                                142 142
142 AA; 15622 MW; 24A265CE4EA4318B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                145 AA; 16081 MW; ECDBIA135E05B8AA CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
VH186.2-D-J-C mu protein (Fragment).
                                                                                                                                                                                                                                                                                                                                                                     62.8%; Score 396; DB 11;
65.0%; Pred. No. 3.5e-32;
11ve 13; Mismatches 28;
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                                                                                                                                                                                      Kozono Y., Kozono H., Azuma T.;
Direct Estimation of Relative Affinity by Flow Cytometry Reveals Affinity Maturation of Relative Affinity By Flow Cytometry Reveals Affinity Maturation of Relative Cell Antigen Receptors in Response to (4-Hydroxy-3-Mitropheny) Acetyl (MP).";
Submitted (AUG-2001) to the EMBL/GenBank/DDBJ databases.
Babbig, ABG57789; Babb63274.1;
InterProj. IPR003006; Ig_MHC.
                                                               Mus muscumus (Mouse).

Bukaryotaf Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sclurognathi; Muridae; Murinae; Mus.

NCBI_Taxīp=10090;
                                                                                                                                                                                                                                                                                                                                                                             62.4%; Score 393.5; DB 11; Length 145; 64.2%; Pred. No. 6.5e-32; ive 13; Mismatches 27; Indels 3;
                                                                                                                                                                                                                                                                                                                              145 145
145 AA; 15979 MW; 0162D0A26C746C04 CRC64;
             01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
VH186.2-DEU-C mu protein (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
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Best Local Similarity
Matches 7%; Conserv
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Search completed: December 23, 2002, 07:29:55 Job time : 49:5233 secs

Sequence Seq

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   FEATURE:
   QQ
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163.250 Million cell updates/sec
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                                                                                                                                                                                                                       December 23, 2002, 07:20:23; Search time 19.4651 Seconds
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1 DIELTQSPAIMSASPGEKVT.....QRSSYPFTFGSGTKLEIKRA 108
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2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep:*
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5: /cgn2_6/ptodata/1/iaa/F0TUS_COMB.pep:*
5: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
6: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
                                 . GenCore version 5.1.3
Copyright (c) 1993 - 2002 Compugen Ltd.
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US-08-661-052-16

US-09-188-082-16

US-09-364-088-16

US-09-423-439-44

US-09-423-439-44

US-09-423-439-44

US-09-423-439-41

US-09-423-439-41

US-09-423-439-61

US-09-423-439-61

US-09-423-439-61

US-08-437-728-1

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Maximum Match 100%
Listing first 45 summaries
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 2000000000
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APPLICANT: Enery, Stephen
APPLICANT: Copley, Citve Graham
APPLICANT: Enery, Capley Citve Graham
APPLICANT: Enery, Citve Graham
APPLICANT: Enery, Citve Graham
APPLICANT: Enery, Monoclonal Antibody to CEA, Conjugates Comprising Said
TITLE OF INVENTION: Antibody, and Their Therapeutic Use in an Adept System
TILE OF INVENTION: Antibody, and Their Therapeutic Use in an Adept System
TILE OF INVENTION: MONBER: US/09/11,945
CURRENT APPLICATION NUMBER: US/09/11,945
CURRENT FILING DATE: 1997-02-14
PRIOR FILING DATE: 1997-02-14
PRIOR FILING DATE: 1996-05-04
PRIOR FILING DATE: 1996-05-04
PRIOR FILING DATE: 1997-02-14
PRIOR FILING DATE: 1997-04-29
NUMBER OF SEQ ID NOS: 131
SOFTWARE: Patentin Ver: 2.1
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US-08-082-842A-83

US-08-839-765-163

US-08-839-765-163

US-08-484-537-16

US-08-484-537-16

US-08-610-838-163

US-08-902-486-11

US-08-902-486-11

US-08-933-385B-111

US-08-469-486-57

US-08-469-486-57

US-08-469-658-57

US-08-469-658-57

US-08-619-619-2

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Pred. No. 1.4e-41;
4; Mismatches 1;
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GENERAL INFORMATION: APPLICANT: Emery, Stephen APPLICANT: Copley, Clive Graham; APPLICANT: Edge, Michael Derek
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 9, Application US/09171945
Patent No. 6277599
GENERAL INFORMATION:
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Best Local Similarity 95.4%;
Matches 103; Conservative
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US-09-171-945-17
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83,

Sequence Sequence

US-08-487-200-16 US-08-488-113B-163 US-08-477-448-1163 US-08-107-669D-49 US-08-472-788A-83 US-08-477-531B-49

Sequence

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24 IVLTQSPAIMSASPGEKVTITCSASSSVSYMHWFQQKPGTSPKLMIYSTSNLASGVPARF 83
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                                                                                                                                                                                        BY SIMILARITY WITH KNOWN SEQUENCE TO TO AN ESTABLISHED CONSENSUS
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WITH KNOWN SEQUENCE OR TO AN ESTABLISHED
CONSENSUS
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WITH KNOWN SEQUENCE OR TO AN ESTABLISHED
CONSENSUS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               /product= "HYPERVARIABLE REGION 1"
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SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: KOIKE, MASAMICHI
APPLICANT: SHITARA, KENYA
APPLICANT: HANAI, NOBUO
APPLICANT: HANAI, NOBUO
APPLICANT: HASBGAMA, MAMORU
APPLICANT: HASBGAMA, MAMORU
NUMBER OF SEQUENCES: 49
CORRESPONDENCE ADDRESS:
ADDRESSEE: NIXON & VANDERHYE P.C.
STREET: 1100 NORTH GLEBE ROAD
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10-MAY-95
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Patent No. 5874255
GENERAL INFORMATION:
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COMPUTER: IBM PC compatible
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME/KEY: domain
LOCATION: 49..55
IDENTIFICATION METHOD:
                                                                                                                                                                                                                                                                                                                                           LOCATION: 24..33
IDENTIFICATION METHOD:
IDENTIFICATION METHOD:
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                                                                                                                                   NAME/KEY: sig_peptide
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                                                                                                                                                               LOCATION: -22..-1
IDENTIFICATION METHOD:
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                                                                    MOLECULE TYPE: protein FEATURE:
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FILING DATE: 10-MAY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     OTHER INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CITY: ARLINGTON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FEATURE:
NAME/KEY:
                                                                                                                                                                                                                                                                                                                  NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-08-116-778E-2
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                                           TOPOLOGY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FEATURE:
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TITLE OF INVENTION: Monoclonal Antibody to CEA, Conjugates Comprising Said
TITLE OF INVENTION: Antibody, and Their Therapeutic Use in an Adept System
FILE REFERENCE: Monoclonal Antibody to CEA
CURRENT APPLICATION NUMBER: US/09/171,945
CURRENT FILENC DATE: 1998-10-29
PRIOR FILING DATE: 1998-10-29
PRIOR FILING DATE: 1997-02-14
PRIOR FILING DATE: 1997-02-14
PRIOR FILING DATE: 1997-04-29
NUMBER OF SEQ ID NOS: 131
SOFTWARE: Matentin Ver. 2.1
SEQ ID NO 17
LENGTH: 235
TYPE: PRT

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FEATURE: OTHER INFORMATION: Description of Artificial Sequence: humanized
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 235
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61 FSGSGSGTSYSLTISRMEAEDAATYYCQQRSSYPFTFGSGTKLEIKR 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDIÚM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ouery Match. 96.6%; Score 539; DB 4;
Best Local Similarity 96.3%; Pred. No. 5e-41;
Matches 103; Conservative 3; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 24 Application US/08116778E
Patent No. 5830470
GENERAL INFORMATION:
APPLICANT: NAKAMURA, KAZUYASU
APPLICANT: SHITRARA, KENYA
APPLICANT: HANI, NOBUO
APPLICANT: HANI, NOBUO
APPLICANT: HANI, NOBUO
TITLE OF INVENTION: HUMANIZED ANTIBODIES
NUMBER OF SEQUENCES: 49
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLÍCATION NUMBER: US/08/116,778E
FILIÑG DATE: 07-SEP-93
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADDREŠSEE: NIXON & VANDERHYE P.C. STREEF; 1100 NORTH GLEBE ROAD CITY: ARLINGTON STATE; VIRGINIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ATTORNEY/AGENT INFORMATION:
NAME: WILSON, MARY J.
REGISTRATION NUMBER: 32,955
REFERENCE/DOCKET NUMBER: 249-
TELECOMMUNICATION INFORMATION:
TELEPHONE: (770))816-4000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEFAX: (703)816-4100
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    129 amino acids
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ZIP: 22201-4714
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CLASŠIFICATION:
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Gaps

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LENGTH: 129 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
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IDENTIFICATION METHOD:
IDENTIFICATION METHOD:
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IDENTIFICATION METHOD:
IDENTIFICATION METHOD:
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IDENTIFICATION METHOD:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME/KEY: sig_peptide LOCATION: -22..-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  IDENTIFICATION METHOD:
    CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        OTHER INFORMATION:
                                    STREET: 1100 NOR:
CITY: ARLINGTON
STATE: VIRGINIA
COUNTRY: U.S.A.
ZIP: 22201-4714
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          domain
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US-08-652-507-2
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WITH KNOWN SEQUENCE OR TO AN ESTABLISHED
CONSENSUS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          BY SIMILARITY WITH KNOWN SEQUENCE OR TO AN ESTABLISHED CONSENSUS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match

95.7%; Score 534; DB 2; Length 129;
Best Local Similarity 97.2%; Pred. No. 7.3e-41;
Matches 103; Conservative 1; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      | IDENTIFICATION METHOD: WITH KNOWN SEQUENCE OR TO AN EDIDENTIFICATION METHOD: CONSENSUS OTHER INFORMATION: /product= "HYPERVARIABLE REGION 3" US-08-438-562-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /product= "HYPERVARIABLE REGION 1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /product "HYPERVARIABLE REGION 2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SGSGSGTSYSLTISRMEAEDAATYYCQQRSSYPFTFGSGTKLEIKR 107
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APPLICANT: SHITARA, KENYA
APPLICANT: HANAI, NOBUO
APPLICANT: KUWANA, YOSHIHISA
APPLICANT: HASEGAWA, MAMORU
TITLE OF INVENTION: HUMANIZED ANTIBODIES
NUMBER OF SEQUENCES: 103
        PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/116,778
FILING DATE: 07-SEP-93
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: WILSON, MARY J.
REGISTRATION NUMBER: 32,955
                                                                                                                                                REFERENCE/DOCKET NUMBER: 249-76
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703)816-4000
TELEFAX: (703)816-4100
INFORMATION FOR SEQ ID NO: 2:
SQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 92, Application US/08483528B Patent No. 5939532 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAKAMURA, KAZUYASU
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....exist 129 amino acids
TYPE: amino acid
TOPOLOGY: 1:--
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IDENTIFICATION METHOD:
IDENTIFICATION METHOD:
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IDENTIFICATION METHOD:
IDENTIFICATION METHOD:
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IDENTIFICATION METHOD:
IDENTIFICATION METHOD:
IDENTIFICATION METHOD:
                                                                                                                                                                                                                                                                                                                                                                 NAME/KEY: sig_peptide
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                                                                                                                                                                                                                                                                                                                       MOLECULE TYPE: protein
CLASSIFICATION: 424
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  OTHER INFORMATION:
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BY SIMILARITY WITH KNOWN SEQUENCE TO TO AN ESTABLISHED CONSENSUS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2 IELTQSPAIMSASPGEKVTITCSASSSVSYMHWFQQKPGTSPKLWIYSTSNLASGVPARF 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      BY SIMILARITY WITH KNOWN SEQUENCE OR TO AN ESTABLISHED CONSENSUS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       OD: WITH KNOWN SEQUENCE OR TO AN ESTABLISHED OD: CONSENSUS /Product= "HYPERVARIABLE REGION 1"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /product= "HYPERVARIABLE REGION 3"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /product= "HYPERVARIABLE REGION
                                                                                                                                                                                                    OPERATING SYSTEM: CONFOCATIONS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/483,528B
FILING DATE: 07-JUN-95
CLASSIFICATION: 536
TELECOMMUNICATION: UNFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        BY SIMILARITY
ADDRESSEE: NIXON & VANDERHYE P.C. STREET: 1100 NORTH GLEBE ROAD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 2, Application US/08652507; Patent No. 5876691
GENERAL INFORMATION: APPLICANT:
                                                                                                                      ZIP: 22201-4714
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-
                                                                                                                                                                                                                                                                                                                                                                                                                                        92:
                                                                                                                                                                                                                                                                                                                                                                              TELEPHONE: (703)816-4000
TELEFAX: (703)816-4100
INFORMATION FOR SEQ ID NO: 92
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4 LTQSPAIMSASPGEKVTITCSASSSVSYMHWFQQKPGTSPKLWIYSTSNLASGVPARFSG 63
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       64 SGSGTSYSLTISRMEAEDAATYYCQQRSSYPFTFGSGTKLEIKRA 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TITLE OF INVENTION: THERAPEUTIC COMPOUNDS COMPRISED TITLE OF INVENTION: OF ANTI-FC RECEPTOR ANTIBODIES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ZIP: 02109-1875
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATCHTIN Release #1.0, Version #1.25
CURRENT APPLICATION DARR:
APPLICATION NUMBER: US/09/188,082
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 532; DB 2; I
Pred. No. 5.3e-40;
2; Mismatches 1;
                                                                                                                   NAME: Arnold, Beth E.
REGISTRATION NUMBER: 35,430
REFERENCE/POCKET NUMBER: MXI-043CP
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)227-7400
TELEPEAX: (617)227-5941
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD
STREET: 60 State Street, Suite 510
CITY: Boston
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MXI-043CP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 16, Application US/09188082
Patent No. 6270765
GEMERAL INFORMATION:
APPLICANT: Yashwant M. Deo
APPLICANT: Joel Goldstein
APPLICANT: Robert Graziano
APPLICANT: Robert Graziano
APPLICANT: Chezian Somasundaram
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION DATA: APPLICATION NUMBER: 08/661,052
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NAME: Arnold, Beth E.
REGIETRATION UNUABER: 35,430
REFRERENCE/DOCKET NUMBER: MXI-
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)227-7400
TELEFAX: (617)227-7400
TELEFAX: (617)227-5941
INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                   TELEFAX: (617)227-5941
INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
LENGTH: 553 amino acids
TYPE: amino acids
                          PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 06
FILING DATE: 07-JUNE-1995
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 95.3%;
Best Local Similarity 97.1%;
Matches 102; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           : 553 amino acids
amino acid
                                                                                                                                                                                                                                                                                                                                                                     , MOLECULE TYPE: protein US-08-661-052-16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Massachusetts
USA
                                                                                                                                                                                                                                                                                                                                                           linear
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                                                                                                                                                                                                                                                                                                                                                         · TOPOLOGY:
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COUNTRY:
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TITLE OF INVENTION: ANTIBODY AGAINST CARCINOEMBRYONIC ANTIGEN TITLE OF INVENTION: NUMBER OF SEQUENCES: 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 270,
                                                                                                                                                                                                                                                                                                                       SOFTWARE: PETENTIN BELEASE #1.0, Version #1.30 (EPO)
CURRENT PPELICATION DATA:
APPLICATION NUMBER: US/08/652,507
FILINGAATION NUMBER: US-011-1996
CLASSIFICATION: 530
ATTORNEY/ACBNT INFORMATION:
NAME: AATHUR R. CTAWFORM
REGISTRATION NUMBER: 15,327
REFERENCE/DOCKET NUMBER: 117-211
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEPHÖNE: 703-816-4000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  64 SGŚGTSYSLTISRMEAEDAATYYCQQRSSYPFTFGSGTKLEIKRA 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            225 SGSGTSYSLTISRMEAEDAATYYCQQRSSYPLTFGAGTKLELKRA 269
                                                                CORRESPONDENCE ADDRESS:
ADDRESSEE: Nixon & Vanderhye, P.C.
STREET J 1100 No. 5876691th Glebe Road, 8th Floor
CITY: Arington
STATE: Virginia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
APPLICANT: Yashwant M. Deo
APPLICANT: Yosh Goldstein
APPLICANT: Robert Graziano
APPLICANT: Robert Graziano
APPLICANT: Robert Graziano
APPLICANT: The OF INVENTION: THERAPEUTIC COMPOUNDS COMPRISE
TITLE OF INVENTION: OF ANTI-FC RECEPTOR ANTIBODIES
NUMBER GOUSDENCES: 16
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match: 95.3%; Score 532; DB 2; Best Local Similarity 97.1%; Pred. No. 2.4e-40; Matches 102; Conservative 2; Mismatches 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    E: LAHIVE & COCKFIELD
60 State Street, Suite 510
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              us/08/661,052
                                                                                                                                                                                                                                                         MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMULTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 16, Application US/08661052
Patent No. 5837243
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEFAX: 703-816-4100
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LENGTH: 270 amino acids TYPE: Famino acid
                                                                                                                                                                                      COUNTRY: USA
ZIP: 22201-4714
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TOPOLOĞY: linear
MOLECULEĞTYPE: protein
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COUNTRY: USA
ZIP: $02109-1875
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STREET: 60 St
CITY: Boston
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RESULT 7

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Gaps

TOPOLOGY:

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RESULT 11
                            RESULT 10
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                                                              Length 553;
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                                                                                                         1; Indels
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                                                                                                                                                                                                                                64 SGSGTSYSLTISRMEAEDAATYYCQQRSSYPFTFGSGTKLEIKRA 108
                                                                                                                                                                                                                                                                                                                                                                      Sequence 16, Application US/09364088
Patent No. 6365161
GENERAL INFORMATION:
TITLE OF INVENTION: THERAPEUTIC COMPOUNDS COMPRISED
TITLE OF INVENTION: OF ANTI-FC RECEPTOR ANTIBODIES
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD, LLP
STREET: 28 State Street, 24th Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPRIATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/364,088
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 95.3%; Score 532; DB 4; L
Best Local Similarity 97.1%; Pred. No. 5.3e-40;
Matches 102; Conservative 2; Mismatches 1;
                                                              95.3%; Score 532; DB 4; 97.1%; Pred. No. 5.3e-40;
                                                                                                     2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 09/188,082
FILING DATE: 07-JUNE-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/484,172
FILING DATE: 07-JUNE-1995
ATTONNEY, AGGNT INFORMATION:
NAME: Remillard, Jane E.
REGISTRATION NUMBER: 38,872
FEDCOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEFAN: (617)242-7400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           INFORMATION FOR SEQ ID NO: 16: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      : 553 amino acids
amino acid
                                                                                                   Matches 102; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MOLECULE TYPE: protein US-09-364-088-16
MOLECULE TYPE: protein
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USA
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                                                                                  Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Boston
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                     US-09-188-082-16
                                                                                                                                                                                                                                                                                                                                                     US-09-364-088-16
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                                                                Query Match
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4 LTQSPAIMSASPGEKVTITCSASSSVSYMHWFQQKPGTSPKLWIYSTSNLASGVPARFSG 63
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                                                                                                                                                                                                 TITLE OF INVENTION: THERAPEUTIC COMPOUNDS COMPRISED OF ANTI-FC RECEPTOR ANTIBODIES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
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                                                                                                                                                                                                                                                                     CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD
STREET: 60 State Street, Suite 510
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REFERENCE/DOCKET NUMBER: MXI-043CP TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          BLAKEY, David Charles
TITLE OF INVENTION: CHEMICAL COMPOUNDS
NUMBER OF SEQUENCES: 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/102,716
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 16:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: 08/661,052.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           % Sequence 44, Application US/09423439

Sequence 46, Application US/09423439

Patent No. 6339070

GENERAL INCREATION:

APPLICANT: EMERY, Stephen Charles
                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ATTORNEY AGENT INFORMATION:
NAME: Arnold, Beth E.
REGISTRATION NUMBER: 35,430
                                                                                                                                                                          Chezian Somasundaram
                  Sequence 16, Application US/09102716
Patent No. 6395272
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE: 22-Jun-1998 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (617)227-7400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LENGTH: 553 amino acids
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INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE: <Unknown>
                                                                                             APPLICANT: Yashwant M. Deo
Joel Goldstein
Robert Graziano
                                                                                                                                                                                                                                                                                                                                                                         STATE: Massachusetts
                                                                                                                                                                                                                                                NUMBER OF SEQUENCES: 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CORRESPONDENCE ADDRESS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Best Local Similarity 97.1
Matches 102; Conservative
                                                                                                                                                                                                                                                                                                                                                                                            COUNTRY: USA
ZIP: 02109-1875
                                                                                                                                                                                                                                                                                                                                                     CITY: Boston
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEPHONE:
US-09-102-716-16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-09-102-716-16
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2 IELTQSPAIMSASPGEKVTITCSASSSVSYMHWFQQKPGTSPKLWIYSTSNLASGVPARF 61
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Patent No. 6046037
GENERAL INFORMATION:
APPLICANT: ANDREW C. HIATT, JULIAN
APPLICANT: K.-C. MA, THOMAS LEHNER
TITLE OF INVENTION: IMMUNOGLOBULINS CONTAINING PROTECTION
TITLE OF INVENTION: PROTEINS IN PLANTS AND THEIR USES
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 105;
                                                                                                                                                                                                                                                             Length 666;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 62 SGSGSGTSYSLTISRMEAEDAATYYCQQRSSYPFTFGSGTKLEIKR 107
                                                                                                                                                                                                                                                          Score 526; DB 4;
Pred. No. 2.2e-39;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 518; DB 3;
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below:
                                                                                                                                                                                                                                                                                                                        3; Mismatches
                                                                                            TOPOLOGY: linear MOLECULE TYPE: protein SEQUENCE DESCRIPTION: SEQ ID NO: 51:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDIUM TYPE: 3.5" Diskette, 1.44 Mb MEDIUM TYPE: storage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER: IBM COMPATIBLE
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: Word Perfect 5.1
CURRENT APPLICATION DATA
APPLICATION NUMBER: US/08/434,000A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA: including app PRIOR APPLICATION DATA: including app PRIOR APPLICATION DATA: described be APPLICATION NUMBER: 08/367,395
FILING DATE: 12/30/94
ATTORNEY/AGENT INFORMATION:
NAME: Guise, Jeffrey W.
REGISTRATION NUMBER: 34,613
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            REFERENCE/DOCKET NUMBER: 212/127
TELECOMMUNICATION INFORMATION:
LENGTH: 666 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
STREET: Suite 4700
                                                                                                                                                                                                                                                          94.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (619) 552-8400
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TELEX: SEQUENCE LISTING
INFORMATION FOR SEQ ID NO: 1
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             105 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (619) 552-0159
                                                                                                                                                                                                                                                                                                                        Matches 101; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STREET: Suite 4700
CITY: Los Angeles
STATE: Callfornia
COUNTRY: U.S.A.
ZIP: 90071
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       amino acid
                                                                                                                                                                                                                                                                                              Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEPHONE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-08-434-000A-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-08-434-000A-12
                                                                                                                                                                                           US-09-423-439-51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEFAX:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LENGTH:
                                                                                                                                                                                                                                                          Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 281;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              62 SGSGSGTSYSLTISRMEAEDAATYYCQQRSSYPFTFGSGTKLEIKR 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               94.3%; Score 526; DB 4; Lv
95.3%; Pred. No. 8.7e-40;
tive 3; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      THE CONTROL OF THE CO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COUNTRY: U.S.A.

ZIP: 20005
COMMUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: MS WORD
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/423,439
FILING DATE: 09-NO. 6339070-1999
CLASSIFICATION: <UNknown>
                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/GB98/01294
APPLICATION NUMBER: 98
APPLICATION NUMBER: GB 9709421.3
APPLICATION TOWNER: GB 71097
INFORMATION FOR SEQ ID NO: 44:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION DATA:

4. APPLICATION NUMBER: PCT/CB98/01294

7. FILING DAYE: 05-MAY-1998

7. APPLICATION NUMBER: GB 9709421.3

5. FILING DAYE: 10-MAY-1997

INFORMATION FOR SEQ ID NO: 51:

SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                 COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: MS WORD
CURRENT APPLICATION DATA:
TOPPLICATION WURBER: US/09/423,439
FILING DATE: 09-NO. 6339070-1999
CLASSIFICATION: CURROWN>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; MOLEGULE TYPE: protein SEQ ID NO: 44: US-09-423-439 44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 51, Application US/09423439
Patent No. 6333070
GENERAL INFORMATION:
                                                                                                                                                             MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH: 281 amino acids TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CHARACTERISTICS:
                                                                                        ZIP: 20005
COMPUMER READABLE FORM:
ITY: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Best_Local Similarity 95.3
Matches 101; Conservative
                                STATE: D.C.
COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STATE: D.C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-09-423-439-51
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APPLICANT: QUEEN, Cary L.
APPLICANT: CO, Man Sung
APPLICANT: CO, Man Sung
APPLICANT: SCHNEIDER, William P.
APPLICANT: LANDOLEI, Wilcholas F.
APPLICANT: SELICK, Harold E.
TITLE OF INVENTION: IMPROVED HUMANIZED IMMUNOGLOBLINS
HUMBER OF SEQUENCES: 113
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend Khourie and Crew
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     OCFTANTING STSIEM:
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/634,278
FILING DATE: 19-DEC-1990
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/590,274
FILING DATE: 13-SEP-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/310,252
FILING DATE: 13-FEB-1989
PRIOR APPLICATION NUMBER: US 07/310,252
FILING DATE: 13-FEB-1989
FILING DATE: 13-FEB-1989
FILING DATE: 13-FEB-1989
ATTORNEY/AGENT INFORMATION:
NAME: SMITH, William M
REGISTRATION NUMBER: 30,233
PREGISTRATION NUMBER: 30,233
PREGISTRATION NUMBER: 30,233
PREGISTRATION NUMBER: 30,233
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                     Sequence 1, Application US/07634278 Patent No. 5530101 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                               STREET: 379 Lytton Avenue CITY: Palo Alto STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          106 amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Best Local Similarity 93.3
Matches 98; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SS: single
unknown
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LOCATION: 1..106
OTHER INFORMATION:
OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME/KEY: Protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               HYPOTHETICAL:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                 COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-07-634-278-1
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                            ;;
                            0; Gaps
                                                                                       1 DIELTQSPAIMSASPGEKVTITCSASSSVSYMHWFQQKPGTSPKLWIYSTSNLASGVPAR 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 DIELTQSPAIMSASPGEKVTITCSASSSVSYMHWFQQKPGTSPKLWIYSTSNLASGVPAR 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ;
0
                                                                                                                                                                                                                                                                                                                                                        APPLICANT: ADDREW C. HIATT, JULIAN
K.-C. MA, THOMAS LEHNER
TITLE OF INVENTION: IMMUNOGLOBULINS CONTAINING PROTECTION
PROTEINS IN PLANTS AND THEIR USES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 105;
                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                         FSGSGSGTSYSLTISRMEAEDAATYYCQQRSSYPFTFGSGTKLEI 105
                                                                                                                                                   61 FSGSGSGTSYSLTISRMEAEDAATYYCQQRSSYPFTFGSGTKLEI 105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Guy's 13 Kappa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 92.8%; Score 518; DB 4; L. Best Local Similarity 93.3%; Pred. No. 1.6e-39; Matches 98; Conservative 4; Mismatches 3;
    93.3%; Pred. No. 1.6e-39;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDIUM TYPE: 3.5" Diskette, 1.44 Mb storage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: WORD PERfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/312,157
FILING DATE: 14-May.1999
CLASSIFICATION: <URKNOWN>
                          4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME: Guise, Jeffrey W.
REGISTRATION NUMBER: 34,613
REFRENCE/DOCKET NUMBER: 212/127
TELECOMUNICATION INFORMATION:
TELEPHONE: (619) 552-8400
TELEFAX: (619) 552-0159
TELEX: 67-351
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; SEQUENCE DESCRIPTION: SEQ ID NO: 12:
US-09-312-157-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: 08/434,000 FILING DATE: CUNKNOWN>
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
Suite 4700
                                                                                                                                                                                                                                                                                               Sequence 12, Application US/09312157 Patent No. 6303341 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LENGTH: 105 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE LISTING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DESCRIPTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               INFORMATION FOR SEQ ID NO: 12: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQUENCES: 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
Best Local Similarity 93.3 Matches 98; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ZIP: 90071
                                                                                                                                                                                                                                                        RESULT 14
US-09-312-157-12
                                                                                                                                                                                        61
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Gaps 2 IELTQSPAIMSASPGEKVTITCSASSSVSYMHWFQQKPGTSPKLWIYSTSNLASGVPARF 61 2 IVLTQSPAIMSASPGEKVTITCSASSSISYMHWFQQKPGTSPKLMIYTTSNLASGVPARF 61 . 92.5%; Score 516; DB 1; Length 106; 93.3%; Pred. No. 2.4e-39; ive 4; Mismatches 3; Indels /note= "Variable region of the mouse anti-Tac antibody light chain." Indels 62 SGSGSGTSYSLTISRMEAEDAATYYCQQRSSYPFTFGSGTKLEIK 106 11823-002600 REFERENCE/DOCKET NUMBER: 11
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 326-2400
TELEFAX: (415) 326-2422
INFORMATION FOR SEQ ID NO: 1: 62

Search completed: December 23, 2002, 07:33:18 Job time : 20.4651 secs

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GenCore version 5.1.3

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OM protein - protein search, using sw model

Run on: December 23, 2002, 07:30:08; Search time 10.0465 Seconds

(without alignments)

180.208 Million cell updates/sec

Title:
US-09-865-198-8

Perfect score: 558

Sequence: 1 DIELTQSPAIMSASPGEKVT......QRSSYPFTFGSGTKLEIKRA 108

Scoring table: BLOSUM62

Gapop 10.0, Gapext 0.5

Searched: 106657 seqs, 16763532 residues

Total number of hits satisfying chosen parameters: 106657

Minimum DB seq length: 0

Maximum Match 0%

Maximum Match 0%

Listing first 45 summaries
```

Published_Applications_AA:*

1: /cgn2_6/ptodata/2/pubpaa/USOB_NEW_PUB.pep:*
2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep:*
3: /cgn2_6/ptodata/2/pubpaa/USO6_NEW_PUB.pep:*
4: /cgn2_6/ptodata/2/pubpaa/USO6_NEW_PUB.pep:*
5: /cgn2_6/ptodata/2/pubpaa/USO7_NEW_PUB.pep:*
6: /cgn2_6/ptodata/2/pubpaa/USO7_NEW_PUB.pep:*
7: /cgn2_6/ptodata/2/pubpaa/USO7_NEW_PUB.pep:*
8: /cgn2_6/ptodata/2/pubpaa/USO8_PUBCOMB.pep:*
9: /cgn2_6/ptodata/2/pubpaa/USO9_NEW_PUB.pep:*
10: /cgn2_6/ptodata/2/pubpaa/USO9_NEW_PUB.pep:*
11: /cgn2_6/ptodata/2/pubpaa/USO9_NEW_PUB.pep:*
11: /cgn2_6/ptodata/2/pubpaa/USO9_NEW_PUB.pep:*
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14: /cgn2_6/ptodata/2/pubpaa/USO0_NEW_PUB.pep:*
14: /cgn2_6/ptodata/2/pubpaa/USO0_NEW_PUB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Description	Sequence 8, Appli	ω,	28	Sequence 27, Appl	Sequence 24, Appl	23, 1	Sequence 29, Appl	Sequence 28, Appl	۵, ۸	17	Α.	Sequence 12, Appl	Sequence 88, Appl		۹	-	06	Sequence 75, Appl	78,
	ID	US-09-976-787-8	US-09-865-198-8	US-09-976-787-28	US-09-865-198-27	US-09-976-787-24	US-09-865-198-23	US-09-976-787-29	US-09-865-198-28	US-09-910-059-9	US-09-910-059-17	US-09-807-721-2	US-09-982-107-12	US-09-144-886-88	US-09-808-037-28	US-09-808-037-6	US-09-144-886-76	US-09-144-886-90	US-09-144-886-75	US-09-144-886-78
	DB	10	10	10	10	10	10	10	10	10	10	6	6	6	10	10	σ	σ	6	σ
	Length DB	108	108	240	240	106	106	238	238	108	235	699	105	107	119	239	107	107	107	107
æ	Query Match	100.0	100.0	100.0	100.0	98.4	98.4	98.4	98.4	97.0	9.96	93.7	95.8	91.2	90.7	90.7	90.5	9.68	87.6	87.6
	Score	558	558	558	558	549	549	549	549	541	539	523	518	509	206	206	505	200	489	489
	Result No.		7	e	4	വ	9	7	œ	6	10	11	12	13	14	15	16	17	18	. 61

Sequence 82, Appl Sequence 91, Appl Sequence 91, Appl Sequence 6, Appl Sequence 11, Appl Sequence 11, Appl Sequence 103, Appl Sequence 103, Appl Sequence 105, Appl Sequence 105, Appl Sequence 97, Appl Sequence 98, Appl Sequence 98, Appl Sequence 99, Appl Sequence 99, Appl Sequence 51, Appl Sequence 51, Appl Sequence 51, Appl Sequence 52, Appl Sequence 52, Appl Sequence 52, Appl Sequence 54, Appl Sequence 55, Appl Sequence 65, Appl Sequence 65, Appl Sequence 65, Appl	
US-09-144-886-82 US-09-144-886-83 US-09-144-886-91 US-09-184-886-91 US-09-144-886-99 US-09-144-886-99 US-09-144-886-79 US-09-144-886-79 US-09-144-886-79 US-09-144-886-79 US-09-144-886-97 US-09-144-886-97 US-09-144-886-98 US-09-144-886-98 US-09-144-886-98 US-09-144-886-98 US-09-144-886-98 US-09-910-059-99 US-09-910-059-71 US-09-910-059-99 US-09-910-059-99 US-09-910-059-99 US-09-910-059-99 US-09-910-059-99 US-09-910-059-99 US-09-910-059-99 US-09-910-059-99 US-09-910-059-99 US-09-910-059-99 US-09-910-059-99 US-09-910-059-99 US-09-910-059-50 US-09-910-059-50	
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ALIGNMENTS

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             Sequence 8, Application US/09976787
; Patent No. US20020064528A1
; GENERAL INNORMATION
; GENERAL INNORMATION;
; APPLICANT: Zhu, Zhenping
; APPLICANT: Witte, Larry
; TITLE OF INVENTION: Antibodies Specific to KDR and Uses Thereof
; TITLE OF INVENTION: Antibodies Specific to KDR and Uses Thereof
; CURRENT APPLICATION NUMBER: US/09/976,787
; CURRENT APPLICATION NUMBER: US 09/493,539
; PRIOR PLILNG DATE: 2000-01-28
; PRIOR PLILNG DATE: 2000-01-28
; PRIOR FILING DATE: 1999-01-29
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: WordPerfect 8.0 for Windows
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100.0%; Score 558; DB 10;
Best Local Similarity 100.0%; Pred. No. 1.7e-31;
Matches 108; Conservative 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: PRT
CORGANISM: Mus musculus
US-09-976-787-8
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3-187-976-90-SU
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Sequence 23, Application US/09865198
Patent No. US2002010334541
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: Bispecific Immunoglobulin-Like Antigen Binding Proteins and Meritate Reference: 11245/47102
FILE REFERENCE: 11245/47102
CURRENT APPLICATION NUMBER: US/09/865,198
CURRENT APPLICATION NUMBER: US/09/865,198
PRIOR APPLICATION NUMBER: US/01.05-24
PRIOR APPLICATION NUMBER: US/05/749
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Patent No. US20020064528A1

GENERAL INFORMATION:
APPLICANT: Zhu, Zhenping

APPLICANT: Zhu, Zhenping

TITLE OF INVENTION: Antibodies Specific to KDR and Uses Thereof
FILE REFERENCE: 11245/46505

CURRENT APPLICATION NUMBER: US/09/976,787

CURRENT FILING DATE: 2001-10-12

PRIOR APPLICATION NUMBER: US 09/493,539

PRIOR FILING DATE: 2000-1.28

PRIOR PLICATION NUMBER: US 60/117,726.
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Best Local Similarity 100.0%; Pred. No. 6.7e-31;
Matches 106; Conservative 0; Mismatches 0;
    CURRENT APPLICATION NUMBER: US/09/865,198
CURRENT FILING DATE: 2001-05-24
PRIOR PAPLICATION UNBER: US 60/206,749
PRIOR FILING DATE: 2000-05-24
NUMBER OF SEQ ID NOS: 34
SOFTWARE: WordPerfect 8.0 for Windows
SEQ ID NO 27
LENGTH: 240
TYPE: PRT
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TITLE OF INTENTION: Bispecific Immunoglobulin-Like Antigen Binding Proteins and Methor TITLE OF INTENTION: Production
FILE REFERENCE: 11245/47102
CURRENT APPLICATION NUMBER: US/09/865,198
CURRENT FILING DATE: 2001-05-24
PRIOR FILING APPLICATION NUMBER: US 60/206,749
PRIOR FILING DATE: 2000-05-24
NUMBER OF $EQ ID NOS: 34
SOFTWARE: WordPerfect 8.0 for Windows
SEQ ID NO 8;
LENGTH: 106
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Sequence 27, Application US/09865198

Patent No WISOURD 10345A1

GENERAL INFORMATION:

APPLICANT: Zhu, Zhenping

TITLE OF INVENTION: Bispecific Immunoglobulin-Like Antigen Binding Proteins and Metholy TITLE OF INVENTION: Production

FILE REFERENCE: 11245/47102
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APPLICANT: Witte, Larry
TITLE OF INVENTION: Antibodies Specific to KDR and Uses Thereof
FILE REFERENCE: 11245/46505
CURRENT APPLICATION NUMBER: US/09/976,787
CURRENT FILING DATE: 2001-10-12
PRIOR FILING DATE: 2000-01-28
PRIOR FILING DATE: 1999-01-29
PRIOR FILING DATE: 1999-01-29
SPRIOR FILING DATE: 1999-01-29
SOFTWARE: WordPerfect 8.0 for Windows
SEQ ID NO 28
LENGTH: 240
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                                                                                                                                                                                                                                                                                                                                                        Length 108;
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                                                                                                                                                                                                                                                    TYPE: PRT
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; ORGANISME Mouse
US-09-976-787-28
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Sequence 17, Application US/09910059
Patent No. US20020142359A1
GENERAL INFORMATION:
APPLICANT: Copley, Clive G
APPLICANT: Edge, Michael Derek
APPLICANT: Emery, Stephen Charles
TITLE OF INVENTION: Monoclonal Antibody to CEA, Conjugates Comprising Said Antibod
TITLE OF INVENTION: Their Therapeutic use in an Adept System
FILE REFERENCE: 1991-209
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                                                                                                                                                                                                                                                              97.0%; Score 541; DB 10;
95.4%; Pred. No. 2.3e-30;
Live 4; Mismatches 1;
                                                                                                               Score 549; DB 10;
Pred. No. 1.2e-30;
                                                                                                  98.4%; Scor.
100.0%; Pred. No. 1...
... 0; Mismatches
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SOFTWARE: PatentIn version 3.1
                                                                                                               Query Match
Best Local Similarity 100.0
Matches 106; Conservative
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Best Local Similarity
                                      ; TYPE: PRT
; ORGANISM: Mouse
US-09-865-198-28
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US-09-910-059-17
     SEQ ID NO 28
LENGTH: 238
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Patent No. US30020103345a1
Patent No. US30020103345a1
Patent No. US30020103345a1
RAPELCANT: Zhu, Zhenping
TITLE OF INVENTION: Bispecific Immunoglobulin-Like Antigen Binding Proteins and Methor TITLE OF INVENTION: Production
FILE REFERENCE: 11245/47102
CUBRENT APPLICATION NUMBER: US/09/865,198
CUBRENT FILING DATE: 2001-05-24
PRIOR PELLON DATE: 2000-05-24
NUMBER OF SEQ ID NOS: 34
SOFTWARE: WordPerfect 8.0 for Windows
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Fatent No. US20020064528A1

GENERAL INFORMATION:

APPLICANT: Zhu, Zhenping

TITLE OF INVENTION: Antibodies Specific to KDR and Uses Thereof

FILE REFERENCE: 11245,46505

CURRENT APPLICATION NUMBER: US/09/976,787

CURRENT FILING DATE: 2010-10-12

PRIOR FILING DATE: 1999-01-29

PRIOR FILING DATE: 1999-01-29

FINDR APPLICATION NUMBER: US 60/117,726

PRIOR FILING DATE: 1999-01-29

NUMBER OF SEQ ID NOS: 40

SOFTWARE: WordPerfect 8.0 for Windows

SEQ ID NO 29

LENGTH: 238
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                                                                                                                                                                   Query Match 98.4%; Score 549; DB 10; Best Local Similarity 100.0%; Pred. No. 6.7e-31; Matches 106; Conservative 0; Mismatches 0;
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100.0%; Pred. No. 1.2e-30;
tive 0; Mismatches 0;
PRIOR FILING DATE: 2000-05-24
NUMBER OF SEQ ID NOS: 34
SOFTWARE: WordPerfect 8.0 for Windows
SEQ ID NO 23
LENGTH: 106
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Best Local Similarity
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                                                                                                            ; ORGANISM: Mouse US-09-865-198-23
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US-09-865-198-28
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                                                                                          TYPE: PRT
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APPLICANT: Marks, James D
APPLICANT: Marks, James D
APPLICANT: Amersdorfer, Peter
TITLE OF INVENTION: Therapeutic Monoclonal Antibodies That Neutralize
TITLE OF INVENTION: Botulinum Neurotoxins
FILE REFERENCE: 2500.1170SO
CURRENT APPLICATION UNBER: US/09/144,886
CURRENT FILING DATE: 1998-08-31
NUMBER OF SEQ ID NOS: 98
SOFTWARE: Patentin Ver. 2.0
TITLE OF INVENTION: METHODS FOR PRODUCING IMMUNOGLOBULINS CONTAINING TITLE OF INVENTION: PROTECTION PROTEINS IN PLANTS AND THEIR USE FILE REPERBENCE: EDISIOLE CURRENT APPLICATION NUMBER: US/09/982,107 CURRENT FILING DATE: 2001-10-16 NUMBER OF SEQ ID NOS: 19 SOFFWARE: Patentin Ver. 2.1 SEQ ID NO 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    OTHER INFORMATION: Description of Artificial Sequence: BoNT/a clone OTHER INFORMATION: 2G5 region VL epitope 2
                                                                                                                                                                                                                                                                                                                                                                                                               OTHER INFORMATION: Description of Unknown Organism: Guy's 13 Kappa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 88, Application US/09144886
Patent No. US20020155114A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                 TYPE: PRT ORGANISM: Unknown Organism
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Matches 98; Conservative
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Best Local Similarity
Matches 97; Conservat
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US-09-808-037-28
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Sequence 2,4Application US/09807721

SERIEMATION: UNIVERSITY

APPLICANT: UNIVERSITY OF CENTRAL FLORIDA

TILLE OF INVENTION: PRODUCTION OF ANTIBODIES IN TRANSCENIC PLASTIDS

FILE REPERENCE: 1463-PCT-US-00

CURRENT APPLICATION NUMBER: US/09/807,721

CURRENT APPLICATION NUMBER: US/09/807,721

PRIOR FILLNG DATE: 2001-02-28

NUMBER OF [SEQ ID NOS: 6

SOFTWARE: PRICE PRICE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match; 96.6%; Score 539; DB 10;
Best Local Similarity 96.3%; Pred. No. 5.6e-30;
Matches 103; Conservative 3; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; OTHER INFORMATION: chimaeric light chain sequence US-09-910-059-17
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                                 PRIOR APPLIGATION NUMBER: US 09/171,945
PRIOR FILING DATE: 1998-10-29
PRIOR FILING DATE: 1998-10-29
PRIOR FILING DATE: 1997-04-29
PRIOR FILING DATE: 1997-04-29
PRIOR PILING DATE: 1997-02-14
PRIOR PILING DATE: 1997-02-14
PRIOR PRIING DATE: 1997-02-14
PRIOR PRIING DATE: 1996-05-04
NUMBER OF SEQ ID NOS: 131
SOFTWARE: Patentin version 3.1
SOFTWARE: 235
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                    2001-07-23
                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: PRT .
ORGANISM: Artificial Sequence
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                    CURRENT FILENG DATE:
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ò qq ò g Sequence 28, Application US/09808037
Patent No. US20020052311A1
GENERAL INFORMATION:
APPLICANT: SOLOMON, Beka
TAPLICANT: HANAN, Eilat
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR THE TREATMENT AND/OR DIAGNOSIS OF
TITLE OF INVENTION: NEUROLOGICAL DISEASES AND DISORDERS

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Sequence 6, Application US/09808037

Sequence 6, Application US/09808037

Fatent No. US20020052311A1

GENERAL INFORMATION:

APPLICANT: SOLOWON, Beka

APPLICANT: HANAN, Eilat

TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR THE TREATMENT AND/OR DIAGNOSIS OF

TITLE OF INVENTION: METHODS AND DISORDERS

FILE REFERENCE: SOLOMON=2D

CURRENT APPLICATION NUMBER: US/09/808,037

FRIOR APPLICATION NUMBER: 09/629,971

PRIOR FILING DATE: 2001-07-31

PRIOR FILING DATE: 1999-12-29

PRIOR FILING DATE: 1999-12-29

PRIOR FILING DATE: 1999-12-29

PRIOR FILING DATE: 1999-10-03

NUMBER OF SEQ ID NOS: 33

SOCTWARKE: PATENTIN VERSION 3.0
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                                                                                                                                                                                                                                                                                                                                                                                                 7; Indels
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Pred. No. 5.3e-28;
3; Mismatches 7;
FILE REFERENCE: SOLOMON-2D
CURRENT APPLICATION NUMBER: US/09/808,037
CURRENT FILING DATE: 2001-03-15
PRIOR APPLICATION NUMBER: 09/629,971
PRIOR FILING DATE: 2000-07-31
PRIOR FILING DATE: 1999-12-29
PRIOR FILING DATE: 1999-12-29
PRIOR FILING DATE: 1999-09-03
NUMBER OF SEQ ID NOS: 33
SOFTWARE: PatentIn version 3.0
SEQ ID NO 28
TENGTH: 119
TENGTH: 119
                                                                                                                                                                                                                                                                                         ) ORGANISM: synthetic construct US-09-808-037-28
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Best Local Similarity 90.6%;
Matches 96; Conservative
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US-09-808-037-6
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US-09-808-037-6
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LENGTH: 239
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1 DIELTQSPAIMSASPGEKVT.....QRSSYPFTFGSGTKLEIKRA 108
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	Description	g kappa cha	q light chain	, 6	kappa chain	g kappa	. 6	g kappa chain	5	ь	5	g kappa chain	g kappa chain V	g light chain V	Ig kappa chain V r	g kappa chain V	q kappa chain V	6	6	Ig kappa chain V r	б	ь	ь	ь	ь	ь	q kappa chain	, 6	שו	ъ
SUMMARIES	ID	3	B54378	S05268	PC4405	D38601	A32513	A30562	B30562	G27887	JL0079	PS0070	S26338	866536	S29591	PD0011	PL0278	G30560	PS0071	B49049	PL0276	PL0277	S25058	S17626	A42848	$^{\circ}$	B32456	S11119	PS0069	805269
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	Score	517	513	492	487	486	483	481	476	474	473	472	470	466	465	465	. 465	464.5	463	461	461	461	460	458	455	455	455	453	453	453
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Ig light chain V r	1g kappa chain v r	Ig kappa chain V r	anti-D-dimer monoc	Ig light chain V r	Ig kappa chain V r	chain	Ig light chain V r	chain	chain	kappa chain	light chain	kappa chain	chain	light chain	kanna chain
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ALIGNMENTS

RESULT 1 PL0013 Iq Kappa chain precursor V region (4C11) - mouse (fragment) C;Species: Mus musculus (house mouse) C;Species: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 21-Jan-2000 C;Accession: PL0013 R;Cheng, H.L.; Sood, A.K.; Ward, R.E.; Kieber-Emmons, T.; Kohler, H. Mol. Immunol. 25, 33-40, 1988 A;Title: Structural basis of stimulatory anti-idiotypic antibodies. A;Reference number: PL0011; MUID:88142863; PMID:3125424	A; Molecule type: mRNA A; Residues: 1-140 <che> A; Residues: 1-140 <che> A; Residues: 1-140 <che> A; Experimental source: cell line 4C11 C; Comment: This protein is an anti-idiotypic antibody that induces an anti-phosphoryl C; Superfamily: immunoglobulin v region; immunoglobulin homology C; Keywords: heterotetramer; immunoglobulin homology C; Keywords: heterotetramer; immunoglobulin homology status predicted <ngp> F; 23-129/Product: Ig heavy chain v region (4C11) #status predicted <nat> F; 38-111/Domain: complementarity-determining 1 F; 71-7/Region: complementarity-determining 3 F; 110-118/Region: complementarity-determining 3 F; 130-140/Domain: constant region (fragment) #status predicted <cor></cor></nat></ngp></che></che></che>	Duery Match 92.7%; Score 517; DB 2; Lengt Best Local Similarity 94.4%; Pred. No. 4.3e-35; Matches 101; Conservative 1; Mismatches 5; Ind 2 IELTQSPAIMSASPGEKVTITCSASSSVSYMHWFOOKPGTSPKLMIYS 4 IVLTQSPAIMSASPGEKVTITCSASSSVSYMHWFOOKPGTSPKLMIYS 62 SGSGSGTSYSLTISRMEAEDAATVXCQASSYPFTGSGTKLEIKRA 61 IIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII	RESULT 2 B54378 Ig light chain V region anti-triplex DNA - mouse (fragment) C;Species: Mus musculus (house mouse) C;Accession: B54378 R;Agazie, Y.M.; Lee, J.S.; Burkholder, G.D. J. B10.1 Chem. 269, 7019-703, 1994 A;Title: Characterization of a new monoclonal antibody to triplex DNA and immunofluor A;Reference number: A54378; MUID:94165109; PMID:7509814 A;Status: preliminary A;Molecule type: mRNA A;Residues: 1-106 <aga></aga>
KEHOOOEXaaa			

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Gaps

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Length 107;

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Ig kappa chain V region (6A7) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Species: Mus 19-191 #sequence_revision 30-Aug-1991 #text_change 21.Jan-2000
C;Accession: D36601
R;Goshorn, S.C.; Retzel, E.; Jemmerson, R.
J. Blol. Chem. 266, 2134-2142, 1991
A;Fitle: Common structural features among monoclonal antibodies binding the A;Reference number: A38601; MUID:91115823; PMID:1703527
                                                                                                                                                                                                                                    1 DIELTQSPAIMSASPGEKVTITCSASSSVSYMHWFQQKPGTSPKLWIYSTSNLASGVPAR 60
                                                                                                                                                                                                                                                       A;Experimental source: spleen cell
C;Superfamily: immunoglobulin V region; immunoglobulin homology
F;16-89/Domain: immunoglobulin homology <IMM>
                                                                                                                                                                                                                                                                                                                                         61 FSGSGSGTSYSLTISRVEAEDAATYXCQQWRDNPPFFGGGTKLEIKR 107
                                                                                                                                                                                                                                                                                                                    61 FSGSGSGTSYSLTISRMEAEDAATYYCQQRSSYPFTFGSGTKLEIKR 107
                                                                                                                                                  Score 487; DB 2;
Pred. No. 8.9e-33;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   86.6%; Score 483; DB 2;
87.9%; Pred. No. 2.2e-32;
                                                                                                                                                                                            Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             F;38-113/Domain: immunoglobulin homology <IMM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         C;Superfamily: immunoglobulin V region; immur
C;Keywords: heterotetramer; immunoglobulin
F;8-81/Domain: immunoglobulin homology <IMM>
                                                                                                                                                                                          4;
                                                                                                                                                  87.3%;
87.9%;
                                                                                                                                                                                            Conservative
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                           A; Molecule type: mRNA
A; Residues: 1-107 <DEN>
                                                                                                                                                                       Similarity
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nes 94; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Molecule type: DNA
A; Residues: 1-130 <KOF>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Accession: D38601
A; Status: preliminary
            A; Accession: PC4405
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                                                                                                                                                                                        94;
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                                                                                                                                                     Query Match
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Best Local 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
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Matches 9
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Matches
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(Species: Mus musculus (house mouse)
(Species: Mus musculus (house mouse)
(Space: 10-Növ-1997 #sequence_revision 23-Jan-1998 #text_change 21-Jan-2000
(Shacession: Pc4405
(Shoression: Pc4405
(Chinese Blochem. J. 12, 648-653, 1996
(A) Title: Genération of a phage display library of the immunoglobulin repertoire from hum A; Reference pumber: Pc4405
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A;Cross-references: GB:S68985; NID:9545746; PIDN:AAB30096.1; PID:9545747
A;Experimental source: spleen and myeloma cell line MOPC 315.43
A;Note: sequence inconsistent with nucleotide translation
A;Note: sequence extracted from NCBI backbone (NCBIN:144174, NCBIP:144175)
C;Superfamily: %immunoglobulin V region; immunoglobulin homology
C;Keywords: immunoglobulin
F;16-89/Domain; immunoglobulin homology <IMM>
                                                                                                                                                                                                               Gaps
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                                                                                                                                                                                                                                                     2 IELTÓSPAIMSASPGEKVTITCSASSSVSYMHWFQQKPGTSPKLWIYSTSNLASGVPARF 61
                                                                                                                                                                                                                                                                          2 IVLTQSPAIMSASPGEKVTITCSASSSVSYMHWFQQKPGTSPKLMIYSTSKLASGVPARF 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A, Accession: 910062
A, Molecule type: mRNA
A, Residues: 19120 <CARA
A, Cross-references: EMBL:X14098
G, Superfamily: immunoglobulin V region; immunoglobulin homology
C, Superfamily: immunoglobulin V region; immunoglobulin homology
F, 1-14/Domain: signal sequence (fragment) #status predicted <SIG>F, 15-124/Product: Ig kappa chain (fragment) #status predicted <MAT>F, 15-108/Domain: immunoglobulin homology <IMM>F; 90-103/Domain: immunoglobulin homology <IMM>F; 90-103/Domain: immunoglobulin homology <IMM>F; 109-132/Domain: J region (J-kappa-4) (fragment) <JRE>
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                                                                                                                                                                     Length 106;
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                                                                                                                                                                                                             4; Indels
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                                                                                                                                                                   Score 513; DB 2;
Pred. No. 7.1e-35;
2; Mismatches 4,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 492; DB 2;
Pred. No. 4.3e-33;
9; Mismatches 6;
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86.1%;
                                                                                                                                                                   91.9%;
ilarity 94.3%;
Conservative
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Les 997 Conserv
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Best Local Similarity
Matches 93; Conserv
                                                                                                                                                                     Query Match
Best Local S
Matches 99
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PC4405
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Rikofler, R.; Strohal, R.; Balderas, R.S.; Johnson, M.E.; Noonan, D.J.; Duchosal, M.A.J. Clin. Invest. 82, 852-860, 1988
A;Title: Immunoglobulin kappa light chain variable region gene complex organization a A;Reference number: A94689; MUID:88331394; PMID:3138286
                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ig kappa chain precursor V region (MRL22) - mouse C;Species: Wus musculus (house mouse) C;Date: 21-May-1990 #sequence_revision 31-bec-1990 #text_change 21-Jan-2000 C;Accession: A32513
                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                     9 AIMSASPGEKVTITCSASSSVSYMHWFQQKPGTSPKLWIYSTSNLASGVPARFSGSGSGT 68
A; Molecule type: mRNA
A; Residues: 1-99 <GOS>
A; Cross-references: GB: M57981; NID:g196408; PIDN:AAA63362.1; PID:g196409
C; Superfamily: immunoglobulin V region; immunoglobulin homology
C; Keywords: heterotetramer; immunoglobulin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Cross-references: GB:M20834; NID:g196943; PIDN:AAA38846.1; PID:g196944 C;Superfamily: immunoglobulin V region; immunoglobulin homology C;Keywords: heterotetramer; immunoglobulin
                                                                                                                                                                                                                                                                                                                                                                                                                         1 AIMSASPGEKVTITCSASSSVSYMHWFQLKPGTSPKLMISSTSNLASGVPARFSGSGSGT
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                                                                                                                                                                                                                                                                                                                     Indels
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                                                                                                                                                                                                                                                87.1%; Score 486; DB 2 94.9%; Pred. No. 1e-32;
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Gaps

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Indels

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A.Accession: G27887
A.Molecule type: DNA
A.Residues: 1-106 <CAT>
A.Experimental source: strain Balb/c
A.Note: this sequence was determined from the germline gene
C.Comment: This chain was isolated from a hybridoma protein that binds influenza viru
C.Superfamily: immunoglobulin V region; immunoglobulin homology
C.Keywords: heterotetramer; immunoglobulin
F:16-89/Domain: immunoglobulin homology <IMM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ig kappa chain precursor V region (anti-phenyloxazolone 6F6) - mouse (Species: Mus musculus (house mouse) (C) Date: 31-Dec-1991 #sequence_revision 09-Aug-1996 #text_change 16-Jul-1999 (Species: 10.0079; A49044; B49044 R;Raartinen, M.; Rocca-Serra, J.; Maekelae, O. Mol. Immunol. 25, 859-865, 1988 A;Tile: Combinatorial association of V genes: one VH gene codes for three non-cross-A;Reference number: JL0076; MUID:89096973; PMID:3211160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Molecule type: mRNA
A; Residues: 1-130 < KAA>
A; Residues: 1-130 < KAA>
A; Cross references: GB:M27792; NID:g197159
A; Cross references: GB:M27792; NID:g197159
A; Experimental source: mRNA clones for anti-phenyloxazolone antibody GF6
A; Note: the authors translated the codon TTC for residue 8 as Pro and TTC for residue 8; Note: the codon given for 1-Met (AGT) is inconsistent with the authors' translation B; Mistelin, C.; Even, J.; Jarvis, J.M.; Gonzalez-Fernandez, A.; Gherardl, E. Eur. J. Immunol. 22, 1627-1634, 1992
A; Title: Non-random features of the repertoire expressed by the members of one V Kapp A; Reference number: A49044; MUID:92289826; PMID:1601044
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                                                                                                                                             EMBO J. 5, 1577-1587, 1986
A;Title: Structural and functional implications of a restricted antibody response A;Reference number: A91043; MUID:86300658; PMID:2427335
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A;Note: sequences extracted from NCBI backbone; partial nucleotide sequences
A;Note: sequence extracted from NCBI backbone (NCBIN:106807, NCBIP:106822)
   Ig kappa chain V region (H18-S415) - mouse
C;Species: Mus musculus (house mouse)
C;Date: 15-Dec-1988 #sequence_revision 15-Dec-1988 #text_change 21-Jan-2000
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NCBIP:106809)
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A;Residues: 114-116 <MIL2>
A;Cross-references: GB:S37664; NID:g250215; PIDN:AAB22332.1; PID:g250218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2 IELTQSPAIMSASPGEKVTITCSASSSVSYMHWFQQKPGTSPKLWIYSTSNLASGVPARF
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A;Molecule type: DNA
A;Residues: 1-25 <-ML>
A;Cross-references: GB:S37663; NID:g250214; PIDN:AAB22331.1;
A;Note: sequence extracted from NCBI backbone (NCBIN:106802,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      62 SGSGSGTSYSLTISRMEAEDAATYYCQQRSSYPFTFGSGTKLEIK 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 474; DB 2; L
Pred. No. 9.9e-32;
6: Mismatches 10;
                                                                                                                        Brownlee, G.G.; Staudt, L.M.; Gerhard,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 84.9%;
Best Local Similarity 84.8%;
Matches 89; Conservative
                                                                                         C; Accession: G27887
R; Caton, A.J.; Brown
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C; Species: Mus musculus (house mouse)
C; Species: Mus musculus (house mouse)
C; Date: 23-Mar-1989 #sequence_revision 23-Mar-1989 #text_change 21-Jan-2000
C; Accession: A30562
R; Sikder, S.K.; Borden, P.; Gruezo, F.; Akolkar, P.N.; Bhattacharya, S.B.; Morrison, S.L.
J. Immunol. 142, 888-893, 1989
A; Title: Amino acid substitutions in V-H CDR2 change the idiotype but not the antigen-bi A; Reference number: A30562; MUID: 89110066; PMID: 2464031
A; Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             R;Sikder, S.K.; Borden, P.; Gruezo, F.; Akolkar, P.N.; Bhattacharya, S.B.; Morrison, S.I. J. Immunol. 142, 888-893, 1989
A;Title: Amino acid substitutions in V-H CDR2 change the idiotype but not the antigen-bi A;Reference number: A30562; MUID:89110066; PMID:2464031
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C;Species: Mus musculus (house mouse)
C;Date: 23-Mar-1989 #sequence_revision 23-Mar-1989 #text_change 21-Jan-2000
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                           24 IVLTQSPAIMSASPGERVTMTCSASSSVSSSYLYWYQQRPGSSPKLWIYSTSNLASGVPA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               IELTQSPAIMSASPGEKVTITCSASSSV--SYMHWFQQKPGTSPKLWIYSTSNLASGVPA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A,Molecule type: mRNA
A;Residues: 1-107 <SIK>
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heteroterramer; immunoglobulin
F;16-89/Domain: immunoglobulin homology <IMM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 107
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                                                                                                                                                   SGSGSGTSYSLTISRMEAEDAATYYCQQRSSYPFTFGSGTKLEIKR 107
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Pred. No. 2.7e-32;
3; Mismatches 9;
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Pred. No. 6.9e-32;
4; Mismatches 10
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Local Similarity 88.7%;
nes 94; Conservative
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86.8%;
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A: Residues: 1-107 <SIK>
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Best Local Simi
Matches 92;
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C;Superfamil
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19 11ght chain V region - mouse (fragment)
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19 11ght chain V region - mouse)
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C;Species: Mus musculus (house mouse)
C;Date: 06-Jan.1995 #sequence_revision 06-Jan-1995 #text_change 21-Jan-2000
C;Accession: S29591
R;Kardler, J
Submitted to the EMBL Data Library, April 1991
A;Reference number: S26459
A;Status: preliminary
A;Status: preliminary
A;Molecule type: mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PID:91103702
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           61
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           2 IVLTQSPAIMSASPGEKVTISCSASSSVSYMYWYQQKPGSSPKPWIYRTSNLASGVPARF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Cross-references: EMBL:X88903; NID:g895870; PIDN:CAA61365.1; C;Superfamily: immunoglobulin V region; immunoglobulin homology F;16-91/Domain: immunoglobulin homology <IMM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Rosidues: 1-103 <a href="https://doi.org/10.103/07/10.104">https://doi.org/10.103/07/10.104</a>
A; Cross-references: EMBL:X59094; NID:g52227; PIDN:CAA41820.1; Pl C; Superfamily: immunogloblin v region; immunoglobulin homology C; Keywords: heterotetramer: immunoglobulin C; Keywords: heterotetramer: immunoglobulin F; 15-88/Domain: immunoglobulin homology <IMM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          59 ARFSGSGSGTSYSLTISRMEAEDAATYYCQQRSSYPFTFGSGTKLEIKR 107
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Pred. No. 4.9e-31;
5; Mismatches 10; Indels
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C;Species: Mus musculus (house mouse)
                                                                                                    SGSGSGTSYSLTISRMEAEDAATYYCQQRSSYPFTFGSGTKLE 104
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ilarity 83.5%;
Conservative
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Best Local Similarity
Matches 91; Conserv
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S29591
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ig Aappa chain V region (38C13.V6.1) - mouse
C; Species: Mus_musculus (house mouse)
C; Species: Mus_musculus (house mouse)
C; Species: Mus_musculus (house mouse)
C; Accession: p50070
R; Levy, S; Campbell, M.J; Levy, R.
J. Exp. Med. #f0, 1-13, 1989
A; Title: Functional immunoglobulin light chain genes are replaced by ongoing rearrangeme A; Reference number: A92781; MUD:89310348; PMID:2501443
A; Accession: p50070
A; Accession: p50070
A; Status: trainslation not shown
A; Mesidues: 1; 106 < LEVy
C; Species: 1; 106 < LEVy
C; Status: immunoglobulin V region; immunoglobulin homology
C; Reywords: héterotetramer; immunoglobulin
F; 16-89/Domaaff: immunoglobulin homology < IMM>
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C;Species: Mus musculus (house mouse)
C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 20-Jun-2000
C;Accession: $256338
R;Stark, S.E; Caton, A.J.
J. Exp. Med:174, 613-624, 1991
A;Title: Antibodies that are specific for a single amino acid interchange in a protein A;Reference number: $26309; MUID:91341421; PMID:1908510
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                                                                                                                                                                                                                                                                 2 IELTŐSPAIMSASPGEKVTITCSASSSVSYMHWFQQKPGTSPKLWIYSTSNLASGVPARF 61
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F;23-130/Product: Ig kappa chain V region (6F6) #status predicted <MAT>F;38-111/Domain: immunoglobulin homology <IMM>F;45-109/Disulfide bonds: #status predicted
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                                                                                                                   Length 130;
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                                                                                                                                                                                 11;
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                                                                                                                   Score 473; DB 1;
Pred. No. 1.4e-31;
3; Mismatches 11
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83.0%; Pred. No. 1
                                                                                                                      84.8%;
86.9%;
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Matches 88; Conserv
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A; Residues: 1-105 <STA>
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                                                                                                                      Query Match
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Best Local
Satches 92
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C;Date: 10-Jul-1998 #sequence_revision 10-Jul-1998 #text_change 21-Jan-2000
C;Accession: PD0011
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Chinese Biochem. J. B.; Han, H.; Su, C.Z.; Chen, C.Q.
Chinese Biochem. J. 12, 648-653, 1996
A;Title: Generation of a phage display library of the immunoglobulin repertoire from hum A;Reference number: PC4405
A;Reference number: PC4405
A;Accession: PD0011
A;Accession: PD0011
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A;Residues: 1-107 < CDEN>
C;Superfamily: immunoglobulin V region; immunoglobulin homology
F;16-89/Domain: immunoglobulin homology <IMM>
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December 23, 2002, 07:16:17; Search time 10.6744 Seconds (without alignments) 419.643 Million cell updates/sec
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558
1 DIELTQSPAIMSASPGEKVT.....QRSSYPFTFGSGTKLEIKRA 108
GenCore version 5.1.3 Copyright (c) 1993 - 2002 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                       Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                               112892 seqs, 41476328 residues
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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D Q C LIFETETETETETETETETETETETETETETETETETETET	688888444444444446080000000000000000000		

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This SWISS-PROT entry is copyright. It is produced through a collaboration
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InterPro; IPR003596; Ig_v.
Pfam; PF00047; Ig; 1.
SMART; SM00406; IGv; 1.
Immunoqlobulin V region; Hybridoma.
DOMAIN
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                                                                                                                                                                                                                                                                                                                                      EMBL; K00744; AAA38689.1; -.
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84.0%;
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107 AA;
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Best Local Simmatches 89;
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SEQUENCE
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KV6H_MOUSE
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                                                                                                                                                                                                 Mus muscijus (Mouse).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
                                                                                                                                                                                                                                                                                SEQUENCE FFROM N.A.
MEDLINE-83271467; PubMed-6877353;
MEDLINE-83271467; PubMed-6877353;
MEDLINE-83271467; PubMed-6877353;
MEDLINE-83271467; PubMed-6877353;
MEDLINE-83271467; PubMed-6877353;
MEDLINE-83271467; PubMed-6877353;
MEDLINE-83271467; MISSERIA OF 187747;
MEDLINE-83271467;
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COMPLEMENTARITY-DETERMINING-1.
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COMPLEMENTARITY-DETERMINING-3.
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62 SGSGSATSYSLTITSMQAEDAATYYCQQWSSNPLFFGAGTKLELKR 107
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Pred. No. 5.5e-39;
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13-AUG-1987 (Rel. 05, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
19 kappa chain V-VI region NQ5-78.2.6.
Mus misculus (Mouse).
                                                                                                                               13-AUG-1987 (Rel. 05, Created)
13-AUG-1987 (Rel. 05, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
Ig kappa chain V-VI region NQ6-8.3.1.
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InterPro I PR003596; Ig_v.
Pfam, PR0047; Ig_1.
Immunoglobulin V region; Hybridoma.
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83.0%;
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                                                                                    KV61_MOUSE
P04943;
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
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                                                                                                                                       SEQUENCE FROM N.A.

MEDLINE-83721467; PubMed=6877353;

Kaartinen M., Griffiths G.M., Markham A.F., Milstein C.;

"mRNA sequences define an unusually restricted IgG response to 2-
phenyloxazolone and its early diversification.";

Nature 304:320-324(198).

-i - FUNCTION: ANTI-2-PHENYL OXAZOLONE (PHOX) ANTIBODY.
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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SEQUENCE FROM N.A.

RABELINE=83271467; PubMed=6877353;

Kaartinen M., Griffiths G.M., Markham A.F., Milstein C.;

"mRAN sequences define an unusually restricted IgG response 1
phenyloxazolone and its early diversification.";

Nature 304:320-324(1983).

-i. FUNCTION: ANTI-2. PHENYL OXAZOLONE (PHOX) ANTIBODY.
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COMPLEMENTARITY-DETERMINING-1.
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COMPLEMENTARITY-DETERMINING-2.
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Pred. No. 5.5e-39;
5; Mismatches 12; Indels
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15-JUL-1999 (Rel. 38, Last annotation update)
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BY SIMILARITY.
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[mmunoglobulin
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between the Swiss Institute of Bioinformatics and the EMBL outstation -
the European Bioinformatics Institute. There are no restrictions on its
use by non-profit institutions as long as its content is in no way
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                                modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                            2 IELTQSPAIMSASPGEKVTITCSASSSVSYMHWFQQKPGTSPKLWIYSTSNLASGVPARF 61
                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus
NCBL_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
MEDLINE-83271467; PubMed-6877353;
Raartinen M., Gilffiths G.M., Markham A.F., Milstein C.;
Ranka sequences define an unusually restricted IgG response to phenyloxazolone and its early diversification.";
Nature 304:1220-334(1983).
                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                                                                                               Length 107;
                                                                                                                                                                             COMPLEMENTARITY - DETERMINING - 1.
                                                                                                                                                                                                    COMPLEMENTARITY-DETERMINING-2.
                                                                                                                                                                                                                          COMPLEMENTARITY-DETERMINING-3.
FRAMEWORK-4.
                                                                                                                                                                                                                                                                                                                      11; Indels
                                                                                                                                                                                                                                                                                                                                                                                          62 SGSGSGTSYSLTISRMEAEDAATYYCQQRSSYPFTFGSGTKLEIKR 107
                                                                                                                                                                                                                                                                                                                                                                                                        11605 MW; CA6C4284ECFCB550 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -1- FUNCTION: ANTI-2-PHENYL OXAZOLONE (PHOX) ANTIBODY.
                                                                                                                                                                                                                                                                                               81.7%; Score 456; DB 1;
83.0%; Pred. No. 6.9e-39;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            13-AUC-1987 (Rel. 05, Created)
13-AUG-1987 (Rel. 05, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
18 kappa chain V-VI region NQ2-48.2.2.
Mus musculus (Mouse).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          107 AA.
                                                                                                                                                                                                                                                                                                                      7; Mismatches
                                                                                                                                                                                                                                                   BY SIMILARITY.
                                                                                                                                                                  FRAMEWORK - 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     or send an email to license@isb-sib.ch).
                                                                                                                                                                                          FRAMEWORK-2
                                                                                                                                                                                                                FRAMEWORK - 3
                                                                                                                                                   Immunoglobulin V region; Hybridoma
                                                                               EMBL; K00739; AAA38684.1; -. HSSP; P01679; 2FBJ.
                                                                                                     InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_V.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_v.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; K00737; AAA38682.1; -
                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STANDARD;
                                                                                                                            Pfam; PF00047; ig; 1.
SMART; SM00406; IGv; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pfam; PF00047; ig; 1.
SMART; SM00406; IGv; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          HSSP; P01679; 2FBJ.
                                                                                                                                                                                                                                                                      107 AA;
                                                                                                                                                                                                                                                                                                           Best Local Similarity
                                                                                                                                                                                                                                                                                                                      88;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           KV6G_MOUSE
                                                                                                                                                                                                                                    DOMAIN
DISULFID
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SEQUENCE
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                                                                                                                                                                                                                                                                                                                       Matches
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                    Gaps
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                          2 IELTQSPAIMSASPGEKVTITCSASSSVSYMHWFQQKPGTSPKLWIYSTSNLASGVPARF
                                                                                                                                                                                                                                                                                                                              1 ILLIQSPAIMSASPGQKVIMTCSASSSVSYMHWYQQKSGISPKRWIYDTSKLASGVPARF
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                                                                                                                                                                                                                                                                  ö
                                  COMPLEMENTARITY - DETERMINING - 1.
                                                    FRAMEWORK-2.
COMPLEMENTARITY-DETERMINING-2.
                                                                                                                                                                                                                            Length 107;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FRAMEWORK-2.
COMPLEMENTARITY-DETERMINING-2.
                                                                                                          COMPLEMENTARITY - DETERMINING - 3.
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3 COMPLEMENTARITY-DETERMINING-48 FRAMEWORK-2.
55 COMPLEMENTARITY-DETERMINING-87 FRAMEWORK-3.
98 COMPLEMENTARITY-DETERMINING-108 FRAMEWORK-3.
108 FRAMEWORK-4.
87 BY SIMILARITY.
108
11713 MW; DABF235CD9680AC6 CRC64;
                                                                                                                                                                                                                                                                    11; Indels
                                                                                                                                                                                                                                                                                                                                                                                    62 SGSGSGTSYSLTISRMEAEDAATYYCQQRSSYPFTFGSGTKLEIKR 107
                                                                                                                                                                                                                                                                                                                                                                                                      72488DA9EF354934 CRC64;
                                                                                                                                                                                                                            Score 455; DB 1;
Pred. No. 8.7e-39;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 450; DB 1;
Pred. No. 2.8e-38;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            13-AUG-1987 (Rel. 05, Created)
13-AUG-1987 (Rel. 05, Last sequence update)
13-UUL-1999 (Rel. 38, Last annotation update)
1g kappa chain V-VI region NO2-6.1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AA.
                                                                                                                                                BY SIMILARITY
                                                                                                                                                                                                                                                                  7; Mismatches
                                                                                          FRAMEWORK-3.
              FRAMEWORK-1
                                                                                                                                FRAMEWORK - 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Immunoglobulin V region; Hybridoma
DOMAIN
region; Hybridoma
                                                                                                                                                                                      11556 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; K00746; AAA38691.1; -. HSSP; P01679; 2FBJ.
                                                                                                                                                                                                                            81.5%;
83.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_V.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           80.6%;
82.2%;
                                                                                                                                                                                                                                                                    88; Conservative
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                  23
33
48
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106
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SMART; SM00406; IGv; 1.
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88
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108
                                                                                                                                                                                                                                                  Similarity
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                                                                                                                                                                                      107 AA;
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34
49
56
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97
107
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    KV6K_MOUSE
P04945;
                                                                                                                              DOMAIN
DISULFID
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DISULFID
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SEQUENCE
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SEQUENCE
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MEDLINE—81054757; PubMed-6776525;

A Rudikoff S., Rao D.N., Glaudemans C.P.J., Potter M.;

Rudikoff S., Rao D.N., Glaudemans C.P.J., Potter M.;

Rudikoff S., Rao D.N., Glaudemans C.P.J., Potter M.;

Combining sites.";

Proc. Natl. Acad. Sci. U.S.A. 77:4270-4274(1980).

LI Proc. Natl. Acad. Sci. U.S.A. 77:4270-4274(1980).

Proc. Natl. Acad. Sci. U.S.A. 77:4270-4274(1980).

BIND GALACTAN.

PROC. PIR, A01941; KVMSX4.

RICHARD. PROC. PROC
                                                                                                                               Biochemistry 17:5555-559(1978).
-1- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM A MYELOMA PROTEIN THAT BIND GALACTAN.
PIR; A01941; KVMSX4.
HSSP; P01679; 2FBJ.
InterPro; IPR003006; Ig_MHC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 DIELTQSPAIMSASPGEKVTITCSASSSVSYMHWFQQKPGTSPKLWIYSTSNLASGVPAR 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
                                                                               Rao D.N., Rudikoff S., Potter M.;
"k Chain variable regions from three galactan binding myeloma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FRAMEWORK-1.
COMPLEMENTARITY-DETERMINING-1..
FRAMEWORK-2.
                                                                                                                                                                                                                                                                                                                                  FRAMEWORK-2.
COMPLEMENTARITY-DETERMINING-2.
                                                                                                                                                                                                                                                                                                                  COMPLEMENTARITY - DETERMINING-1.
                                                                                                                                                                                                                                                                                                                                                                                COMPLEMENTARITY - DETERMINING - 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   61 FSGSGSGTSYSLTISRMEAEDAATYYCQQRSSYP-FTFGSGTKLEIKR 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                  11627 MW; 27A2D022BC0A34D7 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 430; DB 1; I
Pred. No. 2.7e-36;
6; Mismatches 12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
IIG kappa chain V-VI region SAPC 10.
Mus musculus (Mouse).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    107 AA
                                                                                                                                                                                                                                                                                                                                                                                                 FRAMEWORK-4.
BY SIMILARITY
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                                                SEQUENCE.
MEDLINE=79082830; PubMed=103573;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  77.1%;
81.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    · STANDARD;
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SMART; SM00406; IGv; 1.
Immunoglobulin V region.
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                107 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Similarity
                 NCBI_TaxID=10090;
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P01678;
                                                                                                               proteins.
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DISULFID
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SEQUENCE
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-!- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM A MYELOMA PROTEIN THAT
BIND GALACTAN.
 Gaps
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                                                               61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2 IELTØSPAIMSASPGEKVTITCSASSSVSYMHWFQQKPGTSPKLWIYSTSNLASGVPARF 61
                                                21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
15-AUL-1999 (Rel. 38, Last annotation update)
16 kappa chain VI region XRPC 24.

Mus muschius (Mouse)

Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostoml;

Mammaliag. Eutheria; Rodentia; Sciurognathi; Muridae; Musinse; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
15-JUL-1999 (Rel. 38, Last annotation update)
19 kappa chain V-VI region XRPC 44.
Mus musculus (Mouse).
Eukarigta: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   5;
                                                                                                                                                                                                                                                                                                                                                                                                                               Rao D.N. Rudikoff S., Potter M.;
"K Chain variable regions from three galactan binding myeloma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPLEMENTARITY - DETERMINING - 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPLEMENTARITY-DETERMINING-3.
FRAMEWORK-4.
BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 107;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPLEMENTARITY - DETERMINING - 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                12; Indels
                                                                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MW; 36E6D022A5EC34D7 CRC64;
 7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 77.6%; Score 433; DB 1; 82.4%; Pred. No. 1.4e-36;
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5; Mismatches
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 10; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE MEDLINE-799082830; PubMed-103573;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PIR; AO1941; KVMSX4.
HSSP; PO1679; 2FBJ.
InterProf; IPR003006; Ig_MHC.
InterProf; IPR003596; Ig_V.
Pfam; PPR0047; Ig; I.
SMART; SM00406; IGV; I.
Immunoglobulin V region.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  11584
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Local Similarity 82.4 tes 89; Conservative
88% Conservative
                                                                                                                                                                                                                  STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STANDARD;
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                                                                                                                                                                                             MOUSE KV6B_MOUSE P01676;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                KV6A_MOUSE
P01675;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 proteins(.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DOMAIN
DISULFID
NON_TER
SEQUENCE
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ID KV6A_MC
AC PO1675/
DT 21-JUL
DT 21-JUL
DT 15-JUL
DT 15-JUL
OS MUS MUS
OC BUKATY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DOMAIN
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                                                                                                                                                                                                  KV6B_MOUSE
 Matches
                                                                                                  62
                                                                                                                               62
                                                                                                                                                                             RESULT 7
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Length 107;

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Proteins 1:74-80(1986).
-!- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM A MYELOMA PROTEIN THAT
BIND GALACTAN.
 X-RAY CRYSTALLOGRAPHY (2.6 ANGSTROMS).
MEDLINE-8217852; Pubmed-3449953;
Suh S.W., Bhat T.N., Navia M.A., Cohen G.H., Rao D.N., Rudlkoff S.,
Davies D.R.;
                                                                                                                                                                                                                                                                                                                                        "The galactan-binding immunoglobulin Fab J539: an X-ray diffraction study at 2.6-A resolution.";
                                                                                                                                                                                                                                             Rudikoff S., Rao D.N., Glaudemans C.P.J., Potter M.;
Kappa Chabin joining segments and structural diversity of antibody
combining sites.";
Proc. Natl. Acad. Sci. U.S.A. 77:4270-4274(1980).
                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FRAMEWORK - 3.
COMPLEMENTARITY - DETERMINING - 3.
                                         FSGSGSGTSYSLTISRMEAEDAATYYCQQRSSYP-FTFGSGTKLEIKR
                                                                                                                         21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
15 Appa chain V-VI region J539.
Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FRAMEWORK-1.
                                                                                                       107
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                                                                                                                                                                                                                                  MEDLINE-81054757; PubMed-6776525;
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48
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11502 MW;
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PDB; 2FBJ; 15-OCT-90.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_V.
                                                                                                                                                                                                                                                                                                                                                                                                                                       Pfam; PF00047; ig; 1.
SMART; SM00406; IGv; 1.
Immunoglobulin V region;
                                                                                                        STANDARD;
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94
101
107
107 AA;
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                                                                                                      KV6E_MOUSE
P01679;
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KV6E_MOUSE
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                                                                                                                           1 DIELTQSPAIMSASPGEKVTITCSASSSVSYMHWFQQKPGTSPKLWIYSTSNLASGVPAR 60
                                                                                                                                      MEDLINE-81054757; Pubwed-6776525; Red D.N., Glaudemans C.P.J., Potter M.; Rabo D.N., Glaudemans C.P.J., Potter M.; Kappa Chain joining segments and structural diversity of antibody combining sites."; Proc. Natl. Acad. Sci. U.S.A. 77:4270-4274(1980).
-i. MISCELLANBOUG: THESE CHAINS WERE ISOLATED FROM MYELOMA PROTEINS
                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBL_TaxID-10090;
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SEQUENCE (TEPC 601).
MEDLINE-79082830; PubMed=103573;
RAO D.N., Rudikoff S., Potter M.;
"k Chain variable regions from three galactan binding myeloma proteins.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPLEMENTARITY - DETERMINING-1.
 COMPLEMENTARITY - DETERMINING - 2.
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                    COMPLEMENTARITY - DETERMINING - 3
                                                                                  Length 107
                                                                                                                                                                     61 FSGSGSGTSYSLTISRMEAEDAATYYCQQRSSYP-FTFGSGTKLEIKR 107
                                                                                                                                                                                 Score 428; DB 1; Length 10
Pred. No. 4.3e-36;
7; Mismatches 12; Indels
                                                                                                      13; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             11568 MW; 203CD752A5EC34D7 CRC64;
                                                             11554 MW; 27A2D022A5EC34D7 CRC64;
                                                                                 Score 429; DB 1;
Pred. No. 3.4e-36;
5; Mismatches 13,
                                                                                                                                                                                                                                                               21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
18 kappa chain V-VI region TEPC 601/TEPC 191.
Mus musculus (Mouse)
                                                                                                                                                                                                                                             107 AA
                               FRAMEWORK-4.
BY SIMILARITY.
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           FRAMEWORK - 3
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                                                                                                                                                                                                                                                                                                                                                                                                                   Biochemistry 17:5555-5559(1978).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      THAT BIND GALACTAN.
PIR; A01941; KYMSX4.
HSSP; P01679; 2FBJ.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_V.
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80.6%;
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81.5%;
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hes 88; Conservative
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SMART; SM00406; IGv; 1.
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P01677;
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EA30C9A3E903979C CRC64;

1 DIELTQSPAIMSASPGEKVTITCSASSSVSYMHWFQQKPGTSPKLWIYSTSNLASGVPAR 60

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26 LTQSPAIMAASLGQKVTMTCSASSSVSSSVLHWYQQKSGASPKPLIHRTSNLASGVPARF 85
                                                                                                                                                                                                                                                                                                                                              diversity.";
Nature 276:785-790(1978).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                            STANDARD;
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P04430;
                                                                                                                            KV3M_MOUSE
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MEDLINE=82115300; PubMed=6799208;
MEDLINE=82115300; PubMed=6799208;
MEDLINE=82115300; PubMed=6799208;
MEDLINE=8215300; MEDLINE SECONDIAN GROWN STORM TO STORE THE MY SECURATION OF TWO RAPPO AS A THE V-J RECOMBINATION SITE (AFTER POSITION 118), IS SYNTHESIZED BUT NOT SECRETED IN CELLS THAT EXPRESS AND SECRETE THE NORMAL KAPPA CHAIN S107.
                                       Gaps
                                                                  DIELTOSPAIMSASPGEKVTITCSASSSVSYMHWFQQKPGTSPKLWIYSTSNLASGVPAR 60
                                                                                  4; Gaps
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                                                                                                                                                                                                                                                                                                               Mus musculus (Mouse).
Sukaryoja, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
NCBI_TaxiD=10090.
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           Length 107;
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FRAMENORK-1.
COMPLEMENTARITY-DETERMINING-1.
FRAMEWORK-2.
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COMPLEMENTARITY-DETERMINING-3.
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                                                                                                                         Ouery Match

73.5%; Score 410; DB 1; Length 12.
Best Local Similarity 80.2%; Pred. No. 3.3e-34;
Matches 85; Conservative 7; Mismatches 10; Indels
                                      13; Indels
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          Score 413; DB 1;
Pred. No. 1.3e-34;
9; Mismatches 13,
                                                                                                                                                                                                                                                     21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
21-JUL-1999 (Rel. 38, Last annotation update)
19 kappa chain V-IV region S1078 precursor.
                                                                                                                                                                                                                            129 AA
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HSSP; E01679; ZFBJ.
InterPig: IPR003306; Ig_MHC.
InterPig: IPR003306; Ig_W.
Pfam: PF00047; 1g; 1.
SMART; $5000406; IGV.
Immunoglobulin V region; Signal.
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13833 MW;
        74.0%;
nilarity 77.8%;
Conservative 9
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129
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           al Similarity
84; Corr
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129 AA;
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P01680;
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KV4A_MOUSE
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                                      Matches
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Gaps
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Mammalia; Euthazia; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DIELTQSPAIMSASPGEKVTITCSASSSV----SYMHWFQQKPGTSPKLWIYSTSNLAS
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                                                                                                                                                                                                                                                                                                                                                                                        Weigert M., Gatmaitan L., Loh E., Schilling J., Hood L.E.; "Rearrangement of genetic information may produce immunoglobulin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             5.
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Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
111
12002 MW; 7A5FCB586C306D29 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    66.9%; Score 373.5; DB 1;
65.8%; Pred. No. 1.2e-30;
tive 13; Mismatches 20;
                                                                                                                                                                         21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
Mus musculus (Mouse).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                13-AUG-1987 (Rel. 05, Created)
13-AUG-1987 (Rel. 05, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
Ig kappa chain V-I region BAN.
                                                                                                                                        111 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE-86174817; PubMed-3083240;
Dwulet F.E., O'Connor T.P., Benson M.D.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FRAMEWORK - 3
                                                                                                                                      PRT;
                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=79073152; PubMed=103003;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PIR; A01937; KVMS43.
HSSP; P80362; 1WTL.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_V.
Pfam; PF00047; ig; 1.
SWART; SMART; IGY.
Immunoglobulin V region.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 DIELTQSPAIMSASPGEKVTITCSASSSV-SYMHWFQQKPGTSPKLWIYSTSNLASGVPA 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1; Gaps
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Sukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus
NCBI_TaxID=10090;
"Polymorphism in a kappa I primary (AL) amyloid protein (BAN).";
Mol. Immunol. 23:73-78(1986).
HSP; AOLBY 8; KIHUBN.
HSSP; P80362: 1WTL.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003556; Ig_V.
Pfam: PF00047; Ig; 1.
SWART; SM00406; IGV; 1.
Immunoglobulin V region; Amyloid.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE-79073152; PubMed-103003; Weigert M., Gatmaitan L., Loh E., Schilling J., Hood L.E.; "Rearrangement of genetic information may produce immunoglobulin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          .;
2
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COMPLEMENTARITY-DETERMINING-2.
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COMPLEMENTARITY-DETERMINING-1.
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COMPLEMENTARITY-DETERMINING-3.
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21-JUL-1986 (Rel. 01, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
19 kappa chain V-III region PC 6308.
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PIR, C01937; KVMSO8.
HSSP; P80302; JWTL.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_V.
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SMART; SM00406; IGv; 1.
Immunoglobulin V region.
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RV30_MOUSE
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DT 21-JUL
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DT 15-JUL
DT 15-JUL
OC BURATY
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Q9u181 homo sapien

4 Q9UL81

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1 DIELTQSPAIMSASPGEKVT.....QRSSYPFTFGSGTKLEIKRA 108
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Copyright (c) 1993 - 2002 Compugen Ltd.
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8: sp_organelle:* 9: sp_phage:* 10: sp_plant:* 11: sp_rodent:* 12: sp_virus:* 13: sp_virus:* 14: sp_unclassified:* 15: sp_rvirus:* 16: sp_bacteriap:* 17: sp_archeap:* 17: sp_archeap:* 17: sp_archeap:* 18: sp_archeap:* 19: sp_archeap:* 10: sp_archeap:* 10: sp_archeap:* 11: sp_archeap:* 12: sp_archeap:* 13: sp_archeap:* 14: sp_archeap:* 15: sp_archeap:* 16: sp_archeap:* 17: sp_archeap:* 18: sp_archeap:* 19: sp_archeap:* 10: sp_archeap:* 11: sp_archeap:* 12: sp_archeap:* 13: sp_archeap:* 14: sp_archeap:* 15: sp_archeap:* 16: sp_archeap:* 17: sp_archeap:* 18: sp_archeap:* 18: sp_archeap:* 19: sp_archeap:* 19: sp_archeap:* 10: sp_archeap:* 11: sp_archeap:* 12: sp_archeap:* 13: sp_archeap:* 14: sp_archeap:* 15: sp_archeap:* 16: sp_archeap:* 16: sp_archeap:* 17: sp_archeap:* 18: sp_archeap:* 18: sp_archeap:* 19: sp_archeap:* 19: sp_archeap:* 10: sp_archeap:* 11: sp_archeap:* 12: sp_archeap:* 13: sp_archeap:* 14: sp_archeap:* 15: sp_archeap:* 16: sp_archeap:* 16: sp_archeap:* 17: sp_archeap:* 18: sp_archeap:* 18: sp_archeap:* 18: sp_archeap:* 19: sp_archeap:* 19: sp_archeap:* 10: sp_ar

sp_fungi:*
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and is derived by analysis of the total score distribution.	ES	Description	OBVAGO musculu	Q9u410 schistosoma	091w12 mus musculu	Q9j176 mus musculu	Q9j178 mus musculu	Q8r062 mus musculu	Q9rla5 mus musculu	Q9ul77 homo sapien	Q920e9 mus musculu	Q96sa9 homo sapien			Q9ul79 homo sapien	uns	Q8vcp0 mus musculu	Q91ws9 mus musculu
of the tot	SUMMARIES	9	Q8VDD0	Q9U410	Q91W12	09JL76	Q9JL78	Q8R062	Q9R1A5	Q9UL77	Q920E9	Q96SA9	09UL78	Q9UL70	Q9UL79	Q91WF8	Q8VCP0	091WS9
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2 IELTQSPAIMSASPGEKVTITCSASSSVSYMHWFQQKPGTSPKLWIYSTSNLASGVPARF 61

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63.3 107 4 090L81 62.3 109 11 090C86 62.1 108 4 090L83 61.4 107 11 095L84 61.5 109 4 090L83 60.5 108 11 099M37 57.9 238 11 099M37 57.6 123 10 090C5 57.6 123 11 095C89 57.6 123 11 095C89 57.6 123 11 095C89 57.6 123 11 095C89 57.7 10 095C81 57.8 108 4 080C8 57.9 233 4 080C8 57.9 233 4 080C8 57.9 233 4 080C8 57.9 233 4 080C8 57.9 234 11 095C8 57.9 234 1 095C8 60.000C8 60.00C8 6	the EN th	Similarity 89.7%; Score 502; DB Similarity 89.7%; Pred. No. 3.8e-96; Conservative 4; Mismatches
11/ 11/ 11/ 11/ 11/ 11/ 11/ 11/	RESULT 1 Q8VDD0 LD Q8VDD0 DT Q8VDD0; DT 01-MAR-2002 (TrEMBLrel.) DE Anti-MOG Z12 variable 1: GN ANTI-MOG KAPPA. OS MUS MUSCHUS (MOUSE). OC EUKARYOTA: METAZOS; CHOOCO. OX NCBL_TAXID=10090; RN (1) RP SEQUENCE FROM N.A. RC STRAIN=BALB/C; RA CHERTAIN=BALB/C; RA CHERTAIN=BALB/C; RA SEQUENCE FROM N.A. RC STRAIN=BALB/C; RA SEQUENCE FROM N.A. BRANT; SMO04005; IG. 1. DR SMART; SMO04005; IG. 1.	Query Match Best Local Simi Matches 96;
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87; Conservative
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                         Best Local Similarity
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01-OCT-2000 (
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                                                                                                                                                                                                                                                        A SEQUENCE FROM N.A.

A SONG X.T., Feng Z.Q., Qiu Z.N., Li Y.Q., Huang H.L., Guan X.H.;

XT "Amplification, cloning and sequence analysis of the light chain

XT variable region gene of monoclonal anti-idiotypic antibody NP30 of

XI Schistosoma japonicum.";

XI Schistosoma japonicum.";

XI SCHISTOSOMA JAF207620, AAF19434.1;

XI SHESP: PO1679; ZFBJ.

XI INTERPRO: IPR003006; Ig_MHC.

XI INTERPRO: IPR003596; Ig_V.

XI RSPR: SMART; SM00406; IGV.

XI NON_TER
                                                                                                                                                                                                  Schistosoma japonicum (Blood fluke).
Eukaryota: Metazoa; Platyhelminthes; Trematoda; Digenea; Strigeidida;
Schistosomatoidea; Schistosomatidae; Schistosoma.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
             83
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              4 LTQSPAIMSASPGEKVTMTCSASSSVSYVYWYLQKPGSSPRLLIYDTSNLASGVPVRFSG 63
                                                                                                                                                   01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
Monoclonal anti-idiotypic antibody NP30 immunoglobulin light chain
24 IVLTQSPAIMSASPGEKVTMTCSASSSISYMHWYQQRPGTSPRRWIYDTSKLASGVPARF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metaria; Crondata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. NCBI_TaxID=10090;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 106;
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 470; DB 5; Length 10
Pred. No. 6.5e-42;
8; Mismatches 5; Indels
                                 Strausberg R.;
Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases.
Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; BC006643; AAH06643.1; -.
Pfam; PF00047; ig; 2.
PROSITE; PS00290; IG_MHC; UNKNOWN_1.
SEQUENCE 235 AA; 26021 MW; 5FC73BDBBD5EBFEF CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                               NON_TER 106 106
SEQUENCE 106 AA; 11478 MW; F20F544426BAE63E CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          091W12;
01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
Unknown (protein for MGC:6582).
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TISSUE-BREAST TUMOR;
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Q91W12
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                                                                                               2 IELTQSPAIMSASPGEKVTITCSASSSVSYMHWFQQKPGTSPKLWIYSTSNLASGVPARF 61
                                                                                                                       24 IVLIQSPAIMSASPGERVTMICSASSSVSHMHWYQQKSGTSPKRWIYDFFKLISGVPDRF 83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        11 MSASPGEKVTITCSASSSVSYMHWFQQKPGTSPKLWIYSTSNLASGVPARFSGSGSGTSY 70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (Fragment).
Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Malkiel S., Liao L., Cunningham M.W., Diamond B.; "T-Cell-dependent antibody response to the dominant epitope of streptococcal polysaccharide, N-acetyl-glucosamine, is cross-re
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 434.5; DB 11; Length 97;
Pred. No. 3.1e-38;
7; Mismatches 5; Indels 1
  Length 235;
                                                  15; Indels
                                                                                                                                                                                                                62 SGSGSGTSYSLTISRMEAEDAATYYCQQRSSYPFTFGSGTKLEIKRA 108
                                                                                                                                                                                                                                                                                                                                                                                                 01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-OCT-2001 (TrEMBLrel. 19, Last annotation update)
Anti-myosin immunoglobulin light chain variable region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-0CT-2000 (TrEMBLrel. 15, Created)
01-0CT-2000 (TrEMBLrel. 15, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
Anti-myosin immunoglobulin light chain variable region (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE 97 AA; 10542 MW; C9EE1FFE1F49DA1C CRC64;
Score 442; DB 11;
Pred. No. 1.5e-38;
5; Mismatches 15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 71 SLTISRMEAEDAATYYCQQRSS-YPFTFGSGTKLEIK 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           97 AA
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                                                                                                                                                                                                                                                                                                                                                      PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=20448942; Pubmed=10992488;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      with cardiac myosin.";
Infect. Immun. 68:5803-5808(2000).
EMBL; AF206030; AAF69328.1; -.
HSSP; P01679; 2FBU.
79.2%;
81.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             77.9%;
86.6%;
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InterPro; IPR003596; Ig_v.
Pfam; PF00047; ig; 1.
SMART; SM00406; IGv; 1.
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Wide K.G., Yu X., Ekramoddoullah A.K.M., Misra S.;

"Cloning of cDNAs encoding for anti-white pine blister rust monoclonal antibody (MaD 7, its light and heavy chains) and construction of a single chain antibody (scFV).";

Submitted (MAY-1999) to the EMBL/GenBank/DDBJ databases.

EMBL; AF152371; AAD40242.1;

EMBL; AF152371; AAD40242.1;

InterPro; IPR003006; Ig_like.

InterPro; IPR003006; Ig_MHC.

InterPro; IPR003006; Ig_WHC.

SMART; SM00406; Ig', 1.

SWART; SM00406; IG', 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 DIELTQSPAIMSASPGEKVTITCSASSSV-SYMHWFQQKPGTSPKLWIYSTSNLASGVPA 59
 Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         'Myosin-reactive autoantibodies in rheumatic carditis and normal
                                                                                                                                                                                                                                                                                                                                                                                                                                                  1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1;
                                                                                                                                                                                                                                                                                                                                                                                                                 DB 11; Length 214;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
MEDLINE-98277139; PubMed-9614934;
Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-WAY-2000 (TrEMBLrel. 13, Created)
01-WAY-2000 (TrEMBLrel. 13, Last sequence update)
01-DBC-2001 (TrEMBLrel. 19, Last annotation update)
Myosin-reactive immunoglobulin light chain variable region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   60 RFSGSGSGTSYSLTISRMEAEDAATYYCQQRSSYPFTFGSGTKLEIKRA 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 371.5; DB 11; Lews-
Pred. No. 3.3e-31;
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108 AA; 11738 MW; C06681716C4D16F3 CRC64;
                                                                                                                                                                                                                                                                                                                                                                             214 AA; 23922 MW; 52BA205FDE995E2A CRC64;
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63.9%; Pred. No. 6.3e-31;
ive 20; Mismatches 18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Clin. Immunol. Immunopathol. 87:184-192(1998).
EMBL; AF035037; AAD56273.1; -.
HSSP; PO1607; IREI.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_V.
                                                                                                                                                                                                                                                                                                                                                                                                                                                9; Mismatches
                                                                                                                                                                                                                                                                                                                              PROSITE; PS00290; IG_MHC; UNKNOWN_1.
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                                                                                                                                                                                                                                                                                                                                                                                                               66.68;
67.08;
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Best Local Similarity o...
And 73; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pfam; PF00047; 19; 1.
SMART; SM00406; IGV; 1.
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                                                                                    SEQUENCE FROM N.A.
                                                      NCBI_TaxID=10090;
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Q9UL77
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        STRIN-A.CA;

X MEDLINE-20448942; PubMed=10992488;

XA MAIKiel S., Liao L., Cunningham M.W., Diamond B.;

RT "T-Cell-dependent antibody response to the dominant epitope of
RT streptococcal polysaccharide, N-acetyl-glucosamine, is cross-reactive
RT with cardiac myosin.";

RT Linfect. Immun. 68:5803-5808(2000).

DR REMB; AP206028; AAF69326.1; -
DR HSSP; P01679; 2FBJ.

DR HSSP; P01679; 2FBJ.

DR InterPro; IPR003966; Ig_WHC.

DR InterPro; IPR003966; Ig_W.

DR Pfam; PF00047; Ig; 1.

DR SMART; SM00406; IGv; 1.

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 DIQMIQITSSLSASLGDRVIISCSASQGISNYLNWYQQKPDGTVKLLIYYTSSLHSGVPS 80
                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                             1 DIELTQSPAIMSASPGEKVTITCSASSSVS-YMHWFQQKPGTSPKLWIYSTSNLASGVPA 59
                                                                                                                                                                                                                                                                                                                                                                            11 MSASPGEKVTITCSASSSVS--YMHWFQQKPGTSPKLWIYSTSNLASGVPARFSGSGSGT 68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-JUN-2002 (TrEMBLrel. 21, Created)
01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Hypothetical 25.9 kba protein.
Mus musculus (Mouse).
Mus musculus (Mouse).
Musmmalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Musculus)
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                                                                                                                                                                                                                                                                                                       72.3%; Score 403.5; DB 11; Length 101; 80.8%; Pred. No. 5.9e-35; ative 6; Mismatches 10; Indels 3;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Straubberg R.;
Straubberg R.;
Submitted (APR-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; BCO27418; AAH27418.1; -.
Hypothetical protein.
SEQUENCE 234 AA; 25857 MW; 4EB08C81426AEABI CRC64;
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(TrEMBLrel. 13, Last sequence update)
(TrEMBLrel. 19, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                              SYSLTISRMEAEDAATYYCQQRSSYP-FTFGSGTKLEIK 106
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01-WAY-2000 (TrEMBLrel. 13, Last sequ
01-DEC-2001 (TrEMBLrel. 19, Last anno
Kappa light chain of Mab7 (Fragment).
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Matches 80; Conservative
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SEQUENCE FROM N.A.
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Q8R062;
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Q9UL70
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                                                                                                                                                                                                                                                                                                                                                                                                                                1 DIELTQSPAIMSASPGEKVTITCSASSSV----SYMHWFQQKPGTSPKLWIYSTSNLAS 55
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostoml;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-MR-2002 (TrEMBLrel. 20, Last annotation update)
Anti-streptococcal/anti-myosin immunoglobulin kappa light chain variable region (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE-98375893; PubMed-9712075; Adderson E.E., Shikhman A.R., Ward K.E., Cunningham M.W.; Modecular analysis of polyreactive monoclonal antibodies from rheumatic carditis: human anti-N-acety1glucosamine/anti-myosin
                                                                                                                                                                                                                                                                                                                                                                                      DB 11; Length 111;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             56 GVPARFSGSGSGTSYSLTISRMEAEDAATYYCQQRSSYPFTFGSGTKLEIK 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
Pterin-mimicking anti-idiotope kappa chain variable region
                                              60 RFSGSGSGTSYSLTISRMEAEDAATYYCQQRSSYPFTFGSGTKLEIKR 107
                                                                                                                                                                                                                                                                                                                                                                                    Ouery Match 65.5%; Score 365.5; DB 11; Length
Best Local Similarity 64.9%; Pred. No. 6.5e-31;
Matches 72; Conservative 10; Mismatches 24; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      antibody V region genes.";
J. Immunol. 161:2020-2031(1998).
EMBL: UG6396; AAB68785.1;
InterPro: IPR003006; Ig_MHC.
                                                                                                                PRELIMINARY;
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                                                                                                                                                                                                                             NCBI_TaxID=10090;
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NCBI_TaxID=9606;
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                                                                                                                                                                                              Mus musculus
                                                                                                                                                                                  (Fragment)
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NON_TER
SEQUENCE
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Q96SA9
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                                                                                                                                                         1 DIELTQSPAIMSASPGEKVTITCSASSSV-SYMHWFQQKPGTSPKLWIYSTSNLASGVPA 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 DIELTQSPAIMSASPGEKVTITCSASSSV--SYMHWFQQKPGTSPKLWIYSTSNLASGVP 58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (Fragment).
Homo sapiens (Human).
Eukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Myosin-reactive autoantibodies in rheumatic carditis and normal
                                                                                                       5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE-98277139; Pubmed-9614934; Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M., Young D.C.;
                                                 Length 107;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 109;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
Myosin-reactive immunoglobulin light chain variable region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last Sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
Myosin-reactive immunoglobulin light chain variable region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           59 ARFSGSGSGTSYSLTISRMEAEDAATYYCQQRSSYPFTFGSGTKLEIKR 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         61 DRFSGSGSGTDFTLTISRLEPEDCAVYYCQQYGSSPLTFGGGTKVEIKR 109
                                                                                                                                                                                                                                                              60 RFSGSGSGTSYSLTISRMEAEDAATYYCQQRSSYPFTFGSGTKLEIKR 107
                                                                                                                                                                                                                                                                                            61 RFSGSGSGTDFTLTISSLQPEDFATYXCQQSYS-TLTFGGGTKVEIKR 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 23; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            109 AA; 11646 MW; 5F675C52EC7EE197 CRC64;
11520 MW; 4BB43E9C5B577F16 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        fetus.";
Clin. Immunol. Immunopathol. 87:184-192(1998).
EMBL, APO35036; AAD56272.1;
HSSP. P80362; 1WTL.
InterPro: IPR003006; Ig_MHC.
InterPro: IPR003309; Ig_V.
R Ffam; PP00047; Ig; 1.
R SMART; SM00406; IGV; 1.
                                              64.7%; Score 361; DB 4;
64.8%; Pred. No. 1.8e-30;
ive 19; Mismatches 17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           64.7%; Score 361; DB 4;
62.4%; Pred. No. 1.9e-30;
ative 16; Mismatches 23.
                                                                                                                                                                                                                                                                                                                                                                                                                                                   109 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRT;
                                                 Query Match
Best Local Similarity 64.8'
Matches 70; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRELIMINARY;
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107 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=9606;
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us-09-865-198-8.rspt

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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                Q91WF8;
01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                234 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Strausberg R.;
Submitted (DEC-2001) to the EMBL/GenBar EMBL, BC019474.1 aA419474.1;
InterPro: IPR003599; Ig.
InterPro: IPR003599; Ig.
InterPro: IPR003506; Ig_MHC.
InterPro: IPR003506; Ig_MHC.
InterPro: IPR003506; Ig_WHC.
InterPro: IPR003506; Ig_MHC.
InterPro: IPR003506; Ig_MHC.
INTERPRO: IPR003506; Ig_W.
SMART; SM00407; Igc1; 1.
SMART; SM00407; IGc1; 1.
PROSITE; PS00290; IG_MHC; UNKNOWN_1.
Hypothetical protein.
SEQUENCE 234 AA; 25702 MW; 102551C5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRT;
                                                                                                 Hypothetical 25.9 kDa protein.
                                                                                                                                                                                                                                                                                                                                        63.98;
                                                                                                                                                                                                                                                                                                                                PRELIMINARY;
                                                                                                                Mus musculus (Mouse).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
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                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                    NCBI_TaxID=10090;
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                                                                                                                                                                                         TISSUE=COLON,
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                                    Q91WF8
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              RESULT 14
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                                                                                                                                                                                                                                                              1 DIELTQSPAIMSASPGEKVTITCSASSSVS-YMHWFQQKPGTSPKLWIYSTSNLASGVPA 59
                                                                                                                                                                                                                                                                            1 DIELTQSPAIMSASPGEKVTITCSASSSV-SYMHWFQQKPGTSPKLWIYSTSNLASGVPA 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota: Metazoa: Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                       Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M., Young D.C.; "Myosin-reactive autoantibodies in rheumatic carditis and normal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "Myosin-reactive autoantibodies in rheumatic carditis and normal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 4; Length 108;
                                                                                                                                                                                                            64.4%; Score 359.5; DB 4; Length 108; 63.9%; Pred. No. 2.7e-30; ive 17; Mismatches 21; Indels 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
Young D.C.;
                                                                                                                                                                                                                                                                                                                                                                                                                            01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
Myosin-reactive immunoglobulin light chain variable region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RFSGSGSGTSYSLTISRMEAEDAATYYCQQRSSYPFTFGSGTKLEIKR 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       61 RFSGSGSGTDFTLTISCLQSEDEATYYCQQYYSFPPTFGQGTKVEIKR 108
                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                60 RFSGSGSGTSYSLTISRMEAEDAATYYCQQRSSYPFTFGSGTKLEIKR 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                108 AA; 11787 MW; DB5845F19724FB4E CRC64;
                                                                                                                                                                                      108 AA; 11633 MW; B7BEDC3E41FCCA37 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      64.1%; Score 357.5; DB 4;
62.0%; Pred. No. 4.4e-30;
.ive 21; Mismatches 19;
                                                         fetus.";
Clin. Immunol. Immunopathol. 87:184-192(1998).
EMBL, AF035044; AAD56280.1;
HSSP. PO1607; 1REI.
InterPro: IPR003006; Ig_MHC.
InterPro: IPR003359; Ig_V.
Fram: PP00047; 1g; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                fetus.";
Clin. Immunol. Immunopathol. 87:184-192(1998).
EMBL; AF035035; AAD56271.1; -.
HSSP; P01607; IREI.
InterPro; IPR003066; Ig_MHC.
InterPro; IPR003566; Ig_W-V.
                                                                                                                                                                                                                                                                                                                                                                                                       108 AA.
                                                                                                                                                                                                                                                                                                                                                                                                       PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
MEDLINE-98277139; PubMed-9614934;
           PubMed=9614934;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local Similarity 62.0%
nes 67; Conservative
                                                                                                                                                                                                                         Local Similarity 63.9%
Les 69; Conservative
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SMART; SM00406; IGv; 1.
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 SEQUENCE FROM N.A.
              MEDLINE=98277139;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 DIELTQSPAIMSASPGEKVTITCSASSSVS-YMHWFQQKPGTSPKLWIYSTSNLASGVPA 59
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01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Hypothetical 25.7 kba protein.
Mus musculus (Mouse).
Mus musculus (Mouse).
Mammalia; Eutheria: Rodentia; Sciurognathi; Muridae; Musimusia; Eutheria: Rodentia; Sciurognathi; Muridae; Musinae; Musinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            %; Score 356.5; DB 11; Length 234;
%; Pred. No. 1.4e-29;
19; Mismatches 20; Indels 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               63.9%; Score 356.5; DB 11; Length 234; 63.3%; Pred. No. 1.4e-29; ive 15; Mismatches 24; Indels 1;
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Strausberg R.;
Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases.
Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; BC015292, AAH15292.1;
InterPro; IPR001066; Ig_MHc.
InterPro; IPR001066; Ig_MHc.
PROSITE; PS000290; IG_MHC; UNKNOWN_1.
PROSITE; PS000962; RIBOSOMAL_S2_1; UNKNOWN_1.
Hypothetical protein.
SEQUENCE 234 AA; 25929 MW; BOD080E6EB7812D2 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL/GenBank/DDBJ databases
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Search completed: December 23, 2002, 07:29:56 Job time : 45.7907 secs

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December 23, 2002, 07:16:08; Search time 9.12597 Seconds (without alignments) 248.221 Million cell updates/sec
GenCore version 5.1.3 Copyright (c) 1993 - 2002 Compugen Ltd.
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                                                                                - protein search, using sw model
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1 WIDPENGDSDYAPKFQG 17
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Maximum Match 100%
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Maximum DB seq length: 2000000000
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                                                                                OM protein
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/SIDS2/gcgdata/geneseg/geneseqp-embl/AA1993.DAT:*/SIDS2/gcgdata/geneseg/geneseqp-embl/AA1994.DAT:*/SIDS2/gcgdata/geneseg/geneseqp-embl/AA1995.DAT:*/SIDS2/gcgdata/geneseg/genesegp-embl/AA1996.DAT:*/SIDS2/gcgdata/geneseg/genesegp-embl/AA1996.DAT:*/SIDS2/gcgdata/geneseg/genesegp-embl/AA1996.DAT:* /SIDS2/gcgdata/geneseg/genesegp-embl/AA1989.DAT:* /SIDS2/gcgdata/geneseg/genesegp-embl/AA1990.DAT:* /SIDS2/gcgdata/geneseg/genesegp-embl/AA1991.DAT:* /SIDS2/gcgdata/geneseg/genesegp-embl/AA1992.DAT:* /SIDS2/gcgdata/geneseq/geneseqp-embl/AA2000.DAT:*/SIDS2/gcgdata/geneseq/geneseqp-embl/AA2001.DAT:*/SIDS2/gcgdata/geneseq/geneseqp-embl/AA2002.DAT:* /SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1998.DAT:* /SIDS2/gcgdata/geneseq/genesegp-emb1/AA1999.DAT:* /SIDSZ/gcgdata/geneseq/geneseqp-embl/AA1980.DAT:*/SIDSZ/gcgdata/geneseqg-embl/AA1981.DAT:*/SIDSZ/gcgdata/geneseqg-embl/AA1981.DAT:*/SIDSZ/gcgdata/geneseqg-embl/AA1982.DAT:*/SIDSZ/gcgdata/geneseqg-embl/AA1983.DAT:*/SIDSZ/gcgdata/geneseqg-embl/AA1983.DAT:*/SIDSZ/gcgdata/geneseqg-embl/AA1985.DAT:*/SIDSZ/gcgdata/geneseqg-embl/AA1985.DAT:*/SIDSZ/gcgdata/geneseqg-embl/AA1986.DAT:*/SIDSZ/gcgdata/geneseqg-embl/AA1986.DAT:*/SIDSZ/gcgdata/geneseqg-embl/AA1988.DAT:*/SIDSZ/gcgdata/geneseqg/geneseqg-embl/AA1988.DAT:*/SIDSZ/gcgdata/geneseqg/geneseqg-embl/AA1988.DAT:*/SIDSZ/gcgdata/geneseqg/geneseqg-embl/AA1988.DAT:*/SIDSZ/gcgdata/geneseqg/geneseqg-embl/AA1988.DAT:*/SIDSZ/gcgdata/geneseqg/geneseqg-embl/AA1988.DAT:*/SIDSZ/gcgdata/geneseqg/geneseqg-embl/AA1988.DAT:*/SIDSZ/gcgdata/geneseqg/geneseqg-embl/AA1988.DAT:*/SIDSZ/gcgdata/geneseqg/geneseqg-embl/AA1988.DAT:*/SIDSZ/gcgdata/geneseqg/genese

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	Humanised antibody	VEGF antagonist an	Heavy chain comple	Humanised antibody-	VEGF antagonist an	Antiqen-binding pr	Chimeric p1C11 hea	VEGF antagonist an	Antiqen-binding pr	Anti-p53 monoclona
SUMMARIES	ΙD	AAE13138	AAB82704	AAU74416	AAE13143	AAB82709	AAU74417	AAE13145	AAB82701	AAU74420	AAW89162
	DB	22	22	23	22	22	23	22	22	23	20
	Query Match Length DB	17	17	17	117	117	117	136	136	238	17
фP	Query Match	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	93.1
	Score	101	101	101	101	101	101	101	101	101	94
	Result No.	1	7	e	4	5	9	7	8	6	10

(IMCL-) IMCLONE SYSTEMS INC. (CORR) CORNELL RES FOUND INC.

WPI; 2001-662942/76. N-PSDB; AAD21664. Witte L, Rafii S;

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annentary dechain comports anti-p53 monoclos ant	() (1)
AAY97230 AAV74407 AAX70744 AAX70794 AAX90733 AAX70787 AAX39530 AAX39540	AAW60769 AAR75719
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11111111111111111111111111111111111111	243
0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	96
111 112 113 113 114 115 116 117 117 118 118 118 119 119 119 119 119 119 119	44

ALIGNMENTS

RESULT 1

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Vascular endothelial growth factor receptor; VEGFR; antagonist; tumour; cytostatic; heavy chain hypervariable region; VH; myelocytic leukaemia; lymphocytic; erythrocytic; monocytic; multiple myeloma; lymphoid cell; Hodgkin's disease; complementarity determining region-2; CDR-2; mouse.
                                                                                 Humanised antibody murine heavy chain hypervariable region (VH) CDR2.
AAE13138
ID AAE13138 standard; peptide; 17 AA.
                                                                                                                                                                                                                                                             31-MAR-2000; 2000US-0540770.
                                                                                                                                                                                                                                       30-MAR-2001; 2001WO-US10504
                                                        28-JAN-2002 (first entry)
                                                                                                                                                                                        WO200174296-A2.
                                                                                                                                                                                                             11-OCT-2001.
                                   AAE13138;
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                                                                                                                                                                                                                                           The invention relates to a method for inhibiting the growth of non-solid tumour cells that are stimulated by a ligand of vascular endothelial growth factor receptor (VEGFR) in mammals particularly humans. The method involves treating the mammals with humanised VEGFR monoclonal antibodies (antagonidis). Humanised wonstant region, where the humanised mouse variable region of nontains mouse complementarity determining region (CDR) grafted into human variable region. The method is useful for treating jeukaemias such as acute or chronic myelocytic leukaemia, acute or chronic lymphocytic leukaemia, erythrocytic or monocytic leukaemia, multiple myelomas and lymphoid cells, particularly those related to antibody minime heavy chain hypervariable region (VH) CDR-2 used in the exemplification of the invention.
Inhibiting growth of non-solid tumor cells useful to treat bone marrow tumors such as leukemias or multiple myeloma comprises treatment with an antagonist of a vascular endothelial growth factor receptor -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Treating or controlling an angiogenic dependent condition (e.g. neoplasm, collagen-vascular or autoimmune disease) in mammal by administering a combination of an antiangiogenic molecule and a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 17;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       100.0%; Score 101; DB 22;
100.0%; Pred. No. 4.4e-09;
iive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         VEGF antagonist antibody IMC-1C11 VH CDR-2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAB82704 standard; Peptide; 17 AA.
                                                                                                                                                                                 Claim 8; Page 14; 68pp; English.
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2000US-0539692
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Matches 17% Conservat
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Chimeric
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The present sequence is that of complementarity determining region (See also AAB8701) of IMC-ICI, a mouse-human chimeric antibody that has vascular inforced. The inforced and inforced and inforced activity. The antibody, or a fragment of it, can be used as an anti-angiogenic molecule, cor a fragment of it, can be used as an anti-angiogenic molecule, cor or a fragment of it, can be used as an anti-angiogenic molecule, and of properties generally to a method of treating or the invention relates generally to a method of treating or controlling an angiogenic dependent condition by administering an anti-angiogenic molecule and a chemotherapeutic agent, to produce a regression or arrest of the condition while minimising or preventing significant toxicity of the chemotherapeutic agent. The anti-angiogenic molecule inhibits or blocks the action of a vascular endothelium survival factor such as VEGF or its receptor, and is especially IMC-ICII. Conditions that can be treated include
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New bispecific immunoglobulin-like antigen-binding protein for reducing tumour growth and for inhibiting angiogenesis, comprises a complex of two polypeptides and two second polypeptides
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Heavy chain complementarity determining region H2 (CDRH2) version #2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   and is especially IMC-ICII. Conditions that can be treated include a neoplasm, a collagen-vascular disease or an autoimmune disease, especially a solid tumour, including breast carcinoma, unng carcinoma, prostate carcinoma, colon carcinoma, prostate carcinoma, ovarian carcinoma, neuroblastoma, central nervous system tumour, neuroblastoma multiforme or melanoma (all claimed).
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100.0%; Pred. No. 4.4e-09;
ive 0; Mismatches 0;
Disclosure; Pagė 37; 42pp; English.
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Best Local Similarity 100.
Matches 17; Conservative
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N-PSDB; AAS20287.
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The invention describes an antigen-binding protein (I) comprising a complex of two polypeptides (P1) and two second polypeptides (P2) which are stably associated in an immunoglobulin like complex. Pl has an antigen-binding site located to the N terminus of immunoglobulin (Ig) light chain constant domain (CL domain), and P2 has an antigen-binding site located to the N terminus of the Cl domain. (I) is useful for: neutralising the activation of a vaccular endothelial growth factor (VEGF) receptor; reducing tumour growth; inhibiting vEGF induced migration of human leukaemia cells; blocking interaction of a protein and its ligand; promoting interaction; inhibiting vEGF induced migration of human leukaemia cells; blocking interaction of a protein and its ligand; promoting interactions between immune cells and target cells; and in vivo and in vitro for investigative, diagnostic or treatment methods. The design of (I) provides for efficient production so that substantially all of the antigen-binding proteins produced are assembled in the design of (I) provides for efficient and bispecific, homogeneous and in tetrameric form. The heavy chain constant domains which constitute antibody and which provide other antibody functions can be present. There is no requirement for processing in vitro to obtain the complete product. The perpites esquence represents the heavy chain variable domain.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Vascular endothelial growth factor receptor; VEGFR; antagonist; tumour; cytostatic; heavy chain; myelocytic leukaemia; lymphocytic; erythrocytic; monocytic; multiple myeloma; lymphoid cell; Hodgkin's disease; mouse;
                                                                                                                                                                                                                                                                                                                                                                                                                     complementarity determining region H2 (CDRH2) version #2 incorporated into an antigen-binding protein described in the method of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Inhibiting growth of non-solid tumor cells useful to treat bone marrow tumors such as leukemias or multiple myeloma comprises treatment with an antagonist of a vascular endothelial growth factor receptor -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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100.0%; Pred. No. 4.4e-09;
live 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Humanised antibody heavy chain fragment.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAE13143 standard; Protein; 117 AA.
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Matches 17; Conservative
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Chimeric - Mus sp.
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N-PSDB; AAD21669.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    human; chimeric.
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      The invention relates to a method for inhibiting the growth of non-solid tumour cells that are stimulated by a ligand of vascular endothelial growth factor receptor (VEGER) in mammals particularly humans. The method involves treating the mammals with humanised veger monoclonal antibodies (antagonists). Humanised monoclonal antibody comprises humanised mouse variable region joined to human constant region, where the humanised mouse variable region of ontains mouse complementarity determining region (CDR) grafted into human variable region. The method is useful for treating leukaemias such as acute or chronic myelocytic leukaemia, acute or chronic lymphocytic leukaemia, erythrocytic or monocytic leukaemia, multiple myelomas and lymphoid cells, particularly those related to non-Hodgkin's and Hodgkin's disease. The present sequence is humanised antibody heavy chain fragament used in the exemplification of the
                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       IMC-1c11; chimeric antibody; mouse; human; antagonist; VEGF; vascular endothelial growth factor; angiogenesis; antiangiogenic; antitumour; neoplasm; collagen-vascular disease; autoimmune diseast tumour; breast carcinoma; lung carcinoma; prostate carcinoma; colon carcinoma; ovarian carcinoma; neuroblastoma; glioblastoma; qlioblastoma; multiforme; melanoma; therapy; heavy chain.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            VEGF antagonist antibody IMC-1C11 heavy chain variable region.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note= "complementarity determining region 2"
                                                                                                                                                                                                                                                                                             Length 117;
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                                                                                                                                                                                                                                                                                         100.0%; Score 101; DB 22;
100.0%; Pred. No. 3.5e-08;
ive 0; Mismatches 0;
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/label= CDR-H1
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/label= CDR-H2
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/label= CDR-H3
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2000US-0539692
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                                                                                                                                                                                                                                                                                                                                                                               50 WIDPENGDSDYAPKFQG 66
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                                                                                                                                                                                                                                                                                                                             17; Conservative
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Chimeric - Homo sapiens.
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                                                                                                                                                                                                                                                                                                          Best Local Similarity
                                                                                                                                                                                                                                                          117 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WO200154723-A1
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                                                                                                                                                                                                                             invention.
                                                                                                                                                                                                                                                              Sequence
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                                                                                                                                                                                                                                                                                             Query Match
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                                                                                                                                             The present sequence is that of the heavy chain variable region of another in a mouse-human chimeric antibody that has vascular endothelia growth factor (VEGF) antagonist activity. The antibody, or a fragment of it, can be used as an anti-angiogenic molecule, together with a chemotherapeutic acid, for the treatment of an angiogenic dependent condition in a mammal, especially a human. The invention relates generally to a method of treating or controlling an angiogenic dependent condition by administering an inti-angiogenic molecule and a chemotherapeutic agent, to produce a regression or arrest of the condition while minimising or preventing significant toxicity of the chemotherapeutic agent. The antifangiogenic molecule inhibits or blocks the action of a vascularizandothelium survival factor such as vesce tor; and is especially INC-IC11 Conditions that can be treated include a neoplasm, a collagen-vascular disease or an autoimmune disease, especially incommune, including breast carcinoma, lung carcinoma, prostate carcinoma, covarian gearcinoma, neuroblastoma multiforme or melanoma (all claimed).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   bispecific immunoglobulin-like antigen-binding protein for reducing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Antigen-binding protein; antibody heavy chain variable domain; cytostatic; anglogenesis inhibitor; tumour; leukaemia; antibody; vascular endothelial growth factor receptor; VEGF; cell proliferation inhibitor;
                               Treating or controlling an angiogenic dependent condition (e.g. neoplasm; collagen-vascular or autoimmune disease) in mammal by administering a combination of an antiangiogenic molecule and a
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Pred. No. 3.5e-08;
; Mismatches 0;
                                                                                                                   Disclosure; Page 38; 42pp; English
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 WIDPENGDSDYAPKFOG 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               50 WIDPENGDSDYAPKFOG 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              17; Conservative
                                                                                   chemotherapeutic agent
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ouery Match
Best Local'Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            117 AA;
 N-PSDB; AAH26405.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence
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                                                                                                                                                                                                                                     (VEGF) receptor; reducing tumour growth; inhibiting angiogenesis; reducing tumour growth; inhibiting angiogenesis; reducing endothelial cell proliferation; inhibiting VEGF induced migration of human leukaemia cells; blocking interaction of a protein and its ligand; promoting interactions between immune cells and target cells; and in vivo and in vitro for investigative, diagnostic or treatment methods. The design of (1) provides for efficient production so that substantially all of the antigen-binding proteins produced are assembled in the desired configuration. (1) is bivalent and bispecific, homogeneous and in tetrameric form. The heavy chain constant domains which constitute the Fc region (e.g., CH2 and GH3 for an IgG molecule) of a natural antibody and which provide other antibody functions can be present. There
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 is no requirement for processing in vitro to obtain the complete product. This sequence represents a heavy chain variable domain (VH) incorporated into Fv, an engineered protein containing a heavy chain variable domain and a light chain variable domain in one polypeptide chain, described in the method of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         cytostatic; heavy chain; myelocytic leukaemia; lymphocytic; erythrocytic; monocytic; multiple myeloma; lymphoid cell; Hodgkin's disease; chimeric;
                                                                                                   The invention describes an antigen-binding protein (I) comprising a complex of two polypeptides (Pl) and two second polypeptides (P2) which are stably associated in an immunoglobulin like complex. Pl has an antigen-binding site located to the N terminus of immunoglobulin (Ig) light chain constant domain (Cl domain), and P2 has an antigen-binding site located to the N terminus of the CHl domain. (I) is useful for: neutralising the activation of a vascular endothelial growth factor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Vascular endothelial growth factor receptor; VEGFR; antagonist; tumour;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note= "Residue 'O' is present at this location in the sequence shown in fig-11 of the specification"
tumour growth and for inhibiting angiogenesis, comprises a complex of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                sequence shown in fig-11 of the specification"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 117;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   100.0%; Score 101; DB 23;
100.0%; Pred. No. 3.5e-08;
iive 0; Mismatches 0;
                  two polypeptides and two second polypeptides
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ...19
/label= Leader_peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Chimeric plC11 heavy chain fragment.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAE13145 standard; Protein; 136 AA.
                                                             English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          5..54
label- CDR_H1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    9..85
Label= CDR_H2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           50 WIDPENGDSDYAPKFQG 66
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                        61; Page 60; 64pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Chimeric - Homo sapiens
Chimeric - Unidentified
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    human; plC11 vector.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             117 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Misc-difference
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Simi
Matches 17;
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Location/Qualifiers

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02-AUG-2001
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            Peptide
                                  Protein
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                                                                                                                            Region
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                                                                                                                                                                                                                                                                                     The invention relates to a method for inhibiting the growth of non-solid tumour cells that are stimulated by a ligand of vascular endothelial growth factor receptor (VEGFR) in mammals particularly humans. The method involves treating the mammals with humanised VEGFR monoclonal antibodies (antagonists). Humanised monoclonal antibody comprises humanised mouse variable region joined to human constant region, where the humanised mouse variable region contains mouse complementarity determining region (CDR) grafted into human variable region. The method is useful for treating leukaemias such as acute or chronic myelocytic leukaemia, criticalial myelomas and lymphoid cells, particularly those related to non-Hodgkin's and Hodgkin's disease. The present sequence is chimeric picli lige expression vector. Chimeric picli heavy chain fragment which is used for the construction of chimeric contains human lgG1 (gamma) heavy chain contains
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                   Inhibiting growth of non-solid tumor cells useful to treat bone marrow tumors such as leukemias or multiple myeloma comprises treatment with an antagonist of a vascular endothelial growth factor receptor -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 IMC-1C11; chimeric antibody; mouse; human; antagonist; VEGF; vascular endothelial growth factor; angiogenesis; antiangiogenic; antitumour; neoplasm; collagen-vascular disease; autoimmune disease; tumour; breast carcinoma; lung carcinoma; prostate carcinoma; colon carcinoma; ovarian carcinoma; neuroblastoma; glioblastoma multiforme; melanoma; therapy; heavy chain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ő
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             VEGF antagonist antibody IMC-1C11 heavy chain variable region.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 136;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            100.0%; Score 101; DB 22;
100.0%; Pred. No. 4.1e-08;
ive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAB82701 standard; Protein; 136 AA.
                                                                                                                                                                                                                                                                   Example 3; Fig 11; 68pp; English
119..125
/label= CDR_H3
                                                                                                                          (IMCL-) IMCLONE SYSTEMS INC. (CORR ) CORNELL RES FOUND INC.
                                                                              30-MAR-2001; 2001WO-US10504.
                                                                                                    31-MAR-2000; 2000US-0540770.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      69 WIDPENGDSDYAPKFQG 85
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 WIDPENGDSDYAPKFQG 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Chimeric - Mus sp.
Chimeric - Homo sapiens.
                                                                                                                                                                                 WPI; 2001-662942/76.
N-PSDB; AAD21682.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Local Similarity
                                                                                                                                                             Witte L, Rafii S;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       136 AA;
                                 WO200174296-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      15-OCT-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   domain (CH)
                                                        11-OCT-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAB82701:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
 Region
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Matches
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The anti-anglogenic molecule inhibits or blocks the action of a vascular endothelium survival factor such as VEGF or its receptor,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ovarian carcinoma, neuroblastoma, central nervous system tumour, neuroblastoma, glioblastoma multiforme or melanoma (all claimed).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Treating or controlling an angiogenic dependent condition (e.g. neoplasm, collagen-vascular or autoimmune disease) in mammal by administering a combination of an antiangiogenic molecule and a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ő
                                                                                                                                                             /note= "complementarity determining region 1"
                                                                                                                                                                                                                                                          2
                                                                                                                                                                                                                                                                                                                           /label= CDR-H3
/note= "complementarity determining region 3"
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                                                                                                                                                                                         59.85
/label= CDR-H2
/note= "complementarity determining region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
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100.0%; Pred. No. 4.1e-08;
ive 0; Mismatches 0;
                                                          /label= Mature_protein
'label= Signal_peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (SUNN-) SUNNYBROOK HEALTH SCI CENT. (IMCL-) IMCLONE SYSTEMS INC.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Disclosure; Fig 1; 42pp; English.
                                                                                               45..54
/label= CDR-H1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             29-JAN-2001; 2001WO-US02839.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              28-JAN-2000; 2000US-0178791.
31-MAR-2000; 2000US-0539692.
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                                                                                                                                                                                                                                                                                               118..125
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      chemotherapeutic agent
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 2001-514531/56.
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                                                                                                                                                                                                                                                                                                                                                                                                                                  WO200154723-A1.
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AAU74420
ID AAU74
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238 AA;

Seguence

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Antigen-binding protein; single chain variable fragment; svFv; antigen; cytostatic; angiogenesis inhibitor; tumour; leukaemia; antibody; vascular endothelial growth factor receptor; VEGF; cell proliferation inhibitor.
                                                                                                                                                                                                                                                                                                                                                                                                    New bispecific immunoglobulin-like antigen-binding protein for reducing tumour growth and for inhibiting angiogenesis, comprises a complex of two polypeptides and two second polypeptides
                                                                                                                                                                           118..132
/label Linker
/note "15 amino acid linker joins the VH and VL
regions of the single chain variable fragment
protein. Encoded by AAS20285"
                                           Antigen-binding protein, single chain variable fragment version #2.
                                                                                                                                                                /note= "Heavy chain variable domain. Specifically claimed in claim 61"
                                                                                                                                                                                                                                     /label= VL
/note= "Light chain variable domain. Specifically
claimed in claim 61"
                                                                                                                                    Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                          Page 62-63; 64pp; English
                                                                                                                                                                                                                                                                                                                              24-MAY-2000; 2000US-206749P
                                                                                                                                                                                                                                                                                                                                                MUCTONE SYSTEMS INC
                                                                                                                                                                                                                                                                                                           24-MAY-2001; 2001WO-US16924
                                                                                                                                               1..117
/label= VH
                          (first entry)
                                                                                                                                                                                                                                                                                                                                                                                   WPI; 2002-106189/14.
                                                                                                                                                                                                                                                                          WO200190192-A2.
                                                                                                                                                                                                                                                                                            29-NOV-2001.
                         26-MAR-2002
                                                                                                          Mus sp.
Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 635
       AAU74420;
                                                                                                                                                                                                                                                                                                                                                IMCL-)
                                                                                                                                      Key
Region
                                                                                                                                                                                   Region
                                                                                                                                                                                                                              Region
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The invention describes an antigen-binding protein (I) comprising a complex of two polypeptides (P1) and two second polypeptides (P2) which are stably associated in an immunoglobulin like complex. Pl has an antigenablinding site located to the N terminus of immunoglobulin (Ig) antigenablinding site located to the N terminus of immunoglobulin (Ig) (Ight chain constant domain (CL domain), and P2 has an antigen-binding site located to the N terminus of the CH1 domain. (I) is useful for: neutral sing the activation of a vascular endothelial growth factor (VEGF) receptor; reducing tumour growth; inhibiting angiogenesis.

CC (VEGF) receptor; reducing tumour growth; inhibiting vEGF induced migration of human leukaemia cells; blocking interaction of a protein and its ligand; promothing interactions between immune cells and target cells; and in vivo and in vitro for investigative, diagnostic or treatment centended; The design of (I) provides for efficient production so that substantially all of the antigen-binding proteins production so that cand in ferrament for methods. The design of (I) provides for efficient production so that cand in ferrament for provide other antibody functions can be present. There the Fefreedian (e.g., CH2 and CH3 for an IgG molecule) of a natural contained and which provide other antibody functions can be present. There can be equirement for processing in vitro to obtain variable fragment (CF This is the amino acid sequence of a single chain variable light and variable haven the method of the five containing a variable light and variable in the method of the five containing a variable in the method of the containing and the complete produced to the variable in the method of the containing and processing in the method of the containing a variable in the method of the containing a variable in the method of the containing a variable in the method of the containing and processing in the method of the containing and containing and containing and containing and containing and containing and containi invention.

17 AA;

Seguence

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The present invention describes the use of an immunogen (A) to induce anti-tumour immunity; to elicit an increased immune response to tumour associated antigen (TAA) and/Or to induce an immune response to mutant or wild-type forms of TAA in mammals. (A) is: (i) a monoclonal antibody or wild-type forms of TAA in mammals. (A) is: (i) a monoclonal antibody (ADA) to TAA, or its fragment; (ii) a peptide based on a CDR (Complementarity determining region) on the heavy or light chain of MAD (able to elicit antibodies to TAA); or (iii) a DNA that encodes the variable (V) region of MAD, in a gene delivery vehicle. The present sequence represents a peptide based on CDR2 of the heavy chain of sequence represents a peptide based on CDR2 of the heavy chain of sequence represents a peptide based on CDR2 of the heavy chain of specific, anti-DNA antibodies (AD) by immunising a mammal with a MAD directed to a domain containing a DNA-binding site of a DNA-binding content. (A) is used to treat a wide variety of primary and metastatic cancers, particularly those where p53 is involved. Ab are used for diagnosis (e.g to determine critical sequences in animal or plant contentage; in gene sequencing and cloning; also possibly for activation of selected therapeutic genes in plants, animals and humans. (A) induce
                                            ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    an effective anti-tumour response without causing harm to the patient. The method uses (A) to generate anti-TAA by exploiting the anti-idiotype
                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                 Anti-p53; monoclonal antibody 240; immunogen; anti-tumour; immunity; immune response; tumour associated antigen; metastatic cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Use of a monoclonal antibody to a tumour-associated antigen - to induce anti-tumour immunity or elicit an increased immune response
                                                                                                                                                                                                                                                                                                                              Anti-p53 monoclonal antibody 421 CDR2 heavy chain based peptide.
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     Length 238;
                                              Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ruiz
Score 101; DB 23;
Pred. No. 7.6e-08;
• Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Herkel J,
                                                                                                                                                                                                                AAW89162 standard; peptide; 17 AA.
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     Query Match 100.0%;
Best Local Similarity 100.0%;
Matches 17; Conservative 0
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                                                                                                                                                                                                                                                                                         25-MAR-1999 (first entry)
                                                                                 1 WIDPENGDSDYAPKFQG 17
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                                                                                                       $0 WIDPENGDSDYAPKFQG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      09-JUN-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              W09856416-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           09-JUN-1997;
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Wolkowicz R;
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                                                                                                                                                                                                                                                                                                                                                                                                                                         Synthetic.
                                                                                                                                                                                                                                                    AAW89162;
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The immunoglobulin molecules bind specifically to an certracellular domain of the KDR receptor with the same affinity as VEGF. Overexpression of VEGF has been implicated in a number of human tumour cell lines including glioblastoma multiforme, chemangioblastoma, central nervous system neoplasms and AIDS associated Karposi's sarcoma. The antibodies therefore have applications in treating these conditions. This sequence encodes a preferred heavy chain complementary determining region of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Novel immunoglobulin molecules binding kinase insert domain-containing receptor with the same affinity as vascular endothelial growth factor, used to reduce tumour growth
                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Immunoglobulin; antibody; complementary determing region; CDR; VBGF; vascular endothbala growth factor; KDR; kinase insert domain containing receptor; multivalent; monovalent; humanised antibody; chimeric antibody; tumour; diabody; triabody; glioblastoma multiforme; hemandioblastoma; AIDS; central nervous system neoplasms; AIDS associated Karposi's sarcoma; acquired immune deficiency syndrome; AIDS; human.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Complementary determining region (CDRH2) of anti-SI(KDR) antibody.
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                                         Length 17;
Score 94; DB 20; Length 1/, Pred. No. 5.6e-08;
                                                                                                                                                                                                                                                                                                                                                                                                      AAY97230 standard; Protein; 17 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     to reduce tumour growth
                                     93.1%;
88.2%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (IMCL-) IMCLONE SYSTEMS INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (first entry)
                                                                                                                                                                    1 WIDPENGDSDYAPKFQG 17
                                                                                                                                                                                                             15; Conservative
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N-PSDB; AAA53762.
                                                                        Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Shu Z, Witte L;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WO200044777-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               29-JAN-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens.
Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    29-JAN-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     19-DEC-2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAY97230;
                                         Query Match
                                                                                                      Matches
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NAMES OF COLOR OF STREET STREE

Length 17;

Score 94; DB 21; Pred. No. 5.6e-08;

93.1%; 94.1%;

Best Local Similarity

Query Match

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The invention describes an antigen-binding protein (I) comprising a complex of two polypeptides (P1) and two second polypeptides (P2) which are stably associated in an immunoglobulin like complex. Pl has an antigen-binding site located to the N terminus of immunoglobulin (Ig) light chain constant domain (CL domain), and P2 has an antigen-binding site located to the N terminus of the CHI domain. (I) is useful for: neutralising the activation of a vaccular endothelial growth factor (VEGF) receptor; reducing tumour growth; inhibiting vEGF induced migration of human leukaemia cells; blocking interaction of a protein and its ligand; promoting interactions between immune cells and target cells; and in vivo and in vitro for investigative, diagnostic or treatment methods. The design of (I) provides for efficient production so that substantially all of the antigen-binding proteins produced are assembled in the desired configuration. (I) is bivalent and bispecific, homogeneous and in tetrameric form. The heavy chain constant domains which constitute antibody and which provide other antibody functions can be present. There is no requirement for processing in vitro to obtain the complete product. The provides the heavy chain constant domain the complete product. The first performance is no requirement for processing in vitro to obtain the complete product.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New bispecific immunoglobulin-like antigen-binding protein for reducing tumour growth and for inhibiting angiogenesis, comprises a complex of two polypeptides and two second polypeptides
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Heavy chain complementarity determining region H2 (CDRH2) version #1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Complementarity determining region; CDR; CDRH2; antigen; cytostatic; angiogenesis inhibitor; vascular endothelial growth factor receptor; VEGF; tumour; leukaemia; antibody; cell proliferation inhibitor; antibody heavy chain variable domain.
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Pred. No. 5.6e-08;
0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                           AAU74407 standard; peptide; 17 AA.
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94.18;
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Best Local Similarity 94.1:
Matches 16; Conservative
1 WIDPENGDSDYAPKFQG 17
                                                 1 WIDPENGDSGYAPKFQG
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                                                                                                                                                                                                 RESULT 12
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25-MAR-1999 (first entry)
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                                                                                                                                 WO9856416-A1.
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                                                                                                                                                                                                                                                                     Cohen IR, E
Wolkowicz R;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               31-JUL-2000
                                                                                                        Synthetic.
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                                                                                            Mus sp
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                                                                                                                                                                                                       Murine; p59 protein; monoclonal antibody; mAb; PAb-421; PAb-421 H2; heavy chain variable region; VH; complementarity determining region; CDR; dernathological; immunosuppressive; antiinflammatory; autoimmune response; SLE; systemic lupus erythematosus; diagnosis; treatment; autoantigen; DNA-binding domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The patent discloses a method for the treatment of systemic lupus erythematosus (SLE) by down-regulating the autoimmune response to the C-terminal DNA-binding domain of p53 protein by an active compound. The present sequence is a PAD-421 H2 peptide which comprises the complementarity determining region (CDR) of the heavy chain of a monoclonal antibody PAD-421 which is specific to the C-terminal DNA-binding domain of murine p53 protein. The peptide corresponds to residues 48-67 of PAD-421 heavy chain variable region. It is an example of the active compound useful in the diagnosis, prevention
                                                                                                                                                                                     Murine an蝕-p53 PAb-421 mAb heavy chain CDR based peptide PAb-421 H2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Treatment of systemic lupus erythematosus by down-regulating the autoimnume response to the C-terminal DNA-binding domain of the p53 protein by an active compound comprising of antibodies to p53 or fragments of p5.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 peptide; 112 AA.
                                                                                                     AAY70794 standard; peptide; 20 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 78 Fig 10; 87pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                treatment of SLE in humans
                                                                                                                                                                                                                                                                                                                                                                                                                                 EDA RES & DEV CO LTD
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88.2%;
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                                                                                                                                                            (first entry)
                       1 WIDPENGDSGYAPKFQG 17
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                                                                                                                                                                                                                                                                                                                       WO200023082-A1.
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                                                                                                                                                          31-JUL-2000
                                                                                                                                                                                                                                                                                                                                                 27-APR-2000
                                                                                                                               AAY70794;
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                                                                            RESULT 13
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anti-tumour immunity; to elicit an increased immune response to tumour associated antigen (TAA) and/or to induce an immune response to tumour associated antigen (TAA) and/or to induce an immune response to mutant or wild-type forms of TAA in mammals. (A) is: (1) a monoclonal antibody (MAD) to TAA, or its fragment; (ii) a peptide based on a CDR (complementarity determining region) on the heavy or light chain of MAD (complementarity determining region) on the heavy or light chain of MAD (complementarity determining region) on the heavy or light chain of MAD (complementarity determining region) on the heavy or light chain of MAD (complementarity determining region) on the heavy or light chain of MAD (complementarity determined delivery vehicle. The present sequence represents the variable heavy chain sequence from anti-PS3 MAD (compain containing a method for generating sequence-specific, anti-DNA antibodies (AD) by immunising a memmal with a MAD directed to a domain containing a DNA-binding site of a DNA-binding protein. (A) is used to treat a wide variety of primary and metastatic cancers, contentive and other parasites; to determine parentage; in forestic sequencing and cloning; also possibly for activation of selected the characteristic genes in plants, animals and humans. (A) induce an effective anti-tumour response without causing harm to the patient.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          uses (A) to generate anti-TAA by exploiting the anti-idiotype network
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The present invention describes the use of an immunogen (A) to induce
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                         Anti-p53; monoclonal antibody 240; immunogen; anti-tumour; immunity; immune response; tumour associated antigen; metastatic cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Use of a monoclonal antibody to a tumour-associated antigen - to induce anti-tumour immunity or elicit an increased immune response
Anti-p53 monoclonal antibody 421 variable heavy chain sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
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Pred. No. 4.2e-07;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Example 3; Fig 3; 47pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (YEDA ) YEDA RES & DEV CO LTD.
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88.2%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 93.1
Best Local Similarity 88.2
Matches 15; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Erez-Alon N,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 1999-070296/06.
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dermatological; immunosuppressive; antiinflammatory; autoimmune response; SLE; systemic lupus erythematosus; diagnosis; treatment; autoantigen; heavy chain variable region; VH; complementarity determining region; CDR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The patent discloses a method for the treatment of systemic lupus erythematosus (SLE) by down-regulating the autoimmune response to the c-terminal DNA-binding domain of p53 protein by an active compound. The present sequence is a heavy chain variable region of monoclonal antibody PAb-421 which is specific to the C-terminal DNA-binding domain of murine p53 protein. PAb-421 antibody and peptides based on complementarity determining regions of light and heavy chain variable regions of the antibody, are examples of active compounds useful in the diagnosis, prevention and treatment of SLE in humans.
                 Murine; p53 protein; monoclonal antibody; PAb-421; DNA-binding domain;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Treatment of systemic lupus erythematosus by down-regulating the autoimmune response to the C-terminal DNA-binding domain of the p53 protein by an active compound comprising of antibodies to p53 or fragments of p53 -
                                                                                                                                                                                              50..66
//label= CDR
//note= "Complementarity determining region"
//note= "Complementarity determining region"
//label= CDR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 94; DB 21; Length 116;
Pred. No. 4.4e-07;
2; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                   /note= "Complementarity determining region"
                                                                                                                                                                                  "Complementarity determining region"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Cohen IR, Rotter V, Erez-Alon N, Herkel J;
                                                                                                                                Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 78; Fig 9; 87pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                  (YEDA ) YEDA RES & DEV CO LTD.
                                                                                                                                                                                                                                                                                                                                                                                  99WO-US24443.
                                                                                                                                                                                                                                                                                                                                                                                                                   98US-0104816.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     93.1%;
88.2%;
                                                                                                                                                 26..35
/label= CDR
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Best Local Similarity 88.2
Matches 15; Conservative
                                                                                                                                                                                   'note=
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                                                                                                                                                                                                                                                                                                                                                                                  19-0CT-1999;
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Search completed: December 23, 2002, 07:25:09 Job time: 9.12597 secs

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: GOURLIE, BRIAN B
APPLICANT: RIXON, MARK W
APPLICANT: RESS, PETER S
APPLICANT: KAPLAN, DONALD A
APPLICANT: KAPLAN, DONALD A
APPLICANT: SCHLOM, JEFFREY
TITLE OF INVENTION: A NOVEL FAMILY OF ANTI-CARCINOEMBRYONIC
TITLE OF INVENTION: ANTIGEN CHIMERIC ANTIBODIES
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 94; DB 1; Length 124;
Pred. No. 6.2e-08;
2; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Eloppy disk
COMPUTER: Eloppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/017,570
FILING DATE: 19930216
CLASSIFICATION: 424
PCT-US94-01709-6

US-08-652-507-2

US-08-983-035-38-38

US-08-983-052-16

US-09-188-082-16

US-09-108-088-16

US-09-171-945-31

US-09-171-945-75

US-09-171-945-75

US-09-171-945-79

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US-09-171-945-85
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 4, Application US/08017570 Patent No. 5472693
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        34,941
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REFERENCE/DOCKET NUMBER: C-TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            93.1%;
88.2%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ATTORNEY/AGENT INFORMATION:
NAME: ULMER, DUANE C
REGISTRATION NUMBER: 34,9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADDRESSEE: Duane C. Ulm
STREET: P.O. Box 1967
CITY: Midland
STATE: MI
COUNTRY: US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             : 124 amino acids
AMINO ACID
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Matches 15; Conservative
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163.250 Million cell updates/sec
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/cgn2_6/ptodata/1/iaa/5B_COMB.pep:*
/cgn2_6/ptodata/1/iaa/6A_COMB.pep:*
/cgn2_6/ptodata/1/iaa/6B_COMB.pep:*
/cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
/cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
                            GenCore version 5.1.3
Copyright (c) 1993 - 2002 Compugen Ltd.
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US-09-025-403A-5
US-09-025-403A-6
US-09-025-403A-7
US-09-025-403A-8
US-09-025-403A-9
US-09-025-403A-9
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US-09-672-609-4
US-09-672-609-6
US-09-672-609-6
US-09-672-609-9
US-09-672-609-9
US-09-672-609-11
US-09-672-609-12
US-09-672-609-12
US-09-025-403A-1
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Maximum Match 100%
Listing first 45 summaries
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Gapop 10.0 , Gapext 0.5
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length: 2000000000
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Maximum DB seq
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Perfect score:
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APPLICANT: RIXON, MARK W
APPLICANT: REZEN, PETER S
APPLICANT: KAPLEN, DONALD A
APPLICANT: KAPLEN, DONALD A
APPLICANT: SCHLOM, JEFFREY
TITLE OF INVENTION: A NOVEL FAMILY OF ANTI-CARCINOEMBRYONIC
TITLE OF INVENTION: ANTIGEN CHIMERIC ANTIBODIES
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 124;
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                                                          MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/471,426
FILING DATE: 06-JUN-1995
APPLICATION NUMBER: 06-JUN-1995
APPLICATION NUMBER: 06-JUN-1995
APPLICATION NUMBER: 34,941
REFERENCE/DOCKET NUMBER: 34,941
REGISTRATION NUMBER: 34,941
REGISTRATION NUMBER: 34,941
REGISTRATION NUMBER: 34,941
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
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TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION 100: 4:
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ZIP: 48641-1967
COMPUTER READABLE FORM:
MEDIUM TYPE: FORM:
MEDIUM TYPE: FORD
COMPUTER: IBM PC COMPATIBLE
OFFRATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/471,426
FILING DATE: 06-JUN-1995
CLASSIFICATION: 536
PRIOR APPLICATION NUMBER: 08/017,570
FILING DATE: 16-FEB-1993
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 94; DB 1; Le
Pred. No. 6.2e-08;
2; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 6, Application US/08471426
Patent No. 5808033
GENERAL INFORMATION:
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REGISTRATION NUMBER: 34,941
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 93.1%;
Best Local Similarity 88.2%;
Matches 15; Conservative
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STREET: P.O. Box 1967
CITY: Midland
STATE: MI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LENGTH: 124 amino acids
TYPE: amino acid
TOPOLOGY: linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ) MOLECULE TYPE: protein US-08-471-426-4
ZIP: 48641-1967
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        linear
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US-08-471-426-6
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                                                                                    GENERAL INFORMATION:
APPLICANT: GOURLIE, BRIAN B
APPLICANT: GOURLIE, BRIAN B
APPLICANT: RIXON, MARK W
APPLICANT: RIXON, MARK W
APPLICANT: RIXON, MARK W
APPLICANT: RAPLAN, DOMALD A
APPLICANT: SCHLOM, DEFERS S
APPLICANT: MURBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESS: 3
ADDRESSEE: Duane C. Ulmer
STREET: P.O. BOX 1967
CITY: Midland
STATE: MI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 3
US-08-471-426-4
US-08-471-426-4
Sequence 4', Application US/08471426
Fatent No. 5808033
GENERAL INFORMATION:
APPLICANT: GOURLIE, BRIAN B
APPLICANT: MEZES, PETER S
APPLICANT: MEZES, PETER S
APPLICANT: MEZES, PETER S
APPLICANT: MIXIN, MARK W
TITLE OF INVENTION: A NOVEL FAMILY OF ANTI-CARCINOEMBRYONIC
TITLE OF INVENTION: A NOVEL FAMILY OF ANTI-CARCINOEMBRYONIC
TITLE OF INVENTION: ANTIGEN CHIMERIC ANTIBODIES
NUMBERS OF SEQUENCES: 24
CORRESPONDENCE ADDRESS:
ADDRESSEE: Duane C. Ulmer
STREET: P.O. Box 1967
CITY: Midland
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Pred. No. 6.2e-08;
2; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/017,570
FILING DATE: 19930216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE: 19930216
CLASSIFACTION: 424
ATTORNEY AGENT INFORMATION: 424
REGISTRATION NUMBER: 34,941
REFERENCE/DOCKET NUMBER: C-38,777
TELECOMMUNICATION INFORMATION: FOR EACH OF SECULATION INFORMATION: 517,000 INFORMATION: 517,000 INFORMATION: 518,000 INFORMATI
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TYPE: AMINO ACID
TOPOLOGY: 11near
MCDECULD TYPE: protein
US-08-017-570-6
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Best Local Similarity 88.2
Matches 15; Conservative
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48641-1967
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COUNTRY:
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Gaps

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Length 124;

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TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
NAME/KEY: Humanized COL-1 VH, HuVH
LOCATION: 1..124
OTHER INFORMATION: Humanized heavy chain variable region containing human OTHER INFORMATION: Ile-29, Lys-30, Asn-97, and Thr-98
US-09-672-609-3
                                                                                                                                                                                                                     Query Match 93.1%; Score 94; DB 4; Le Best Local Similarity 88.2%; Pred. No. 6.2e-08; Matches 15; Conservative 2; Mismatches 0;
                                                                                                                                                                                                                                                                                                  1 WIDPENGDSDYAPKFQG 17
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Best Local Similarity
Matches 15; Conserv
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US-09-672-609-5
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        LENGTH: 124
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APPLICANT: Anderson, W.H. Kerr
APPLICANT: Tempest, Philip R.
APPLICANT: Carr, Frank J.
APPLICANT: Harris, William J.
APPLICANT: Armour, Kathryn
TITLE OF INVENTION: High Affinity Humanized Anti-CEA Monoclonal Antibodies
FILE REFERENCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Anderson, W.H. Kerr
APPLICANT: Tempest, Philip R.
APPLICANT: Carr, Frank J.
APPLICANT: Harris, William J.
APPLICANT: Armour, Kathryn
TITLE OF INVENTION: High Affinity Humanized Anti-CEA Monoclonal Antibodies
FILE REPERENCE:
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Pred. No. 6.2e-08;
2; Mismatches 0; Indels
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CURRENT FILING DATE: 2000-09-28
PRIOR APPLICATION NUMBER: 09/025,403
PRIOR FILING DATE: 1998-02-18
NUMBER OF SEQ ID NOS: 50
SOFTWARE: Microsoft Word 97 SR-2
SEQ ID NO 1
LENGTH: 124
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CURRENT FILING DATE: 2000-09-28
PRIOR APPLICATION NUMBER: 09/025,403
PRIOR FILING DATE: 1998-02-18
NUMBER OF SEQ ID NOS: 50
                                                                                                                                                                                                                                                                                                                                                                                              Sequence 1, Application US/09672609
Patent No. 6333405
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Patent No. 6333405
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                                                                                                                                                                                93.1%;
88.2%;
TELEPHONE: (517) 636-8104 INFORMATION FOR SEQ ID NO: 6: SEQUENCE CHARACTERISTICS:
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88.2%;
                                                             LENGTH: 124 amino acids TYPE: amino acid
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Best Local Similarity 88.2
Matches 15; Conservative
                                                                                                                                                                                                                                                            1 WIDPENGDSDYAPKFQG 17
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; LOCATION: 1..124
US-09-672-609-1
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                                                                                               TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-471-426-6
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Best Local Similarity
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APPLICANT: Anderso
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US-09-672-609-3
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US-09-672-609-1
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SEQ ID NO 3
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LOCATION: 1..124
OTHER INFORMATION: Humanized heavy chain variable region containing human
OTHER INFORMATION: NEWM VH FRS, murine COL-1 VH CDRS, and Ala-24, Phe-27, Asn-28,
OTHER INFORMATION: Ile-29, Lys-30, Asn-97, and Thr-98
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                                                                            APPLICANT: Anderson, W.H. Kerr
APPLICANT: Tempest, Philip R.
APPLICANT: Carr, Frank J.
APPLICANT: Haris, William J.
APPLICANT: Armour, Kathryn
TITLE OF INVENTION: High Affinity Humanized Anti-CEA Monoclonal Antibodies
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Armour, Kathryn TITLE OF INVENTION: High Affinity Humanized Anti-CEA Monoclonal Antibodies
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Pred. No. 6.2e-08;
2; Mismatches 0; Indels
                                                                                                                                                                                                                                        FILE REFERENCE:

CURRENT APPLICATION NUMBER: US/09/672,609
CURRENT FILING DATE: 2000-09-38
PRIOR APPLICATION NUMBER: 09/025,403
PRIOR FILING DATE: 1998-02-18
NUMBER OF SEQ ID NOS: 50
SOFTWARE: MICROSOFT WORD 37 SR-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILE REFERENCE:
CURRENT APPLICATION NUMBER: US/09/672,609
CURRENT FILING DATE: 2000-09-28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME/KEY: Humanized COL-1 VH, HuVHA
; Sequence 4, Application US/09672609; Patent No. 6333405; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 5, Application US/09672609
Patent No. 633405
GENERAL INFORMATION:
APPLICANT: Tempest, Philip R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 93.1%;
88.2%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ORGANISM: Artificial Sequence
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NAME/KEY: Humanized COL-1 VH, HuVHATAY
LOCATION: 1.124
OTHER INFORMATION: Humanized heavy chain variable region containing human
OTHER INFORMATION: NEWM VH FRS, murine COL-1 VH CDRS, and Ala-24, Phe-27, Asn-28,
OTHER INFORMATION: Ile-29, Lys-30, Thr-78, Ala-79, Tyr-80, Asn-97, and Thr-98
                                                                                                                                                                                                                                                                                                                                                                                    OTHER INFORMATION: Humanized heavy chain variable region containing human OTHER INFORMATION: NEWM VH FRs, murine COL-1 VH CDRs, and Ala-24, Phe-27, Asn-28, OTHER INFORMATION: Ile-29, Lys-30, Tyr-80, Asn-97, and Thr-98
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APPLICANT: Tempest, Philip R.
APPLICANT: Carr, Frank J.
APPLICANT: Harris, William J.
APPLICANT: Armour, Kathryn
TITLE OF INVENTION: High Affinity Humanized Anti-CEA Monoclonal Antibodies
APPLICANT: Armour, Kathryn
TITLE OF INVENTION: High Affinity Humanized Anti-CEA Monoclonal Antibodies
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Pred. No. 6.2e-08;
2; Mismatches 0; Indels
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Pred. No. 6.2e-08;
2; Mismatches 0;
                                                              CURRENT APPLICATION NUMBER: US/09/672,609
CURRENT FILING DATE: 2000-09-28
PRIOR APPLICATION NUMBER: 09/025,403
PRIOR FILING DATE: 1998-02-18
NUMBER OF SEQ ID NOS: 50
SOFTWARE: Microsoft Word 97 SR-2
SEQ ID NO 7
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CURRENT APPLICATION NUMBER: US/09/672,609
CURRENT FILING DATE: 2000-09-28
PRIOR APPLICATION NUMBER: 09/025,403
PRIOR FILING DATE: 1998-02-18
NUMBER OF SEQ ID NOS: 50
SOFTWARE: MICROSOFT WORD 97 SR-2
                                                                                                                                                                                                                                                                                                                                       NAME/KEY: Humanized COL-1 VH, HuVHAY
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Patent No. 6333405
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88.2%;
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88.2%;
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Best Local Similarity 88.2
Matches 15; Conservative
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Best Local Similarity 88.2
Matches 15; Conservative
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                                               FILE REFERENCE
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US-09-672-609-8
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LENGTH: 124
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US-09-672-609-9
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                                                                                                              LENGTH: 124

LENGTH: 124

ORGANISM: Artificial Sequence

ORGANISM: Artificial Sequence

FEATURE:

NAME/KEY: Humanized COL-1 VH, HuVHAT

LOCATION: 1...124

OTHER INFORMATION: NEWH VH FRs, murine COL-1 VH CDRs, and Ala-24, Phe-27, Asn-28, OTHER INFORMATION: Ile-29, Lys-30, Thr-78, Asn-97, and Thr-98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           OTHER INFORMATION: Humanized heavy chain variable region containing human OTHER INFORMATION: NEWM VH FRS, murine COL-1 VH CDRS, and Ala-24, Phe-27, Asn-28, OTHER INFORMATION: Ile-29, Lys-30, Ala-79, Asn-97, and Thr-98
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APPLICANT: Tempest, Philip R.
APPLICANT: Tempest, Philip R.
APPLICANT: Tempest, Philip R.
APPLICANT: Carr, Frank J.
APPLICANT: Harris, William J.
APPLICANT: Harris, William J.
APPLICANT: Harris, William J.
APPLICANT: Recent Rethryn
TITLE OF INVENTION: High Affinity Humanized Anti-CEA Monoclonal Antibodies FILE REFERENCE:
CURRENT APPLICATION NUMBER: US/09/672,609
PRIOR APPLICATION NUMBER: 09/025,403
PRIOR FILING DATE: 1998-02-18
NUMBER: OFFESTO ID NOS: 50
SOFTWARE: Microsoft Word 97 SR-2
SEQ ID NO 6
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Pred. No. 6.2e-08;
2; Mismatches 0; Indels
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PRIOR APPLICATION NUMBER: 09/025,403
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence f7, Application US/09672609; Sequence f7, Application US/09672609; Patent No. 633405; GENERAL INFORMATION: APPLICANT: Anderson, W.H. Kerr; APPLICANT: Tempest, Philip R.; APPLICANT: Carr, Frank J.; APPLICANT: Harris, Alliqua, J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 6, Application US/09672609 Patent No. 6333405
                 PRIOR FILING DATE: 1998-02-18
NUMBER OF SEQ ID NOS: 50
SOFTWARE: MICROSOFT WORD 97 SR-2
SEQ ID NO 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: PRT
ORGANISM: Artificial Sequence
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Best Local Similarity 88.2%;
Matches 115; Conservative
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Matches 15% Conserve
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US-09-672-609
                                                                                                                                                                                                                                                                                                                                                                                         Query Match
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FEATURE:
NAME/KEY: Humanized COL-1 VH, HuVHSTAY
LOCATION: 1.1.124
LOCATION: 1.1.124
COTHER INFORMATION: Humanized heavy chain variable region expressed from ATCC
OTHER INFORMATION: CRL-12208, and containing human NEWM VH FRs, murine COL-1 VH C
OTHER INFORMATION: and Phe-27, Asn-28, Ile-29, Lys-30, Ser-76, Thr-78, Ala-79,
OTHER INFORMATION: Tyr-80, Asn-97, and Thr-98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
APPLICANT: Anderson, W.H. Kerr
APPLICANT: Tempost, Philip R.
APPLICANT: Tempost, Philip R.
APPLICANT: Tempost, Philip R.
APPLICANT: Armour, Railiam J.
APPLICANT: Harris, William J.
APPLICANT: Harris, William J.
APPLICANT: Armour, Railiam J.
APPLICANT: Armour, Railiam J.
APPLICANT: Armour, Railiam J.
APPLICANT: Armour, Railiam J.
APPLICANT: APPLICANTON
HIGH AFFLING
CURRENT FILING DATE: 2000-09-28
PRIOR FILING DATE: 1998-02-18
PRIOR PLING DATE: 1998-02-18
NUMBER OF SEQ ID NOS: 50
SOFTWARE: MICROSOft Word 97 SR-2
SEQ ID NO 12
SEQ ID NO 12
                                                                                                                                                      APPLICANT: Anderson, W.H. Kerr
APPLICANT: Tempest, Philip R.
APPLICANT: Tempest, Philip R.
APPLICANT: Tempest, Prank J.
APPLICANT: Ternk J.
APPLICANT: Harris, William J.
APPLICANT: Armour, Kathryn
TITLE OF INVENTION: High Affinity Humanized Anti-CEA Monoclonal Antibodies
FILE REFERENCE:
CURRENT APPLICATION NUMBER: US/09/672,609
GURRENT FILING DATE: 2000-09-28
PRIOR FILING DATE: 1998-02-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LOCATION: 1..124

TOTER INFORMATION: Humanized heavy chain variable region containing human OTHER INFORMATION: NEWM VH FRs, murine COL-1 VH CDRs, and Phe-27, Asn-28, OTHER INFORMATION: Ile-29, Lys-30, Ser-76, Asn-97, and Thr-98
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 94; DB 4; Length 124
Pred. No. 6.2e-08;
2; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME/KEY: Humanized COL-1 VH, HuVHS
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                                                                               Sequence 11, Application US/09672609 Patent No. 6333405
                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQ ID NOS: 50
SOFTWARE: Microsoft Word 97 SR-2
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Best Local Similarity 88.28;
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US-09-672-609-12
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LENGTH: 124
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APPLICANT: Tempest, Philip R.
APPLICANT: Carr, Frank J.
APPLICANT: Harris, William J.
APPLICANT: Harris, William J.
APPLICANT: Armour, Kathryn
TITLE OF INVENTION: High Affinity Humanized Anti-CEA Monoclonal Antibodies
APPLICANT: Anderson, W.H. Kerr
APPLICANT: Tempest, Philip R.
APPLICANT: Tempest, Philip R.
APPLICANT: Tempest, Philip R.
APPLICANT: Harris, William J.
APPLICANT: Harris, William J.
APPLICANT: Armour, Kathryn
TITLE OF INVENTION: High Affinity Humanized Anti-CEA Monoclonal Antibodies
FILE REPERBNCE:
CURRENT APPLICATION NUMBER: 05/09/672,609
PRIOR APPLICATION NUMBER: 09/025,403
PRIOR FILING DATE: 1998-02-18
NUMBER OF SEQ ID NOS: 50
SOFTWARE: Microsoft Word 97 SR-2
SEQ ID NO 9
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Pred. No. 6.2e-08;
2; Mismatches 0; Indels
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88.2%; Pred. No. 6.2e-08;
tive 2; Mismatches 0;
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CURRENT FILING DATE: 2000-09-28
PRIOR APPLICATION NUMBER: 09/025,403
PRIOR FILING DATE: 1998-02-18
NUMBER OF SEQ ID NOS: 50
SEQ ID NO 10
LENGTH: 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME/KEY: Humanized COL-1 VH, HUVHASTAY LOCATION: 1..124
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Patent No. 6333405
                                                                                                                                                                                                                                                                                                                                                                                              TYPE: PRT
ORGANISM: Artificial Sequence
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88.2%;
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Best Local Similarity 88.2
Matches 15; Conservative
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Gaps

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Length 124;

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Best Local Similarity 88.2%; Pred. No. 6.2e-08; Matches 15; Conservative 2; Mismatches 0; Indels 0; Gaps

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Search completed: December 23, 2002, 07:33:18 Job time : 3.06395 secs

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December 23, 2002, 07:17:57; Search time 3.36047 Seconds (without alignments) 486.327 Million cell updates/sec
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GenCore version 5.1.3
Copyright (c) 1993 - 2002 Compugen Ltd.
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                                                                               - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 200000000
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution. pirl:*
pir2:*
pir3:*

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

PIR_73:*

Database

Ig heavy chain v r gamma chain (WM gheavy chain V-D gamma-1 chain heavy chain V r heavy chain V r heavy chain V r Description SUMMARIES D37262 PH1013 PH1012 S31680 S18551 S36265 S03471 S06823 D33548 PH1403 S46393 S49530 S29594 S03484 S49220 6465 Query Match Length DB Score Result No.

RESULT 2 S25174

monoclonal antibodies to core hist

Ug heavy chain V region - mouse .
C; Species: Mus musculus (house mouse)
C; Species: Mus musculus (house mouse)
C; Species: Mus musculus (house mouse)
C; Accession: S25174; S3133
R; Monestier, M.; Fasy, T.M.; Losman, M.J.; Novick, K.E.; Muller, S. submitted to the EMBL Data Library, July 1992
A; Description: Structure and binding properties of monoclonal antibodies to A; Reference number: S25174
A; Status: preliminary
A; Status: preliminary
A; Molecule type: mRNA
A; Residues: 1-118 < MON>

A;Cross-references: EMBL:X67622; NID:951854; PIDN:CAA47880.1; PID:9938259 A;Accession: S33133 A;Status: preliminary A;Molecule type: mRNA

Ig heavy chain V r Ig gamma chain V r Ig heavy chain V r	ALIGNMENTS	RESULT 1 A36025 Id heavy chain V region (PR8-1) - mouse (fragment) C; Date: 11-Jan-1991 #sequence_revision 11-Jan-1991 #text_change 23-Jul-1999 R; Caton, A.J.; Koprowski, H. Proc. Natl. Acad. Sci. U.S.A. 87, 6450-6454, 1990 A; Title Influence virus hemagglutinin-specific antibodies isolated from a combinator A; Reference number: A36025; MUD:90349634; PMID:16966733 A; Acatous: preliminary A; Residues: 19-82 < CAT> A; Residues: 19-82 < CAZ> A; Accas-references: GB:M55999; NID:9194963; PIDN:AAA38112.1; PID:9194964 A; Rocas-references: GB:M55273; NID:9194963; PIDN:AAA38116.1; PID:9194964 A; Mote: PR8-12 A; Mote: PR8-12 A; Mote: PR8-12 C; Superfamily: immunoglobulin V region; immunoglobulin homology C; Superfamily: immunoglobulin V region; immunoglobulin Nowlogy C; Superfamily: immunoglobulin V region; immunoglobulin V V V V V V V V V V V V V V V V V V V
\$31600 \$29544 \$16028 \$24289 \$24289 \$16028 \$24289 \$1666 \$26911 \$1999 \$23623 \$31999 \$23623 \$31999 \$23623 \$31999 \$23623 \$31999	ALIGN	SULT 1 6025 heavy chain V region (PR8-1) - mouse (fra Species: Mus musculus (house mouse) Date: 11-Jan.1991 #sequence_revision 11-Ja. Accession: A36025; E36025 Caton, A.J.; Koprowski, H. Ccton, A.J.; Koprowski, H. Ccton, A.J.; Koprowski, H. Title: Influenza virus hemagglutinin-speci Reference number: A36025; MUID:90349634; P. Accession: A36025 Accession: A36025 Accession: B36025 Ccoss-references: GB:M55999; NID:g194955; Note: PR8-1 Accession: E36025 Status: preliminary Molecule type: mRNA Redidues: 19-82 CCAN> Ccoss-references: GB:M55999; NID:g194963; Note: PR8-1 Accession: B36025 Actus: preliminary Molecule type: mRNA Redidues: 19-82 CCAN> Ccoss-references: GB:M57273; NID:g194963; Note: clone PR8-21 Superfamily: immunoglobulin V region; immu Reywords: heterotetramer; immunoglobulin Ouery Match Best Local Similarity 88.2%; Pred. No. Matches 15; Conservative 2; Mismatc 1 WIDPENGDSPAPKFQG 17 1 WIDPENGDYAPKFQG 28
000000000000000		-1). se mce_ree aggll mUID MUID MIID immu immu 17 17 28
136 97 97 97 111 111 112 120 120 127 127		region (PR8-1) - mouse mouse) 91 #sequence_revision 25; E36025 Prowski, H. Sci. U.S.A. 87, 645 a virus hemagglutini 1: A36025; MUID:9034 2: A36025; MUID:9034 2: GA17 mRNA cCAT7 s: GB:M5599; NID:91 25 nary mRNA cRA 125 nary mRNA cGA2> 125 nary mRNA cGA2> 126 nary mRNA cGA2> 127 128 1318; Scc larity 88.28; Pre Conservative 2; DSDYAPKFOG 17 1:: DTEYAPKFOG 17 1:: DTEYAPKFOG 28
00000000000000000000000000000000000000		hain V region (PRM Mus musculus (hou Jan - 1991 #sequenon: A36025; E36025 . J.; Koprowski, H . Acad. Sci. U.S.; Acad. Sci. U.
8 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2		y chain V region less: Mus musculus sion: A36025; E3 N. A.J.; Koprowsk wall. Acad. Sci. Influenza viru ence number: A36 ssion: A36025 ssion: A36025 ssion: A36025 ssion: B36025 ssion: B
0.11 0.00 0.00 0.00 0.00 0.00 0.00 0.00		RESULT 1 A36025 Ig heavy chain V region (PR8-1) - mouse (S.Species: Mus musculus (house mouse) C.Species: Mus musculus (house mouse) C.Species: Mus musculus (house mouse) C.Accession: A36025, E36025 A;Title: Influenza Virus hemagglutinin- A;Reference number: A36025; MUID:903496 A;Accession: A36025 A;Status: preliminary A;Molecule type: mRNA A;Residues: 1-82 < CAT> A;Cross-references: GB:M55999; NID:g194 A;Note: PR8-1 A;Accession: E36025 A;Status: preliminary A;Molecule type: mRNA A;Accession: E36025 A;Status: preliminary A;Molecule type: mRNA A;Residues: 19-82 < CAZ> A;Cross-references: GB:M55999; NID:g194 A;Note: clone PR8-21 C;Superfamily: immunoglobulin V region; C;Superfamily: immunoglobulin V region; C;Superfamily: immunoglobulin V redion; C;Superfami

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A Map position: 14q32.33-14q32.33
C; Superfamily: immunoglobulin V region; immunoglobulin homology
C; Superfamily: immunoglobulin V region; immunoglobulin; pyroglutamic acid
C; Seywords: heterotetramer; immunoglobulin; pyroglutamic acid
F; 1-15/Domain: signal sequence #status predicted <SIG>
F; 16-143/Porduct: Ig heavy chain V-I region (Nd) #status predicted <NAT>
F; 30-113/Domain: immunoglobulin homology <IMM>
F; 16/Modified site: pyrrolidone carboxylic acid (Gln) (in mature form) #status experi
F; 37-111/Disulfide bonds: #status experimental
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Cispecies: Homo sapiens (man)
Cibate: 11.Mar-11801 Hasquence_revision 05-Apr-1983 #text_change 21-Jan-2000
Cibate: 31.Mar-11801 Hasquence_revision 05-Apr-1983 #text_change 21-Jan-2000
Ciracession: A93933; A02026
R;Kenten, J.H.; Molgaard, H.V.; Houghton, M.; Derbyshire, R.B.; Viney, J.; Bell, L.O. Proc. Natl. Acad. Sci. U.S.A. 79, 661-6665, 1982
A;Title: Cloning and sequence determination of the gene for the human immunoglobulin A;Reference number: A93933; MUID:83065234; PMID:6815656
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Accession: A93933
A; Molecule type: mRNA
A; Residues: 1-143 < KEN>
R; Bennich, H.H.; Johansson, S.G.O.; Von Bahr-Lindstrom, H.
in Immediate Hypersensitivity: Modern Concepts and Developments, Bach, M.K., ed., pp.
A; Reference number: A94418
A; Contents: annotation; partial sequence
A; Note: this epsilon chain was isolated from a myeloma protein
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Ig heavy chain V region (6H2) - mouse (fragment)
C.Species: Mus musculus (house mouse)
C.Spate: 30-Aug-1991 #sequence_revision 30-Aug-1991 #text_change 09-May-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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C; Superfamily: inmunoglobulin V region; immunoglobulin homology
C; Keywords: heterotetramer; immunoglobulin
F; 34-115/Domain: immunoglobulin homology <IMM>
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Pred. No. 0.0016;
5; Mismatches 2; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 78; DB 2; Pred. No. 3.8e-05;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Cross-references: GDB:128528; OMIM:147070
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58.8%;
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Best Local Similarity 76.5%;
Matches 13; Conservative
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65 WINPNSGGTNYAPRFQG 81
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Matches 10; Conservative
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C; Species: Mushmusculus (house mouse)
C; Date: 04-Dec_1992 #sequence_revision 04-Dec-1992 #text_change 21-Jan-2000
C; Accession. SQ4576
R; Kofler, R.; Moonan, D.J.; Strohal, R.; Balderas, R.S.; Moller, N.P.H.; Dixon, F.J.; The Eur. J. Immunol. 17, 91-95, 1987
A; Title: Molecular analysis of the murine lupus-associated anti-self response: involveme A; Reference number: S04573; MUID:87133856; PMID:3102255
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 C;Accession § S15672
R;Tempest, P.R; Brenner, P.; Lambert, M.; Taylor, G.; Furze, J.M.; Carr, F.J.; Harris, B10/Technology 9, 266-271, 1991
A;Title: Reshaping a human monoclonal antibody to inhibit human respiratory syncytial vi A;Reference funmber: S15672; MUID:91337412; PMID:1367535
A;Accession § S15672
A;Status: preliminary; nucleic acid sequence not shown
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C;Superfamily immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;1-19/Domain; signal sequence #status predicted <SIG>
F;20-136/Product: Ig heavy chain V region (fragment) #status predicted <WAT>
F;34-117/Domain: immunoglobulin homology <IMM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ig heavy chain V region - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 18-Eeb-1994 #sequence_revision 10-Nov-1995 #text_change 21-Jan-2000
                                               A;Cross-references: EMBL:X67622; NID:951854; PIDN:CAA47880.1; PID:9938259 Cs. Superfamilty: immunoplobulin V region; immunoglobulin homology C;Keywords: hererotetramer; immunoglobulin P:15-98/Domain: immunoglobulin homology <IMM>
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A; Residues: 1-116 <TEM>
A; Cross-references: EMBL:X58835; NID:951978; PIDN:CAA41644.1; PID:951979
C; Superfamily: immunoglobulin V region; immunoglobulin homology
C; Keywords; heterotetramer; immunoglobulin
F;15-98/Domain: immunoglobulin homology <IMM>
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ilarity 82.4%; Pred. No. 4.1e-06;
Conservative 1; Mismatches 2;
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82.4%; Pred. No. 7.2e-06;
Live 0; Mismatches 3;
                                                                                                                                                                                              Score 86; DB 2;
Pred. No. 1.7e-06;
                                                                                                                                                                                                                                                    2; Mismatches
                                                                                                                                                                                              Query Match 85.1%;
Best Local Similarity 82.4%;
Matches 14; Conservative
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es 14; Conserv
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A; Residues: 12136 <KOF>
                          A; Residues: 1-118 <MO2>
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Matches
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Best Loc Matches

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C;Accession: S26912
R;Tomlinson, I.M.; Walter, G.; Marks, J.D.; Llewelyn, M.B.; Winter, G.
J. Mol. Biol. 227, 776-798, 1992
A;Title: The repertoire of human germline V(H) sequences reveals about fifty groups o A;Reference number: S26885; MUID:93021117; PMID:1404388
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Joheavy chain V region (2E5) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Species: Mus musculus (house mouse)
C;Species: 30-Aug-1991 #sequence_revision 30-Aug-1991 #text_change 21-Jan-2000
C;Accession: J37-202
R;Goshorn, S.C.; Retzel, E.; Jemmerson, R.
J. Biol. Chem. 266, 2134-2142, 1991
A;Title: Common structural features among monoclonal antibodies binding the same anti A;Reference number: A38601; MUID:91115823; PMID:1703527
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C; Species: Mus musculus (house mouse)
C; Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 21-Jan-2000
C; Accession: PH1013
B; Tillman, D.M.; Jou, N.T.; Hill, R.J.; Marion, T.N.
J. Exp. Med. 176, 761-779, 1992
A; Title: Both IgM and IgG anti-DNA antibodies are the products of clonally selective A; Reference number: PH0971; MUID:92381444; PMID:1512540
                                                                                                                                                                                                                                C;Species: Homo sapiens (man)
C;Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 23-Jul-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Residues: 1-98 <TOM>
A; Residues: 1-98 <TOM>
A; Cross-references: EMBL.212310; NID:932979; PIDN:CAA78180.1; PID:932980
C; Superfamily: immunoglobulin V region; immunoglobulin homology
C; Keywords: heterotetramer; immunoglobulin
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A;Residues: 1-99 <GOS>
A;Cross-references: GB:M57990; NID:g195046; PIDN:AAA63328.1; PID:g195047
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;7-90/Domain: immunoglobulin homology <IMM>
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58.8%; Pred. No. 0.0066;
11ve 4; Mismatches 3;
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Pred. No. 0.0067;
2; Mismatches 3;
                                                                                                                                                                                                      Ig heavy chain V region (DP-8) - human (fragment)
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68.8%;
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                   1 WIDPENGDSDYAPKFQG 17
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Matches 10; Conservative
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IDPANGNTKYDPKFQG 58
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Best Local Similarity
Matches 11; Conserv
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A; Status: preliminary
A; Molecule type: DNA
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C; Accession: E37262
R; Gosborn, S.C.; Retzel, E.; Jemmerson, R.
J. Biol. Chem. 266, 2134-2142, 1991
A;Title: Common structural features among monoclonal antibodies binding the same antiger A; Reference number: A38601; MUID:91115823; PMID:1703527
A; Accession: E37262
A; Status: preliminary; not compared with conceptual translation
A; Molecule type: mRNA
A; Residues: 1-85 GGOSA
A; Residues: 1-85 GGOSA
A; Cross-references: GB:M57991
C; Superfamily: immunoglobulin V region; immunoglobulin homology
C; Keywords: heterotetramer; immunoglobulin
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C; Date: 22-Nov-1993 #sequence_revision 17-Nov-1995 #text_change 23-Jul-1999
C; Date: 22-Nov-1993 #sequence_revision 17-Nov-1995 #text_change 23-Jul-1999
C; Date: 22-Nov-1993 #sequence_revision 17-Nov-1995 #text_change 23-Jul-1999
C; Accession: S6938
R; Tominson, I.M.; Walter, G.; Marks, J.D.; Llewelyn, M.B.; Winter, G.
J. Mol. Biol. 227, 776-798, 1992
A; Mol. Biol. 227, 776-798, 1992
A; Recession: S26885; MulD: 93021117; PMID:1404388
A; Recession: S26938
A; Recession: S26938
A; Recession: S26938
A; Recession: S26938
A; Residues: 1-98 < TOM>
A; Molecule type: DNA
A; Residues: 1-98 < TOM>
A; Molecule type: DNA
A; Residues: 1-98 < TOM>
A; Molecule type: DNA
A; Residues: 1-98 < TOM>
A; Molecule type: DNA
A; Cross references: EMBL:24071; NID:932969; PIDN:CAA78451.1; PID:932970
A; Mote: the nucleotide sequence was submitted to the EMBL Data Library, July 1992
C; Superfamily: immunoglobulin V region; immunoglobulin homology < IMM>
F; 15-98/Domain: immunoglobulin homology < IMM>
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C; Species: Homo sapiens (man)
C; Species: Homo sapiens (man)
C; Species: Homo sapiens (man)
C; Accession: S54912
R; Tomlinson, M.; Walter, G.; Cook, X.Y.Z.; Winter, G.
submitted to the EMBL Data Library, November 1992
A; Reference number: S54912
A; Reference number: S54912
A; Accession: S54912
A; Accession: S54912
A; Accession: Breal inhary
A; Molecule type: DNA
A; Residues: 1-86 < TOM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Cross-references: EMBL:218904; NID:9840779; PIDN:CAA79341.1; PID:9840780 C;Superfamily: immunoglobulin V region; immunoglobulin homology F;3-86/Domain: immunoglobulin homology <IMM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 63; DB 2; Length 98;
Pred. No. 0.0066;
4; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                         Score 67; DB 2; Length 85;
Pred. No. 0.0013;
1; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ig heavy chain V region (DP-75) - human (fragment)
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58.8%;
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75.0%;
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Best Local Similarity 64.7
Matches 11; Conservative
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Best Local Similarity
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RESULT 9

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Gaps

RESULT 8

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Gaps

1 WIDPENGDSDYAPKFQG 17

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Search completed: December 23, 2002, 07:31:39 Job time : 4.36047 secs
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C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Accession: 831680
R;Cuisinier, A.M.; Gauthier, L.; Boubli, L.; Fougereau, M.; Tonnelle, C. Submitted to the EMBL Data Library, June 1992
A;Description: Mechanisms that generate human immunoglobulin diversity operate from the A;Reference number: 831585
A;Accession: 331680
                                                                                                                                                                                                                                                                                                                                                                                               In heavy chain, V region (clone 17p.73) - mouse (fragment)
C; Species: Mus musculus (house mouse)
C; Species: Mus musculus (house mouse)
C; Species: Mus musculus (house mouse)
C; Accession: PH1012
R; Tillman, D.M; Jou, N.T.; Hill, R.J.; Marion, T.N.
J. Exp. Med. 176, 761-779, 1992
A; Title: Both iggm and IgG anti-DNA antibodies are the products of clonally selective B. A; Reference number: PH0971; MUID:92381444; PMID:1512540
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C; Superfamily; Immunoglobulin V region; Immunoglobulin homology
C; Keywords: hèterotetramer; Immunoglobulin
F;15-98/Domaiñ: immunoglobulin homology <IMM>
                                        A;Experimental gource: B cell, strain [NZB x NZW]F1
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heteroterramer; immunoglobulin
F;15-98/Domain: immunoglobulin homology <IMM>
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C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: {heterotetramer; immunoglobulin
F;34-117/Domain: immunoglobulin homology <IMM>
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                                                                                                                                                      Length 107
                                                                                                                                                      Score 63; DB 2; Length 107
Pred. No. 0.0073;
2; Mismatches 2; Indels
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Pred. No. 0.0073;
2; Mismatches 2; Indels
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58.8%; Pred. No. 0.008;
iive 4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Status: nucleic acid sequence not shown
                                                                                                                                                    62.4%;
illarity 73.3%;
Conservative
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Best Local Similarity 73.3%;
Matches 11; Conservative
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                                                                                                                                                                                                                                             2 IDPENGDSDYAPKFQ 16
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                                                                                                                                                      Query Match
Best Local Similarity
Matches 11; Conserv
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A; Residues: 1-108 <TIL>
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A;Molecule type: mRNA
A;Residues: 1-117 <CUI>
A; Residues: 1-107
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A;Cross-references: EMBL:X62106; NID:g37831; PIDN:CAA44016.1; PID:g37832
R;Olee, T.; Lu, E.W.; Huang, D.F.; Soto-Gil, R.W.; Deftos, M.; Kozin, F.; Carson, D.A.
J. Exp. Med. 175, 831-842, 1992
                          C; Species: Homo sapiens (man)
C; Species: Homo sapiens (man)
C; Date: 13-4m-1995 # sequence_revision 06-Jun-1997 # text_change 23-Jul-1999
C; Date: 13-5m-1995 # sequence_revision 06-Jun-1997 # text_change 23-Jul-1999
C; Date: 13-5m-1995 # sequence_revision 06-Jun-1997 # text_cession: S18551; S23625
EMBO J. 10, 3641-3645, 1991
A; Title: Physical map of the 3' region of the human immunoglobulin heavy chain locus: A; Reference number: S18551; MUID:92037524; PMID:1935893
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Title: Genetic analysis of self-associating immunoglobulin G rheumatoid factors fro
A;Reference number: S23623; MUID:92156804; PMID:1740665
A;Accession: S23625
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A; Residues: 1-117 <OLE>
A; Cross-references: EMBL:X59704; NID:932552; PIDN:CAA42225.1; PID:932553
C; Genetics:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          C;Superfamily: immunoglobulin V region; immunoglobulin homology C;Keywords: heterotetramer; immunoglobulin
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Ig heavy chain V region precursor (VI-2) - human (fragment)
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A; Residues: 1-117 <SHI>
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December 23, 2002, 07:16:17; Search time 1.68023 Seconds (without alignments) 419.643 Million cell updates/sec
GenCore version 5.1.3
Copyright (c) 1993 - 2002 Compugen Ltd.
                                                                                                     OM protein - protein search, using sw model
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US-09-865-198-21 101 1 WIDPENGDSDYAPKFOG 17 Title: Perfect score: Sequence: Scoring table:

112892 seqs, 41476328 residues BLOSUM62 Gapop 10.0 , Gapext 0.5 Searched:

112892 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

SwissProt_40:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Description	DOIT44 homo sanden	3 homo	3 homo	homo	Q9bzz2 homo sapien	m snm g	snw /	P06327 mus musculu	0	Q9m8d3 arabidopsis	7	P30589 neurospora		P23306 escherichia	P37124 solanum mel	P40596 azotobacter	P97838 rattus norv	P97929 mus musculu	P01746 mus musculu	P03982 caiman croc	Sa	Q11190 c probable	P01750 mus musculu	P06329 mus musculu	Q9s7b5 arabidopsis		Q14162 homo sapien	014490 homo sapien	6 rattu	2 homo	_	Q19311 caenorhabdi	P35421 drosophila
SUMMAKIES	ID	HV1C HIMAN	HV1G HUMAN	HV1B_HUMAN	NUD9_HUMAN	SN_HUMAN	HV12_MOUSE	HV13_MOUSE	HV52_MOUSE	HV51_MOUSE	PUR4_ARATH	MCE1_SCHPO	CHS2_NEUCR	HV03_MOUSE	YIGB_ECOLI	C772_SOLME	HYPF_AZOVI	DLP3_RAT	BRC2_MOUSE .	HV02_MOUSE	HV03_CAICR	YG1F_YEAST	ETFD_CAEEL	HV06_MOUSE	HV50_MOUSE	THRC_ARATH	HELS_HALN1	SREC_HUMAN	DLP1_HUMAN	DLP1_RAT	EPA8_HUMAN	PUR4_HUMAN	PUR4_CAEEL	PUR4_DROME
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P15368 p fatty aci P36704 human adeno									
FAS2_PENPA DNBI ADE12	HV1A_HUMAN	RNP_HUMAN YG24_HAEIN	MOX1_HUMAN	YMY9_YEAST	PAI2_RAT	PACR_MOUSE	PACR_RAT	GFA1_CANAL	MTO1_HUMAN
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ALIGNMENTS

KESULT HV1C_H ID H	HV1C_HUMAN ID HV1C_HUMAN	STAN	STANDARD;	PRT;	147 A	AA.				
N E	21-JUL-1986	(Rel. 0	01, Created)	(þa						
i di	16-0CT-2001 16-0CT-2001	(Rel. 4	(Rel. 40, Last sequence update) (Rel. 40. Last annotation updat	sequence update)	update n upda	(t)				
DE	Ig heavy chain V-I region ND precursor (Fragments)	in V-I	region NE	brecurs	or (Fr	agments				
SO	Homo sapiens (Human)	(Human								
8	Eukaryota; Metazoa;	letazoa;	Chordata;		ta; Ve	rtebrat		stom	.;	
ပွ	Mammalia; Eutheria;	theria;			hini;	Catarrhini; Hominidae;	ае; ношо.			
<u> </u>	NCB1_Tax1D=9606;	: 909								
X t	[1]									
국 5 5	SEQUENCE FROM N.A.	M N.A.	LO DA GOL							
Z Z	Kenten J.H., Molgaard H.V., Houghton M., Derbyshire	Molgaa	rd H.V.	Houghton	Ξ.	erbyshi	R. B.	Vinev	J.,	
RA	Bell L.O., Gould H.J.;	ould H.	٦.,			1		•		
RT	"Cloning and sequence determination of	sequen	ce detern	ination	of the	the gene for		nan		
RŢ	1mmunoglobulin epsilon chain expressed in a myeloma	in epsi	lon chair	express	ed in	a myelo	ma cell line."	".eu	•	
Z Z	Proc. Natl.	Acad. S	ct. U.S.	۸. 79:666	1-6665	(1982).				
Z ([2]									
¥ 5	SEQUENCE OF ZU-14/	./#I-U2		. Horatopati-wated act.	7 - 24 - 0	1000				
5 2	(Tr) Bach M K (eds):	X COLIAL			Daill 1	ייייייייייייייייייייייייייייייייייייייי	· · · · ·			
R.	Immediate hypersensitivity: modern concepts and	persens	itivity:	modern c	oncept	s and d	developments, pp.1-36,	id 's:	5.1-36,	
R.	Marcel Dekke	ir, New	York (197	.8).	•		•			
ပ္ပ	-!- MISCELLANEOUS: THIS EPSILON CHAIN WAS	ANEOUS:	THIS EPS	CLON CHAI	N WAS	ISOLATE	ISOLATED FROM A MYELOMA	AYELOI	ΨA	
ນູ	PROTEIN.									
DR	PIR; A02026; E1HUND.	ETHUNE								
DR	HSSP; P01789	9; IMCP.								
DR		IPR003006;								
DR	InterPro; IP	IPR003596;	, Ig_v.							
DR	Ptam; PF00047; 1g; 1.	17; 19;	1.							
Ä.	SMART; SMU04	106; IGV	. ;	-						
X E	Immunogrobutin V region;	110 V re		signal.						
. E	CHAIN	70	147	TG HEAV	Y CHAI	N V-T R	TO HEAVY CHAIN V-T REGION ND			
댎	MOD RES	20	20	PYRROLI	DONE	ARBOXYL	PYRROLIDONE CARBOXYLIC ACID.			
FŢ	DISULFID	41	115							
FT	CONFLICT	21	21	T -> V (IN REF.	(IN RE	6				
FT	CONFLICT	53	54	IH -> HI (IN REF.	NI) I					
FI	CONFLICT	29	89	VG -> GV		(IN REF. 2)				
FT	CONFLICT	125	125	MISSING (IN REF.	(IN I	(4				
FΤ			147							
SO	SEQUENCE 1	147 AA;	16491 MW;		F72A5	948F9F72A5366C20 CRC64;	RC64;			
no o	Query Match	***************************************	67.38;	Score 68;		DB 1; Le	Length 147;			
X a	10;	Similarity 20.0 10; Conservative	Jo.00; rative	5; Mismat		2;	Indels	0;	Gaps	
οy	1 WIDPENGDSDYAPKFQG	SDSDYAPR	(FQG 17							
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RESULT 2

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
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SEQUENCE FROM N.A.

MEDLINE-83144028; PubMed-6298778;

Rechave G., Ram D., Glazer L., Zakut R., Givol D.;

Rechave G., Ram D., Glazer L., Zakut R., Givol D.;

Rechave G., Ram D., Glazer L., Zakut R., Givol D.;

Rechave G., Ram D., Glazer L., Zakut R., Givol D.;

(VH) Gene subgroups.";

Rechave G., Natl. Acad. Sci. U.S.A. 80:855-859(1983).

Proc. Natl. Acad. Sci. U.S.A. 80:855-859(1983).
                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
MEDLINE-88296408; Pubmed-2841108;
MEDLINE-88296408: Pubmed-2841108;
Matsuda F.; Lee K.H., Nakai S., Sato T., Kodaira M., Zong S.O.,
Ohno H., Fukuhara S., Honjo T.;
"Dispersed localization of D segments in the human immunoglobulin
                                                                                                                                                                                                                                                  Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
NCBI_TaxIQ=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryōta; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 52; DB 1; Length 117;
Pred. No. 0.21;
4; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         13009 MW; BE61CE63F8CE97BD CRC64;
                                                                               01-NOV-1991 (Rel. 20, Created)
01-NOV-1991 (Rel. 20, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
18 heavy chain V-I region V35 precursor.
Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
19 heavy chain V-I region HG3 precursor.
Homo sapiens (Human)
                             117 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; X03448; -; NOT_ANNOTATED_CDS. PIR; S00476; HVHU35. INSP. PO$\text{T72}$. 2Fe4 InterProf. IPR003006; Ig_MHC. InterProf. IPR003506; Ig_V. Pfan; PR0047; Ig' 1. SMART; SM00406; IGV; 1. Immunog1\text{Cobultn} V region; Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        51.5%;
56.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBO J. 751047-1051(1988).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best Local Similarity 56.2
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     |:|| :| ::|. | || || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10
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                             STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2 IDPENGDSDYAPKFOG 17
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117 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                heavy-chain locus."
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                   HV1G_HUMAN, P23083;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              HV1B_HUMAN
ID HV1B_HUMAN
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HV1G_HUMAN
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            and for commercial
use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDITRE-2179171; PubMed-11385575;
Perraud A.-L., Fleig A., Dunn C.A., Bagley L.A., Launay P.,
Schmitz C., Stokes A.J., Zhu Q., Bessman M.J., Penner R., Kinet J.-P.,
Scharenberg A.M.,
"ADP-ribose gating of the calcium-permeable LTRPC2 channel revealed by
Nudix motif homology.";
Nature 411:595-599(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        phosphate.
-1- TISSUE SPECIFICITY: Ubiquitous.
-1- SIMILARITY: BELONGS TO THE NUDIX HYDROLASE FAMILY. NUDF SUBFAMILY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             15-JUN-2002 (Rel. 41, Created)
15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
15-JUN-2002 (Rel. 41, Last annotation update)
ADP-ribose pyrophosphatase (EC 3.6.1.13) (ADP-ribose diphosphatase)
Addenosine diphosphoribose pyrophosphatase) (ADP-ribose phosphohydrolase) (Nucleoside diphosphate-linked moiety X motif 9).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Chordata; Craniata; Vertebrata; Euteleostomi;
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                                                                                                                                                                                                                                                                                                                                                                                                                                        IG HEAVY CHAIN V-I REGION HG3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 117;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eutese
Mammalla; Eutherla; Primates; Catarrhini; Hominidae; Homo
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              50.5%; Score 51; DB 1; 56.2%; Pred. No. 0.31;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          350 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2; Mismatches
                                                                                                                                                  EMBL, J00240; AAA52988.1; -. PTR, A02024; HVHDHG. HSSP, P01772; ZFB4. InterPro: IPR003066; Ig_MRC. InterPro: IPR003596; Ig_V. Pfam: PF00047; 1g; 1. SMART; SM00406; IGV; 1. SMART; SM00406; IGV; 1. SMART; SM0406; IGV; 1. 1. 19
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           117 AA;
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SEQUENCE
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         HID DESCRIPTION OF STREET 
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Genew; HGNC:8056; NUDT9

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RAY PEQUENCE FROM N.A. (ISOFORMS 1 AND 2).

RECURSE SEQUENCE FROM N.A. (ISOFORMS 1 AND 2).

RECURSE SEQUENCE FROM N.A. (ISOFORMS 1 AND 2).

RECURSE SEQUENCE SEC. Almedda J.P., Babbage A.K., Bagguley C.L.,

RA JONES M., Stavides G., Almedda J.P., Babbage A.K., Bagguley C.L.,

RA Bailey J., Barlow K.F., Bates K.N., Beard L.M., Beare D.M.,

RA Basley O.P., Bird C.P., Blakey S.E., Bridgeman A.M., Brown A.J.,

RA Buck D., Burrill W.D., Butler A.P., Carder C., Carter N.P.,

RA Coulson A., Coville G.J., Deadman R.E., Connor R.E., Corby N.R.,

Coulson A., Coville G.J., Deadman R.E., Corby N.R.,

RA Ellington A.G., Frankland J.A., Fraser A., French L., Garner P.,

RA Blington A.G., Frankland J.A., Heath P.D., HO.S., Holden J.L., Howden P.J.,

RA Bamond S., Harley J.L., Heath P.D., HO.S., Holden J.L., Howden P.J.,

RA Huckle E., Hunt A.R., Hunt S.E., Jekosch K., Johnson C.M., Johnson D.,

RA Marsh V.L., Martin S.L., McConnachie L.J., McLay K., McMurray A.A.,

RA Milne S.A., Mistry D., Moore M.J.F., Mullikin J.C., Nickerson T.,

RA Phillimore B.J.C.T., Prathalingam S.R., Plumb R.W., Ramsay H.,

RA Phillimore B.J.C.T., Prathalingam S.R., Plumb R.W., Ramsay H.,

RA Swann R.M., Sycamore N., Taylor R., Tee L., Thomas D.W., Thorpe A.,

RA Tracey A., Tromans A.C., Vaudin M., Wallis J.M.,

RA Tracey A., Tromans A.C., Vaudin M., Wallis J.M.,

Mitchead S.L., Withtaker P., Willey D.L., Williams L., Williams S.A.,

Whitchead S.L., Witay P.W., Hubbard T., Durbin R.M., Bentley D.R., Beck S.,

RA Rogers J.:
                                                                                                                                       ö
                                                                                                                                                                                                                                                          SN_HUMAN STANDARD; PRT; 1709 AA. O9B2Z2; 09H1H5; Q9H1H7; Q9GZS5; 16-C7-2001 (Rel. 40, created) 16-CCT-2001 (Rel. 40, Last sequence update) 15-JUN-2002 (Rel. 41, Last annotation update) 5ialoadhesin precursor (Sialic acid binding Ig-like lectin-1) (Siglec-
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Hartnell A., Steel J., Turley H., Jones M., Jackson D., Crocker P.R.; "Characterisation of human sialoadhesin (siglec-1), a sialic acid binding receptor expressed on resident and inflammatory macrophage populations."; Submitted (JAN-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        the DNA sequence and comparative analysis of human chromosome 20."; ture 414:865-871(2001).
                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ohara O., Nagase T., Kikuno R., Okumura K.; "The nucleotide sequence of a long cDNA clone isolated from human
                                                                                                                                       ö
                                                                                                       50.5%; Score 51; DB 1; Length 350; 46.7%; Pred. No. 1; Live 5; Mismatches 3; Indels
                                                                   NUDIX BOX.
2EA5B24B88FB3420 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE OF 733-1709 FROM N.A. (ISOFORMS 1 AND 2).
       PITE, PRO00086; NUDIX_hydrolase. Pfam; PF00293; NUDIX; 1. PROSITE; PS00893; NUDIX; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A. (ISOFORM 1).
                                                                237 N
39125 MW;
                                                                                         Query Match
Query Match
Best Local Similarity 46./*,
7; Conservative
                                                                                                                                                                             | | | : :|::|||
110 WADPQISESNFSPKF 124
                                                                                                                                                               WIDPENGDSDYAPKF 15
                                                                215 23
350 AA;
                                                                                                                                                                                                                                                                                                                                              (CD169 antigen).
                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=9606;
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MIM; 606022;
                                                     Hydrolase.
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                                                                               SEQUENCE
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                                                                                                                                                                                                                                   RESULT 5
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DR DR DR SO FT
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                                       STALIC-ACID DEPENDENT TYPE I MEMBRANE PROTEIN (ISOFORM 1) AND SOLUBLE (ISOFORM 2).

-I- FUNCTION: MACROPHAGE-RESTRICTED ADHESION MOLECULE THAT MEDIATES STALIC-ACID DEPENDENT BINDING TO CELLS.

-I- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN (ISOFORM 1) AND SOLUBLE (ISOFORM 2).

-I- ALTERNATIVE PRODUCTS: 2 1soforms; 1 (shown here) and 2; are produced by alternative splicing.

-I- SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUBERFAMILY.

-I- SIMILARITY: CONTAINS 1 IMMUNOGLOBULIN-LIKE V-TYPE DOMAINS.

-I- SIMILARITY: CONTAINS 16 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAINS.

-I- DATABBASE: NAME-PROW, NOTE-PROW, 2:18-22(2001); WWW-"http://www.ncbi.nlm.nih.gov/prow/guide/985165905_g.htm".
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pfam; PF00047; 1g; 14.
SMART; SM00409; 1G; 17.
SMART; SM00409; 1G-11ke; 1.
SMART; SM00408; 1G-2; 14.
Signal; Glycoprotein; Cell adhesion; Immunoglobulin domain; Repeat; Transmembrane; Alternative splicing; Antigen.
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CYTOPLASMIC (POTENTIAL)
IG-LIKE C2-TYPE DOMAIN 1.
IG-LIKE C2-TYPE DOMAIN 2.
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IG-LIKE C2-TYPE DOMAIN 3.
IG-LIKE C2-TYPE DOMAIN 4.
IG-LIKE C2-TYPE DOMAIN 5.
IG-LIKE C2-TYPE DOMAIN 6.
IG-LIKE C2-TYPE DOMAIN 9.
IG-LIKE C2-TYPE DOMAIN 10.
IG-LIKE C2-TYPE DOMAIN 11.
IG-LIKE C2-TYPE DOMAIN 11.
IG-LIKE C2-TYPE DOMAIN 11.
IG-LIKE C2-TYPE DOMAIN 11.
IG-LIKE C2-TYPE DOMAIN 12.
IG-LIKE C2-TYPE DOMAIN 13.
IG-LIKE C2-TYPE DOMAIN 14.
IG-LIKE C2-TYPE DOMAIN 15.
IG-LIKE C2-TYPE DOMAIN 15.
IG-LIKE C2-TYPE DOMAIN 15.
IG-LIKE C2-TYPE DOMAIN 15.
IG-LIKE C2-TYPE DOMAIN 16.
BY SIMILARITY.
                       (AUG-2000) to the EMBL/GenBank/DDBJ databases
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InterPro; IPR003598; Ig_C2.
InterPro; IPR003600; Ig_like.
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EMBL; AK024479; BAB15769.1;
HSSP; Q62230; 1QFO.
Genew; HGNC:11127; SN.
MIM; 600751; -.
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Schilling J., Clevinger B., Davie J.M., Hood L.;

"Amino acid sequence of homogeneous antibodies to dextran and DNA
rearrangements in heavy chain V-region gene segments.";

Nature 283:35-40(1980).

--- MISCELLANEOUS: THE SEQUENCES OF 10 HYBRIDOMA PROTEINS THAT ALSO
BIND DEXTRAN DIFFER FROM THAT SHOWN AT 1-7 POSITIONS, MANY OF

WHICH OCCUR IN THE D AND J SECMENTS.

--- MISCELLANEOUS: THIS PROTEIN BINDS DEXTRAN.

PRIR, AZG242; MHMS-J5.

RSSP, P01789; 1MPS-

InterPro; IPR003006; Ig_MHC.

RICHEPTO; IPR003006; Ig_MHC.

RICHEPTO; IPR003006; Ig_W.

Pram; PF00047; ig; 1.

RMART; SM00406; IGV.

PRAM; SM00406; IGV.

THE MISCELLANEOUS THIS PROTEIN BINDS DEXTRAN.

Pram; PF00040; Igv.

Pram; PF00040; Igv.

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PRAM; SM00406; IGV.

RMART; SM00406; IGV.

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THE MINDOGLOBULIN V REGION.
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Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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Yancopoulos G.D., Alt F.W.;
"Developmentally controlled and tissue-specific expression unrearranged VH gene segments.";
Cell 40:271-281(1985).
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01-JAN-1988 (Rel. 06, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
heavy chain V region VH558 Al/A4 precursor.
Mus musculus (Mouse).
                                                                                                                                                                                                                                                          21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
15-Pur-1999 (Rel. 38, Last annotation update)
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51 INPNNGGTSYNQKFKG 66
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51 INPNNGGTSYNQKFKG 66
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P06327;
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HV13_MOUSE
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HV52_MOUSE
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21-JUL-1986 (Rel. 01, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
19 heavy chain V region MOPC 104E.
Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus.
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MEDILNE-83075344; PubMed-6816276;
KENLY M.R., Fuhrman J.S., Schilling J.W., Rogers J., Sibley C.H.,
Hood L.E.;
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A -> T (IN REF. 1).
A -> V (IN REF. 3; BAB15749/BAB1576
MW; 587C7CCA0B789A6D CRC64;
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        HV12_MOUSE
P01756;
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HV12_MOUSE
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Dildrop R., Bovens J., Siekevitz M., Beyreuther K., Rajewsky K.;
"A V region determinant (idiotope) expressed at high frequency in B
lymphocytes is encoded by a large set of antibody structural genes.";
EMBO J. 3:517-523(1984).
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
NCBL_TaxID=10090;
                                                                                                                                                                    IG HEAVY CHAIN V REGION VH558 A1/A4 FRAMEWORK-1.
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01-JAN-1988 (Rel. 06, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
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                                                                                                                                                                                                                                      BY SIMILARITY.
                                                                                                                                                                                                                                                                                                         3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3; Mismatches
                                                                                                                                                                                                      FRAMEWORK-2
                                                                                                                                                                                                                           FRAMEWORK-3
 European Bioinformatics Institute.
                                                                                                                                                                                                                                                                                                                                                                                                          PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ig heavy chain V region AC38 205.12.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pfam; PF00047; ig; 1. SMART; SM00406; IGv; 1. Immunoglobulin V region; Signal.
                                                                                      HSSP; P01810; 2FBJ.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_v.
                                                                 EMBL; M13787; AAA38499.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         50.0%;
                                                                                                                                                                                                                                                                                                                                            69 WIYPGDGSTKYNEKFKG 85
                                                                                                                                                                                                                                                                                                                               1 WIDPENGDSDYAPKFOG 17
                                                                                                                                                                                                                                                                                                         8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                           STANDARD;
                                                                                                                                                                              54
54
68
85
1117
1115
                                                                             PIR; A02029; HVMSA1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (Wonse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       118 AA;
                                                                                                                                                                                                                                                            117 AA;
                                                                                                                                                                                                                                                                                             Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mus musculus
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8
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P06330;
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DISULFID
NON_TER
SEQUENCE
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                                                                                                                                                                               DOMAIN
DOMAIN
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DOMAIN
                                                                                                                                                          SIGNAL
                                                                                          HSSP;
                                                                                                                                                                                                                                                                                                                                                                                               HV51_MOUSE
                                                                                                                                                                       CHAIN
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2 IDPENGDSDYAPKFQG 17

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                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

SEQUENCE TO Columbia;

A Theologis A., Ecker J.R., Palm C.J., Federspiel N.A., Kaul S.,

Milte O., Alonso J., Altafi H., Araujo R., Bowman C.L., Brooks S.Y.,

White O., Alonso J., Chao Q., Chen H., Cheuk R.F., Chin C.W.,

RA Dunn P., Ety P., Feldblyum T.V., Feng J.-D., Fong B., Fujil C.Y.,

A Dunn P., Ety P., Feldblyum T.V., Feng J.-D., Fong B., Fujil C.Y.,

RA Dunn P., Ety P., Feldblyum T.V., Feng J.-D., Fong B., Huizar L.,

RA Hunter J.L., Jenkins J., Johnson-Hopson C., Khan S., Khankin B.,

RIM C.J., Koo H.L., Kremenetskaia I., Kurtz D.B., Kwan A., Lam B.,

Langin Hooper S., Lee A., Lee J.M., Lenz C.A., Li J.H., Li Y.-P.,

Lin X., Liu S.X., Liu Z.A., Luros J.S., Maiti R., Marziali A.,

Lin X., Liu S.X., Liu Z.A., Luros J.S., Maiti R., Marziali A.,

RA Pai G., Peterson J., Pham P. K., Nguyen M., Ngoreng T., Rowley D.,

Sakano H., Salzberg S.L., Schwartz J.R., Shinn P., Southwick A.M.,

RA Utterback T., Van Aken S., Vaysberg M., Vysotskaia V.S., Walker M.,

"The State of Chromosome I of the plant Arabidopsis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; AC020579; AAG52403.1; -.
InterPro; IPR000728; AIRS_related.
Pfam; PF00586; AIRS_t. 1.
Ptam; PF00789; AIRS_C; 2.
Purine biosynthesis; Ligase; ATP-binding; Glutamine amidotransferase; Chloroplast; Transit peptide.
CHLOROPLAST 1 ? PROBABLE
CHAIN ? 1387
                                                                                                                                                                                                                                                                          Arabidopsis thaliana (Mouse-ear cress).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Nature 408 816-820(2000).

-!- CATALYTIC ACTIVITY: ATP + N(2)-formyl-N(1)-(5-phospho-D-ribosyl)glycinamide + L-glutamine + H(2)0 - ADP + phosphate + 2-formamido)-N(1)-(5-phospho-D-ribosyl)acetamidine + L-glutamate.
-!- PATHWAY: De novo purine blosynthesis; fourth step.
-!- SUBCELLULAR LOCATION: Chloroplast (Probable).
-!- SIMILARITY: IN THE N-TERMINAL SECTION; BELONGS TO THE FGAMS

    -!- SIMILARITY: CONTAINS 1 TYPE-1 GLUTAMINE AMIDOTRANSFERASE DOMAIN.

                                                                                                                 16-OCT-2001 (Rel. 40, Last sequence update)
15-UNN-2002 (Rel. 41, Last annotation update)
15-UNN-2002 (Rel. 41, Last annotation update)
Purbable phosphorthosylformylglycinamidine synthase, chloroplast
Precursor (EC 6.3.5.3) (FCAM synthase) (FGAMS) (Formylglycinamide
ribotide amidotransferase) (FGARAT) (Formylglycinamide ribotide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PHOSPHORIBOSYLFORMYLGLYCINAMIDINE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        387 398 ATP (POTENTIAL).
1215 1215 GATASE (BY SIMILARITY).
1387 AA; 151778 MW; 65E9920DF83F0E95 CRC64;
                                                 PRT; 1387 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SYNTHASE.
                                                                                              16-OCT-2001 (Rel. 40, Created)
                                                   STANDARD;
                                                                                                                                                                                                                                    synthetase).
ATIG74260 OR F1017.7.
                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=3702;
                                                 PUR4_ARATH
O9M8D3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NP_BIND
ACT_SITE
SEQUENCE
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RESULT 10
PUR4_ARATH
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RA MEDLINE-21848401; PubMed=11859360;

RA Goulos J., Peat N., Hayles J., Basker S., Basham D., Bowman S.,

RA Brooks W., Brown D., Brown S., Chillingworth T., Churcher C.M.,

RA Brooks W., Brown D., Brown S., Chillingworth T., Churcher C.M.,

RA Collins M., Connor R., Cronin A., Davis P., Feltwell T., Fraser A.,

RA Gentles S., Goble A., Hamlin N., Harris D., Hidalgo J., Hodgson G.,

RA Holroyd S., Hornsby T., Howarth S., Huckle E.J., Hunt S., Jagels K.,

RA Holroyd S., Hornsby T., Howarth S., Huckle E.J., Hunt S., Jagels K.,

RA Holroyd S., Mungall K., Murphy L., Niblett D., Odell C.,

RA Mucher Cord R., Studers M., Seeger K., Sharp S.,

Ruther Cord K., Rutter S., Saudres S., Stevens K.,

RA Taylor K., Taylor R., Taylor R., Walsh S.V., Warren T., Whitehead S.,

RA Taylor R., Taylor R., Tivey A., Walsh S.V., Warren T., Whitehead S.,

RA Taylor R., Langer T., Beck R., Lehrach H., Reinhardt R., Pohl T.M.,

RA Borzym K., Langer I., Beck A., Lehrach H., Reinhardt R., Pohl T.M.,

RA Borzym K., Langer I., Beck A., Lehrach H., Reinhardt R., Pohl T.M.,

RA Golfeau A., Cadleu E., Dreano S., Gloux S., Lelaure V., Mottier S.,

RA Lucas M., Rochet M., Gaillardin C., Tallada V.A., Garzon A., Thode G.,

RA Lucas M., Rochet M., Gaillardin C., Tallada V.A., Garzon A., Thode G.,

RA Daga R.R., Cruzado L., Jimenez J., Sanchez M., del Rey F., Benito J.,

ROMINGUEZ A., Revuelta J.L., Moreno S., Armstrong J., Forsburg S.L.,

RA Shakoyski G.V., Ussery D., Barrell B.G., Nurse P.;

Wathre G. Stills R. Sarles 
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FUNCTION: SECOND STEP OF M-RNA CAPPING. TRANSFER OF THE GMP MOIETY OF, GTP TO THE 5'END OF RNA YIELDING A 52 KDa ENZYME-GMP COVALENT
                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Shuman Sg. Liu Y., Schwer B.; "Covableng catalysis in nucleotidyl transfer reactions: essential motifs in Saccharomyces cerevisiae RNA capping enzyme are conserved in Schizösaccharomyces pombe and viral capping enzymes and among
                                                                                   ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REACTION INTERMEDIATE (BY SIMILARITY).
CATALYTIC ACTIVITY: GTP + (5')PP-pur-mRNA - diphosphate + G(5')PPP-pur-mRNA.
                                                                                                                                                                                                                                                                                                                                                                       01-FEB-1995 (Rel. 31, Created)
01-FEB-1995 (Rel. 31, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
mRNA on enzyme alpha subunit (mRNA guanylyltransferase)
(EC 2.77, 78, 50) (GTP-RNA guanylyltransferase) (GGSC) OR PCEI OR SPBC2F12.08C.
                           Length 1387;
                                                                                5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Buratowski S.;
to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota Fungi; Ascomycota; Schizosaccharomycetes;
Schizosa charomycetales; Schizosaccharomycetaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            polynucleotide ligases.";
Proc. Natl. Acad. Sci. U.S.A. 91:12046-12050(1994)
                              DB 1;
                           Score 45; DB Pred. No. 41; 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Schizosaccharomyces pombe (Fission yeast).
Eukaryota Fungi; Ascomycota; Schizosaccha
                                                                                                                                                                                                                                                                                                                        PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE-95083638; PubMed-7991582;
                                                                                ö
                           44.68;
                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Nature 415:871-880(2002)
                                                                                                                                                                                                                                                                                                                           STANDARD;
                                                                                                                                                            11 F | 11 | 11 | 11 | 148 IDASNGASDYGNKF 461
                                                                                                                                   2 IDPENGDSDYAPKF 15
Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Fresco L.D., Woo S.,
Submitted (DEC-1994)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Schizosaccharomyces.
NCBI_Taxib=4896;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                     MCE1_SCHPO
P40997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN-972
                                                                                                                                                                                                                                                                         RESULT 11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1;
SUBUNIT: THE M-RNA CAPPING ENZYME IS COMPOSED OF TWO SEPARATE CHAINS ALPHA AND BETA, RESPECTIVELY A MRNA GUANYLYLTRANSFERASE AND AN RNA 5'-TRIPHOSPHATASE (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "Classification of fungal chitin synthases.";
"Classification of fungal chitin synthases.";
Proc. Natl. Acad. Sci. U.S.A. 89:519-523(1992).
-!- FUNCTION: PLAYS A MAJOR ROLE IN CELL WALL BIOGENESIS.
-!- CATALYTIC ACTIVITY: UDD-N-acetyl-D-glucosamine + {(1,4)-(N-acetyl-beta-D-glucosaminyl)}(N) = UDP + {(1,4)-(N-acetyl-beta-D-glucosaminyl)}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               glucosaminyl)}(N+1).
-!- SUBCELLULAR LOCATION: Integral membrane protein. Plasma membrane.
-!- SIMILARITY: BELONGS TO THE CHITIN SYNTHASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Interpro; IPR001339; mRNA_cap_enzyme.
Pfam; PF01331; mRNA_cap_enzyme; 1.
Transferase; Nucleotidyltransferase; mRNA processing; mRNA capping;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDIJINE-95039879; PubMed-7952169;
Din A.B., Yarden O.;
"The Neurospora crassa chs-2 gene encodes a non-essential chitin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-FEB-1996 (Rel. 33, Last sequence update)
01-FEB-1996 (Rel. 33, Last annotation update)
Chitin synthase 2 (EC 2.4.1.16) (Chitin-UDP acetyl-glucosaminyl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
Sordariales; Sordariaceae; Neurospora.
NCBI_TaxID=5141;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE OF 250-438 FROM N.A.
MEDLINE-92115692; Pubmed-1731323;
BOSWEN A. Chen-Wu J.L., Momany M., Young R., Szaniszlo P.J.,
Robbins P.W.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 44; DB 1; Length 402;
Pred. No. 15;
2; Mismatches 2; Indels
                                                                                             -i- SUBCELLULAR LOCATION: Nuclear.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GUANYLYLATION SITE.
K->A: LOSS OF FUNCTION.
76B1E2052DABB974 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           944 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Microbiology 140:2189-2197(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-APR-1993 (Rel. 25, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   46875 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            43.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; U16143; AAA64996.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; U18811; AAA58715.1; -. EMBL; 297211; CAB10156.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PENGDSDYA--PKFQ 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      29
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best_Local Similarity
Matches 9; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      [1]
SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Neurospora crassa.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Nuclear protein.
ACT_SITE 67
MUTAGEN 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  transferase 2).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          synthase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDINE=83131846; PubMed=6186498;
MEDINE=83131846; PubMed=6186498;
MEDINE=83131846; PubMed=6186498;
Marshak-Rothstein A.;
Marshak-Rothstein A.;
"The genetic basis of antibody production: the dominant anti-arsonate idiotype response of the strain A mouse.";
Bur. J. Immunol. 12:1023-1032(1982).
-:- TIMMUNOL. 12:1023-1032(1982).
-:- MISCELLANEOUS: FROM ANALYSIS OF THE SIZES OF SEVERAL OTHER DIFFERENTIATED GENES THAT HYBRIDIZE TO THIS ONE, THE AUTHORS CONCLUDE THAT ALL OF THESE V REGIONS HAVE REARRANGED TO THE SAME J
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                        Gaps
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus
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                                                                                                                                Transferase; Glycosyltransferase; Transmembrane; Cell wall;
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Pred. No. 39;
3; Mismatches 6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         42.6%; Score 43; DB 1; Length 120;
47.1%; Pred. No. 5.8;
tive 4; Mismatches 5; Indels
                                                                                                                                                                  654 POTENTIAL.
689 POTENTIAL.
733 POTENTIAL.
106816 MW; F70052AEE083060D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                        21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                   120 AA.
                                                                                                                                                         POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                  PRT;
                                                   EMBL; X77782; CAA54816.1; -.
EMBL; M82951; AAA33582.1; -.
PIR; B45189; B45189.
InterPro; IPR004834; Chitin_synth.
Pfam; PF01644; Chitin_synth; 1.
ProDom; PD002998; Chitin_synth; 1.
                                                                                                                                                                                                                                           Watch 43.6%;
Local Similarity 47.1%;
nes 8; Conservative
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Best Local Similarity 47.1%;
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49 YINPGNGYTKYNEKFKG 65
                                                                                                                                                                                                                                                                                              1 WIDPENGDSDYAPKFQG 17
                                                                                                                                                                                                                                                                                                                                                                                   STANDARD;
                                                                                                                                                                                                                    944 AA;
                                                                                                                                            Multigene family.
TRANSMEM 597
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713
873
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P01747;
                                                                                                                                                                                                                     SEQUENCE
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RESULT 14 YIGB_ECOLI

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                                                                                                                                                                                                         SEQUENCE FROM N.A.
STRAIN=KIZ / MG1655,
STRAIN=KIZ / MG1655,
Daniels D.L., Plunkett G. III, Burland V.D., Blattner F.R.;
Daniels D.L., Plunkett G. III, Burland P.D., Blattner F.R.;
"Analysis of the Escherichia coli genome: DNA sequence of the region Efrom 84.5 to 86.5 minutes.";
Science 257:771-778 (1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE OF 183-238 FROM N.A.
MEDILINE-84169504; PubMed-6324092;
Easton A.M., Kushner S.R.;
"Transcription of the uvrD gene of Escherichia coli is controlled by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Colloms S.D., Sykora P., Szatmari G., Sherratt D.J.;
"Recombination at ColE1 cer requires the Escherichia coli xerC gene product, a member of the lambda integrase family of site-specific recombinases.";
                                                                                                                                                                                                                                                                                                                                                                STRAIN-KIZ / MG1655;
MEDLINE-97426617; PubMed-9278503;
Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,
Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.,
Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
                                                                                                                                        Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "The complete genome sequence of Escherichia coli K-12."; Science 277:1453-1474(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE OF 183-238 FROM N.A.
MEDLINE-84272255; PubMed-6379604;
Finch P.W., Emmerson P.T.;
"The nucleotide sequence of the uvrD gene of E. coli.";
Nucleic Acids Res. 12:5789-5799(1984).
YIGB_ECOLI STANDARD; PRT; 238 AA. P23306; P7675; 20. Created) 15-UNOV-1991 (Rel. 20, Created) 15-JUL-1998 (Rel. 36, Last sequence update) 15-JUL-2002 (Rel. 41, Last annotation update) YIGB OR B3812.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 the lexA repressor and by attenuation.";
Nucleic Acids Res. 11:8625-8640(1983).
-1- SIMILARITY: TO E.COLI YJJG.
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Hypothetical protein; Complete proteome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            or send an email to license@isb-sib.ch)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EcoGene, EG11202, yigB.
InterPro, IPR001454; Hlgnase/hydrlase.
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EMBL; X00738; -; NOT_ANNOTATED_CDS.
PIR; D37841; D37841.
PIR; S30702; S30702.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=91072248; PubMed=2254268;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   J. Bacteriol. 172:6973-6980(1990)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; M87049; AAA67608.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                        Escherichia coli
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mau B., Shao Y.;
                                                                                                                                                                           NCBI_TaxID=562;
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                                                                                                                                                        Escherichia
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                                                                                                                                                                                                                         P37124; Created)
01-OCT-1994 (Rel. 30, Created)
01-OCT-1995 (Rel. 37, Last sequence update)
15-DEC-1996 (Rel. 37, Last annotation update)
Cytochrome P450 77A2 (EC 1.14.-.-) (CYPLXXVIIA2) (P-450EG5).
CYP77A2 ORCYPEG5.
Solanum melongena (Eggplant) (Aubergine)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Asteridae, euasterids I; Solanales; Solanaceae; Solanum.
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STRAIN=CVE Sinsadoharanasu; TISSUE-Hypocotyl;
MEDLINE-9413942; Pubmed=8307197;
TOGUTI T. TOKNGAWR K.;
"Cloning of eggplant hypocotyl cDNAs encoding cytochromes P450
belonging of a novel family (CYP77).";
FEBS Lett 338:290-294(1994).
-1- SIMILARITY: BELONGS TO THE CYTOCHROME P450 FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                               Query Match 4 42.6%; Score 43; DB 1; Length 238; Best Local Similarity 87.5%; Pred. No. 12; Matches 7; Conservative 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 43; DB 1; Length 511;
Pred. No. 28;
2; Mismatches 7; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         00067; p450; 1.
PS00086; CYTCCHROME P450; 1.
Uctase; Monooxygenase; Heme: Multigene family.
456 456 HEME (BY SIMILARITY).
511 AA; 58114 MW; 4B2A185D4DAFE023 CRC64;
238 AA; 27122 MW; 9C1BDE710641E0D6 CRC64;
                                                                                                                                                                                                                     511 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PIR; S41598, S41598.
PIR; S40266, S40266.
InterProf IPR001128; Cytochrome_P450.
                                                                                                                                                                                                                     PRT;
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P37124;
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SQ SEQUENCE
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Search completed: December 23, 2002, 07:26:13 Job time : 3.68023 secs

479 WADPENTRVDFTEKLE 494

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Scoring table:

Searched:

Database

Perfect score:

Title:

Sequence:

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Run on:

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031916 bacillus su

09stk0 arabidopsis

09343 arabidopsis

069834 streptomyce

099403 aeropyrum p

09shd8 arabidopsis

09stal arabidopsis

09lm1 mus musculu

09lm3 arabidopsis
                                                                                                                                                          099104 rattus norv
0921c4 mus musculu
0921c4 mus musculu
0951c8 carbidopsis
09x182 arabidopsis
09x182 arabidopsis
016334 arabidopsis
016334 rabidopsis
08y02 vigna ungui
08y074 ralstonia s
034915 bacillus su
QBrydB arabidopsis (QBylu7 ralstonia s QByla6 mus musculu QB1je3 methanosarc Q91wtl mus musculu Q92x12 mus musculu Q94x60 mus musculu Q96xe9 mus sapien
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01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Similar to Riken cDNA 1810060009 gene.
Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musines; Musch_TaxID=10090;
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A Strausberg R.;
Submitted (FEB-2001) to the EMBL/GenBank/DDBJ databases.
L Submitted (FEB-2001) to the EMBL/GenBank/DDBJ databases.
R HSSP; PO1842; 7FAB.
R InterPro; IPR003599; Ig.
R InterPro; IPR003509; Ig.
R InterPro; IPR003606; Ig_Alike.
R InterPro; IPR003606; Ig_Alike.
R InterPro; IPR003606; Ig_Alike.
R InterPro; IPR003606; Ig_Alike.
R Ffam; PR00047; ig; 2.
R SMART; SM00409; IG; 2.
R SMART; SM00409; IG; 2.
R SMART; SM00406; IG; 1.
R SMART; SM00406; IG_Alike; 1.
R SMART; PS00290; IG_Alike; 1.
R PROSITE; PS00290; IG_Alike; UNKNOWN_1.
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Pred. No. 0.00095;
Mismatches 1; Indels
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69 WIDPEDGETKYAPKFQ 84
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Q955s3 mus musculu
Q9sts2 arabidopsis
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09u195 homo s
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                  GenCore version 5.1.3
Copyright (c) 1993 - 2002 Compugen Ltd.
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                                                                                                                                                                                                                                                                                                                     671580 seqs, 206047115 residues
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Listing first 45 summaries
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sp_invertebrate:*
sp_manmal:*
sp_mhc:*
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sp_vertebrate:*
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sp_bacteriap:*
sp_archeap:*
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Maximum DB seq length: 200000000
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2: sp_bacteria:*
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Match 1
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76 60 59 59 57 57 55 55 51 51 51 51 50 48

Score

Мо.

Result

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08WY24; Q8WY24 RESULT 2 Q8WY24

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SEQUENCE FROM N.A.

MEDILINE-98322155; Pubmed-9657749;

MEDILINE-98322155; Pubmed-9657749;

MEDILINE-98322155; Pubmed Fist L.P.L.;

Jacquemin M.G., Vander Elst L.P.L.;

Indehanism and kinetics of factor VIII inactivation: study with an inhibitor.;

I gG4 monclonal antibody derived from a hemophilia A patient with inhibitor.;

EMBL; AJ224083; CAA11829.1; -.

R BASE; PO1772, 2FB4.

R InterPro; IPR003006; Ig_MG.

R InterPro; IPR003596; Ig_V.

R Pfam; PF00047; ig; 1.

SMART; SMO0406; IGV; 1.
                                                                                                                                                                 Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           57.4%; Score 58; DB 11; Length 109; 68.8%; Pred. No. 0.12;
                                                                                01-0CT-2000 (TrEMBLrel. 15, Created)
01-0CT-2000 (TrEMBLrel. 15, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
Anti-myosin immunoglobulin heavy chain variable region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         11944 MW; DFE615FE6CED4EDE CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Q9Y298 PRELIMINARY; PRT; 150 AA.
Q9Y298;
01-NOV-1999 (TrEMBLrel. 12, Created)
01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
                                                109 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     IgG VH protein precursor (Fragment).
                                                    PRT;
                                                    PRELIMINARY;
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Matches 11; Conservative
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NON_TER 109
SEQUENCE 109 AA;
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                                                                                                                                                          (Fragment).
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                                                                  Q9JL85;
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Q9Y298
                RESULT 4
                                     09JL85
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                                                                                                                                                                                                         Zheng S., Shao X., Cao J., Geng L., Fang Y., Dong Q.;
"Identification and characterization of SNC66, a Ig-like gene which is down-regulated in colorectal cancer.";
Submitted (JUN-2000) to the EMBL/GenBank/DDBJ databases.
EMBL, AF293666; AAL36987.1;
InterPro; IPR003599; Ig.
InterPro; IPR003597; Ig.cl.
InterPro; IPR003596; Ig_MHC.
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01-DEC-2001 (TEMBLE1 19, Created)
01-DEC-2001 (TEMBLE1 19, Last sequence update)
01-MAR-2002 (TEMBLE1 20, Last annotation update)
Unknown (protein for MGC:15420)
Unknown (From 10 MGC:15420)
Eukaryota: Merazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostoml;
Mammalia; Futheria; Primates; Catarrhini; Hominidae; Homo.
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Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.
Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.
EMBL, BC009851.1; -.
Interpro; IPR000005; HTHATAC.
Interpro; IPR0003006; Ig_MHC.
R Pfam: PE00047; Ig. 5.
SMART; RM00408; IGC.2; 2.
R PROSITE; PS00041; HTH_ARAC_FAMILY_1; UNKNOWN_1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 60; DB 4; Length 497;
Pred. No. 0.35;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 7 Match 58.4%; Score 59; DB 4; Length 614; Local Similarity 62.5%; Pred. No. 0.64; les 10; Conservative 3; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2; Indels
                                                                                                                                                                                                                                                                                                                                                         Pfam: PF00047; 19; 4.

SMART; SM00407; 1G: 4.

SMART; SM00407; 1G: 1.

SMART; SM00406; 1G: 1.

PROSITE; PS00290; 1G_MHC; UNKNOWN_1.

SEQUENCE 497 AA; 53665 MW; F24D08DFA5A663E5 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  614 AA; 67921 MW; 55EF536E77AA9BBB CRC64;
                                  Created)
Last sequence update)
Last annotation update)
497 AA.
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                       OBWY44;
01-MAR-2002 (TrEMBLrel. 20,
01-MAR-2002 (TrEMBLrel. 20,
01-JUN-2002 (TrEMBLrel. 21,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               69 WMNPOTGNTEFAQKFOG 85
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 WIDPENGDSDYAPKFOG 17
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PRELIMINARY;
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                                                                                    SNC66 protein.
Homo sapiens (Human)
                                                                                                                                                                                         SEQUENCE EROM N.A.
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                                                                                                                                                        NCBI_TaxID=9606;
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RESULT 3

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096GA6

Query Match

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50 WINPNSWTTNYAQKFQG 66
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69 YIDPYNGGSSYNQKFKG 85
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 WIDPENGDSDYAPKFQG 17
                                                                                                                                                                      1 WIDPENGDSDYAPKFQG 17
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Best Local Similarity 58.8
Matches 10; Conservative
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                                                                                                                                                                                                                                                   PRELIMINARY;
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                                                                                                    SEQUENCE
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NON_TER
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Q9UL92;
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                                                                   Gaps
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "Myosin-reactive autoantibodies in rheumatic carditis and normal fecus.";
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                                           56.9%; Score 57.5; DB 4; Length 150; 55.0%; Pred. No. 0.21; ive 4; Mismatches 2; Indels
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BEDILINE-98277139; Pubmed-9614934;
Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
Young D.C.;
                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.

BEDLINE-98277139; Pubmed-9614934;
Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
Young D.C.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
Myosin-reactive immunoglobulin heavy chain variable region (Fragment).
                                                                                                                                                                                        01-MAY-2000 (TrEMBLrel. 13, Created)
1-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
Myosin-reactive immunoglobulin heavy chain variable region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 55.4%; Score 56; DB 4; Length 125; 52.9%; Pred. No. 0.29; tive 4; Mismatches 4; Indels
                                                                  2; Indels
1 19 POTENTIAL.
150 150
150 Aa; 16031 MW; 563D164AB22802D5 CRC64;
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125 AA; 13516 MW; 0D3CD5C23248BEAC CRC64;
                                                                                                                                                                                                                                                                                                                                                                     Clin. Immunol. Immunopathol. 87:184-192(1998).
EMBL; AF035019; AAD56255.1; -
HSSP; PO1810; ZFBJ.
INTERPOO! ZFBJ.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_V.
Pfam; PF00047; ig; 1.
SMART; SM00406; IGv. 1.
                                                                                                                                                                    125 AA.
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                                                                                                                                                                   PRT;
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| 66 WVGSFDPESGESIYAREFQG 85
                                                                                       1 WI---DPENGDSDYAPKFQG 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Best Local Similarity 55.0
Matches 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 WIDPENGDSDYAPKFQG 17
                                                                                                                                                                      PRELIMINARY;
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                                                                                                                                                                                                                                              Homo sapiens (Human).
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les 9; Conserv
                                                                                                                                                                                                                                                                                 NCBI_TaxID=9606;
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SEQUENCE
           NON_TER
SEQUENCE
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                                             Query Match
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SIGNAL
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Matches
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Q9UL94
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
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Pred. No. 3;
2; Mismatches 5; Indels
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
Myosin-reactive immunoglobulin heavy chain variable region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TISSUE-MAMMARY TUMOR;
Strausberg R.;
Submitted (DEC-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; BC010455; AAH18455.1; -.
InterPro; IPR003599; Ig.
InterPro; IPR003597; Ig_c1.
InterPro; IPR003597; Ig_c1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-WAR-2002 (TrEMBLrel. 20, Created)
01-WAR-2002 (TrEMBLrel. 20, Last sequence update)
01-UNN-2002 (TrEMBLrel. 21, Last annotation update)
Hypothetical 52.3 kba protein.
Mus musculus (Mouse).
Clin. Immunol. Immunopathol. 87:184-192(1998).
EMBL; AF035020; AAD56256.1; -.
HSSP; P01810; 2FBJ.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003506; Ig_v.
Pfam; PF00047; ig; 1.
SMART; SM00406; IGV; 1.
                                                                                                                                                                                                                                                                     Query Match 54.5%; Score 55; DB 4; Best Local Similarity 52.9%; Pred. No. 0.4; Matches 9; Conservative 4; Mismatches
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58.8%;
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1 WIDPENGDSDYAPKF 15
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SEQUENCE FROM N.A.

STRAIN-657BL/6J; TISSUE-EMBRYO;

KRAWAI JM, Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,

KRAWAI JM, Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,

KRAWAI JM, Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,

KRAWAI JM, Shinagawa A., Shibata K., Yoshino H., Adachii J., Fukuda S.,

Alzawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,

Saito TK, Matsuda H.A., Ashburner M., Batalov S., Casavant T.,

KRAGOTA K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,

KRAGOTA K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,

KRAGOTA K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,

KRAGOTA K., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,

Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,

Blake JM, Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,

Rushingich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,

KASARAI H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,

Nordone P., Ring B., Ringwald M., Rodiiguez I., Sakamoto N.,

Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,

K., Wynshaw, Bootis A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,

M. Wanshaw, Bootis A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
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                                                                                                                                                                                                                                                         Gaps
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Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
NCBL_TaxID=10090;
                                    Young D.C. \frac{1}{2}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "Functional annotation of a full-length mouse cDNA collection."; Nature#409:685-690(2001).
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                          Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
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                                                                                                                                                                                                                             Score 51; DB 4; Length 124;
Pred. No. 1.8;
2; Mismatches 5; Indels
                                                                                                                                                                                    124 124
124 AA; 13580 MW; 1BAAACBD96ACD2A2 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                    Last sequence update)
Last annotation update)
                                                                           Clin. Immunol. Immunopathol. 87:184-192(1998).
EMBL; AF035022; AAD56258.1; -.
HSSP; P01772; 2F84.
InterPro; IFPR003006; Ig_MHC.
InterPro; IPR00356; Ig_v.
Pfam; PF00047; 1g; 1.
SMART; SM00406; IGv; 1.
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MGD; MGI:1921417; Nudt9.
InterPro; IPR000086; NUDIX_hydrolase.
                                                                                                                                                                                                                                                                                                                                                                                                        Created)
                                                                                                                                                                                                                                                                                                                                                                              PRT;
             PubMed-9614934;
                                                                                                                                                                                                                                                                                                                                                                                       095002;
01-JUN-2001 (TrEMBLEE1.17, C)
01-JUN-2001 (TrEMBLEE1.17, L6
01-JUN-2002 (TrEMBLEE1.21, L6
11900020071k protesin.
NUDT9 OR 1190002COTRIK.
Mus muscallus (Mouse)
                                                                                                                                                                                                                             50.5%;
56.2%;
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Matches 7; Conservative
                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                               PRELIMINARY;
                                                                                                                                                                                                                             Query Match
Best Local Similarity
               MEDLINE-98277139;
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NON_TER
SEQUENCE 1
                                                                 fetus.";
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TISSUE-EEMBRYO, AND MAINLY HEAD;
TISSUE-EEMBRYO, TISSUE H., Kondo H., Sugawara M.,
TISHABABHI M., Chlba Y., ISHIGA S., MUNAKWAR K., ONO Y., TAKIGUCHI S.,
TAKABABHI M., Chlba Y., ISHIGA S., MUNAKWAR K., ONO Y., TAKIGUCHI S.,
TAKABABHI M., Chlba Y., ISHIGA S.,
TAKABABHI M., Chlba Y., ISHIGA S.,
TAKABABHI M., Chlba Y., ISHIGA S.,
TAKABABHI M., Chlba Y., Saito K.,
TAKABABHI T.,
TAKABABHI Y., Saito K.,
TAKABABHI Y., MASHABI Y., Saito K.,
TAKABABHI Y., MASHABI T.,
TAKABABHI Y., Saito K.,
TAKABABHI Y., Saito K.,
TAKABABHI Y., Saito K.,
TAKABABHI Y.,
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Sukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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TISSUE-PROSTATE;
Strausberg R.;
Strausberg R.;
Strausberg R.;
Strausberg R.;
Strausberg R.;
Submitted (ARP-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; BC005951; AAH05951.1; -.
EMBL; BC005951; AAH05951.1; -.
InterPro; IPR003599; Ig.-C1.
InterPro; IPR003509; Ig.-d1.
InterPro; IPR003600; Ig.-like.
InterPro; IPR003606; Ig.-MHC.
InterPro; IPR003569; Ig.-V.
Pfam; PF00047; ig; 4.
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Last annotation update)
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01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
Hypothetical 54.2 kDa protein.
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                                                                                                                                                                                                                                                                   350 AA.
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Best Local Similarity 46.7%; Pred. No. 6.1;
Matches 7; Conservative 5; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CDNA FLJ14389 fis, clone HEMBA1002876
                                                                                                                                                                                                                                                                                                                                                                    01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last seq
01-MAR-2002 (TrEMBLrel. 20, Last ann
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SMART; SM00407; IGC1; 2.
SMART; SM00406; IGv; 1.
SMART; SM00410; IG_like; 1.
                                                                                                                                                                                                                                                                   PRELIMINARY;
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60 WADPOISESNESPKF 74
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Malkiel S., Liao L., Cunningham M.W., Diamond B.;
"T-Cell-dependent antibody response to the dominant epitope of
streptococcal polysaccharide, N-acetyl-glucosamine, is cross-reactive
                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                      0883H6;
01-JUN-2002 (TERBLrel. 21, Created)
01-JUN-2002 (TERBLrel. 21, Last sequence update)
01-JUN-2002 (TERBLrel. 21, Last annotation update)
Hypothetical 51.7 kba protein.
Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Musmmalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
NCBI_TaxID=10090;
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                                                                  4; Length 500;
                                                                                                                  5; Indels
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Submitted (MAR-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; BC025447; AAH25447.1; -.
Hypothetical protein.
SEQUENCE 474 AA; 51748 MW; 8608B57C6CD2874A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
Anti-myosin immunoglobulin heavy chain variable region
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                     500 AA; 54154 MW; 0A9BF43F2A3CC6D9 CRC64;
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                                                                                                                                                                                                                                                                                                                        474 AA
                                                                49.5%; Score 50; DB 47.1%; Pred. No. 13;
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50.0%; Pred. No. 22;
iive 3; Mismatches
                                                                                                             4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 with cardiac myosin.";
Infect. Immun. 68:5803-5808(2000).
EMBL; AF206027; AAF69325.1; --
HSSP; P01772; 2FB4.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_V.
Pfam; PF00047; ig; 1.
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66 WIGRIFPGDGDTHYSGKFQG 85
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69 WISPSSDNTRFAKKFQG 85
                                                                                                                                                           1 WIDPENGDSDYAPKFQG 17
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Best Local Similarity 50.0
Matches 10; Conservative
                                                                                                             8; Conservative
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Hypothetical protein. SEQUENCE 500 AA; 5
                                                                  Query Match
Best Local Similarity
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Q8R3H6
                                                                                                             Matches
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Cui D., Zeng G., Yan X., Li X., Su C.;
Cli D., Zeng G., Tan X., Li X., Su C.;
"Cloning of mouse genes related to repairing of intestinal epithelium of the irradiated mice by treatment with the intestinal RNA of mice of
                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Su C.; "Mechanism of exogenous nucleic acids and their precursors improving the repair of intestinal epithelium after irradiation in mice."; World J. Gastroenterol. 6:709-717(2000).
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Int. J. Radlat. Biol. Relat. Stud. Phys. Chem. Med. 19:71-80(2001).
EMBL; AF240166; AAK43731.1; -.
InterProy. IPR003006; Ig_MHC.
Pfam; PF00047; 19; 1.
SEQUENCE 147 AA; 16274 MW; 800594A12B97191F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN=BALB/C;
PubMed=11819679;
Cul D., Zeng G., Yan X., Wang F., Tian F., Ren D., Zhao T., Li X.,
                                                                                                                                                                                                                                                                                                                                                                                                                                     Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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47.1%; Pred. No. 6.6;
Live 3; Mismatches 6; Indels
  Score 48; DB 11; Length 102;
Pred. No. 4.3;
                                                                                                                                                                                                                                                                                                                                   01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
                                                                                                                                                                                                                                                                                      147 AA
                                                       Mismatches
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47.58;
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52 WIFPGEGSTEYNEKFKG 68
                                                                                                          1 WIDPENGDSDYAPKFQG 17
                                                                                                                                       | | | : | | : | | | | | | | 35 WINTETGEPTYADDFKG 51
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                                                       8; Conservative
                                                                                                                                                                                                                                                                                      PRELIMINARY;
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Best Local Similarity
Matches 8; Conserv
     Query Match
Best Local Similarity
Matches 8; Conserv
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Sequence 4, Al Sequence 2, Al Sequence 2, Al Sequence 7, Al Sequence 10, Al Sequence 110, Al

Sequence Sequence

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US-08-646-265A-29 US-08-232-081B-38 US-08-232-081B-39 US-08-822-830B-13 US-08-822-830B-2 US-08-9250-660-2 PCT-US93-00030-2 PCT-US93-00030-2 PCT-US93-0024-2 US-08-561-521-4 PCT-US95-01219-4 US-08-792-824-4 US-08-792-824-10 US-08-792-824-13 US-08-792-824-13 US-08-792-824-13 US-08-792-824-13 US-08-792-824-13 US-08-792-824-13 US-08-792-824-13 US-08-792-824-13 US-08-792-824-13

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163.250 Million cell updates/sec
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                                                                  December 23, 2002, 07:20:23 ; Search time 21.0872 Seconds
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                                                                                                        US-09-865-198-22
631
1 QVKLQQSGAELVGSGASVKL.....AYYGDYEGYWGQGTTVTVSS
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/cgn2_6/ptodata/1/iaa/5B_COMB.pep:*
/cgn2_6/ptodata/1/iaa/6A_COMB.pep:*
/cgn2_6/ptodata/1/iaa/6B_COMB.pep:*
/cgn2_6/ptodata/1/iaa/PcTUS_COMB.pep:*
/cgn2_6/ptodata/1/iaa/PcTUS_COMB.pep:*
        GenCore version 5.1.3
Copyright (c) 1993 - 2002 Compugen Ltd.
                                                                                                                                                                                                   Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PCT-US94-01709-6
US-08-661-052-16
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US-09-102-716-16
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US-08-471-426-4
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                                                                                                                                                                                262574 seqs, 29422922 residues
                                                                                                                                                                                                                                                                                                                                                                                                                     SUMMARIES
                                                                                                                                                                                                                                                    Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                               OM protein – protein séarch, using sw model
                                                                                                                                                            Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                              Issued_Patents_AA:*
                                                                                                                                                                                                                      Minimum DB seq length: 0 Maximum DB seq length: 2000000000
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length
                                                                                                                                                   BLOSUM62
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506.5
506.5
506.5
503.5
503.5
502.5
502.5
502.5
484.5
481.5
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                                                                   Run on:
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Sequence 38, Application US/08983035A
Patent No. 6326464
GENERAL INFORMATION:
APPLICANT: CONSEILLER, EMMANUEL
APPLICANT: CONSEILLER, EMMENUEL
TITLE OF INVENTION: P53 PROTEIN VARIANTS AND THERAPEUTICAL
USES THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 535;
                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
MEDIUM TYPE: Floppy disk
COMPUTER: Law PC compatible
ODERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURENT APPLICATION DATA:
APPLICATION NUMBER: US/08/983,035A
FILING DATE: 20-Feb-1998
CLASSIFICATION: CUNKNOWN>
PRIOR APPLICATION: CUNKNOWN>
PRIOR APPLICATION: NUMBER: PCT/FR96/01111
FILING DATE: 17-JUL-1996
FILING DATE: 19-JUL-1995
                                                                                                                                                                            NUMBER OF SEQUENCES: 59
CORRESPONDENCE ADDRESS:
ADDRESSEE: FINNEGAN, HENDERSON, FARABOW, GARRETT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 558.5; DB 4;
Pred. No. 6.5e-49;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME: Strauss, William L.
REGISTRATION NUMBER: 47,114
REFERENCE/DOCKET NUMBER: 03804.0142
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-408-4090.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; TOPOLOGY: linear; ; MOLECULE TYPE: protein; ; SEQUENCE DESCRIPTION: SEQ ID NO: 38: US-08-983-035A-38
                                                                                                                                                                                                               STREET: 1300 I Street, NW CITY: Washington STATE: DC COUNTY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LENGTH: 535 amino acids TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEPHONE: 202-408-400
TELEFAX: 202-408-4400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 INFORMATION FOR SEC ID NO: 38
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88.9%;
                                                                                                                                                                                                                                                                                                                                           COUNTRY: USA
ZIP: 20005-3315
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
US-08-983-035A-38
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Sequence Sequence Sequence

Sequence

PCT-US94-01709-4

-09-672-609-1

US-09-423-439-44 US-09-423-439-26 US-09-171-945-19

-09-423-439-51

US-09-025-403A-1

Sequence

Sequence Sequence Sequence

Sequence Sequence Sequence Sequence Sequence Sequence Sequence

US-09-171-945-11 US-08-348-548-8 PCT-US95-15716-8 JS-08-290-592E-18 PCT-US95-10053-15 PCT-US96-09448-18

481 481 478 478 478

PCT-US95-01219-44

JS-08-561-521-44

Length 118;

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Query Match
Best Local Similarity
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| 144 VSS 146
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                                                                                                                                                                                                                  -08-652-507-2
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 Gaps
                              1 QVKLQQSGAELVGSGASVKLSCTTSGFNIKDFYMHWVKQRPEQGLEWIGWIDPENGDSDY 60
                                              ADDRESSEE: Merchart, Gould, Smith, Edell, Welter & Sch
STREET 3100 No. 6111079west Center, 90 South Seventh
Indels
                                                                                                                                                                                                                                                                          APPLICANTE MURRAY, PETER JOSEPH
APPLICANTE GOEBEL, PETER
TITLE OF ÉNVENTION: LEAD BINDING POLYPEPTIDES AND
TITLE OF ÉNVENTION: NUCLEOTIDES CODING THEREFORE
NUMBER OF SEQUENCES: 46
CORRESPONDENCE ADDRESS:
5;
7; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE: 04-DEC-1996
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US96/09258
FILING DATE: 05-JUN-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICĀTION NUMBER: US/08/767,128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      JATAL.
JATAL.
JAPATE: 05-0cm.
JEATION DATA:
JEATION NUMBER: 08/541,373
JATATE: 10-0CT-1995
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RELICATION DATA:
GATION NUMBER: 08/462,798
GG DATE: 05-JUN-1995
WAGENT INFORMATION:
                                                                                                                                                                                                  Sequence 22, Application US/08767128
Patent No. 6111079
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SYSTEM: DOS
FastSEQ Version 1.5
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TELECOMMUNICATION INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM COMPATIBLE
                                                                                                                                                                                                                                              WYLIE, DWANE E. LOPEZ, OSVALDO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: Carter, Charles G
REGISTRATION NUMBER: 35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LENGTH: 118 amino acids TYPE: amino acid.
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CURRENT APPLICATION DATA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: protein ICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRANDEDNESS: sibgle
                                                                                                                                                                                                                                                                                                                                                                                                    Minneapolis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           linear
                                                                                                                                                                                                                              GENERAL INFORMATION:
APPLICANTE WYLIE,
APPLICANTE LOPEZ,
                                                                                                                                                                                                                                                                                                                                                                                                                                  USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           õ
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Matches 104;
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                                                                                   1 OVKLOOSGAELVGSGASVKLSCTTSGFNIKDFYMHWVKQRPEQGLEWIGWIDPENGDSDY 60
                                                                                                      1 QVKLQQSGAELVGSGASVKLSCTTSGFNIKDFYMHWVKQRPEQGLEWIGWIDPENGDSDY 60
                                                                                                                                                                                        61 APKFOGKATMTADSSSNTAYLQLSSLTSEDTAVYYCNAY-YGDYEGYWGQGTTVTVSS 117
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                                            Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADDRESSEE: Nixon & Vanderhye, P.C. STREET: 1100 No. 5876691th Glebe Road, 8th Floor CITY: Arlington STATE: Virginia
Score 536.5; DB 3;
Pred. No. 1.8e-47;
7; Mismatches 9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 517.5; DB 2;
Pred, No. 4.2e-45;
5; Mismatches 9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         5; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/652,507
FILING DATE: 02-011-1996
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Arthur R. Crawford
REGISTRATION NUMBER: 25,327
REFERENCE/DOCKET NUMBER: 117-211
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                       Sequence 2, Application US/08652507 Patent No. 5876691
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; Sequence 6, Application US/08017570
  85.0%;
85.6%;
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81.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 82.0°
Best Local Similarity 81.3°
Matches 100; Conservative
                                         Matches 101; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEFAX: 703-816-4100
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                       TITLE OF INVENTION: AN IITLE OF INVENTION: NUMBER OF SEQUENCES: 8 CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 amino acid
                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION: APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ZIP: 22201-4714
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 4
US-08-017-570-6
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61 APKFQGKATMTADSSSNTAYLQLSSLTSEDTAVYYCNA-----YYGDYEGYWGQG 110
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 QVKLQQSGAELVGSGASVKLSCTTSGFNIKDFYMHWVKQRPEQGLEWIGWIDPENGDSDY 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       81.1%; Score 511.5; DB 1; Length 124; 77.2%; Pred. No. 6.7e-45; Live 9; Mismatches 7; Indels 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 6, Application PC/TUS9401709
GENERAL INFORMATION:
APPLICANT: THE DOW CHEMICAL COMPANY
APPLICANT: THE DOW CHEMICAL COMPANY
APPLICANT: U.S.A. DEPT. OF HEALTH AND HUMAN SERVICES
TITLE OF INVENTION: A NOVEL FAMILY OF ANTI-CARCINOEMBRYONIC
TITLE OF INVENTION: ANTIGEN CHIMERIC ANTIBODIES
NUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESS:
                                                                                               MEDIUM TYPE: Floppy disa

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/471,426

FILING DATE: US/08/471,426

FILING DATE: US/08/471,426

FILING DATE: US/09/08/471,426

PROJUCTION NUMBER: 346/11,426

PRICE APPLICATION NUMBER: 34,941

REGISTRATION NUMBER: 34,941

RECIECOMMUNICATION INFORMATION:

TELECOMMUNICATION INFORMATION:

TELECOMMUNICATION INFORMATION:

SEQUENCE CHARACTERISTICS:

LENGTH: 124 amino acids

TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ZIP: 48641-1967
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: 12 PACHOLIN ROLF PC-DOS/MS-DOS
SOFWARE: PACHOLIN Rolease #1.0, Version #1.25
CURRENT APPLICATION DATR:
APPLICATION NUMBER: PCT/US94/01709
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ....oreSSEE: Duane C. Ulm
STREET: P.O. Box 1967
CITY: Midland
STATE: MI
COUNTRY: US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ATTORNEY/AGENT INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 77.29
Matches 98; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; MOLECULE TYPE: protein US-08-471-426-6
                                                                               COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                   COUNTRY: US
ZIP: 48641-1967
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 111 TTVTVSS 117
Midland
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           118 TTVTVSS 124
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PCT-US94-01709-6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 13;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 6. Application US/08471426
Patent No. 5808033
GENERAL INFORMATION:
APPLICANT: GOURLIE, BRIAN B
APPLICANT: RINO, MARK W
APPLICANT: RAPLAN: DONALD A
APPLICANT: SCHLOM, JEFFREY
TITLE OF INVENTION: A NOVEL FAMILY OF ANTI-CARCINOEMBRYONIC
TITLE OF INVENTION: A NOVEL FAMILY OF ANTIBODIES
                                 APPLICANT: GOURLIE, BRIAN B
APPLICANT: RIXON, MARK W
APPLICANT: MEZES, PETER S
APPLICANT: KAPLAN, DONALD A
APPLICANT: SCHLOM, JEFFREY
TITLE OF INVENTION: A NOVEL FAMILY OF ANTI-CARCINOEMBRYONIC
TITLE OF SEQUENCES: 24
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
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77.2%; Pred. No. 6.7e-45;
ilve 9; Mismatches 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: US/08/017,570
ELLASIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: ULMER, DUANE C
REGISTRATION NUMBER: C-38,777
FELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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P.O. Box 1967
                                                                                                                                                                                                                                 Ulmer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LENGTH: 124 amino acids TYPE: AMINO ACID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best Local Similarity 77.2
Matches 98; Conservative
                                                                                                                                                                                                                                 E: Duane C. U. P.O. Box 1967
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; MOLECULE TYPE: protein US-08-017-570-6
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ADDRESSEE: Duane C. (
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                 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                     48641-1967
                                                                                                                                                                                                                                                                       Midland
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                                                                                                                                                                                                                                                   STREET:
CITY: Mi
                                                                                                                                                                                                                                                                                                                   COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-08-471-426-6
                                                                                                                                                                                                                                                                                             STATE:
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Gaps

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62 PKFQGKATMTADSSSNTAYLQLSSLTSEDTAVYYCN-----AYYGDYEGYWGQGTTVTV 115
                                                                                                                                               62 PKFQGKATMTADSSSNTAYLQLSSLTSEDTAVYYCN-----AYYGDYEGYWGQGTTVTV 115
                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2 VKLQQSGAELVGSGASVKLSCTTSGFNIKDFYMHWVKQRPEQGLEWIGWIDPENGDSDYA 61
                                                                                                                         2 VKLQQSGAELVGSGASVKLSCTTSGFNIKDFYMHWVKQRPEQGLEWIGWIDPENGDSDYA
                                                                                6
                                         Length 553;
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                                                                                Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Yashwant M. Deo
APPLICANT: Joel Goldstein
APPLICANT: Robert Graziano
APPLICANT: Chezian Somasundaram
APPLICANT: Chezian Somasundaram
TITLE OF INVENTION: THERAPEUTIC COMPOUNDS COMPRISED
TITLE OF INVENTION: OF ANTI-FC RECEPTOR ANTIBODIES
NUMBER OF SEQUENCES: 16
                                       Score 511.5; DB 2;
Pred. No. 4.1e-44;
6; Mismatches 9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match

81.1%; Score 511.5; DB 4
Best Local Similarity 80.3%; Pred. No. 4.1e-44;
Matches 98; Conservative 6; Mismatches 9
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STREET: 60 State Street, Suite 510
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STATE: Massachusetts
COUNTRY: USA
ZIP: 02109-1875
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPALIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US/09/188,082
                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 16, Application US/09188082 Patent No. 6270765
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/661,052
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ATTORNEY AGENT INFORMATION:
NAME: Arnold, Beth E.
REGIESTRATION UNDRER: 35,430
REFERENCE/DOCKET NUMBER: MXI-
TELECOMMUNICATION INFORMATION:
TELEPAX: (617)227-7400
TELEPAX: (617)227-5941
INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
                                         81.1%;
80.3%;
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                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; MOLECULE TYPE: protein US-09-188-082-16
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CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER:
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                                       Query Match
Best Local Similarity
Matches 98; Conserv
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CITY: Boston
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                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 8
US-09-188-082-16
US-08-661-052-16
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                                                                                                                                                                                                                                                                                                                                   395 SS 396
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                                                                                                                                                                                                                                                                                                                 Gaps
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                                                                                                                                                                                                                                                         Score 511.5; DB 5; Length 124; Pred. No. 6.7e-45; O. Mismatches 7; Indels 13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Yashwant M. Deo
APPLICANT: Yashwant M. Deo
APPLICANT: Robert Graziano
APPLICANT: Robert Graziano
APPLICANT: Robert Graziano
APPLICANT: Chezian Somasundaram
TITLE OF INVENTION: THERAPEUTIC COMPOUNDS COMPRISED
TITLE OF INVENTION: OF ANTI-FC RECEPTOR ANTIBODIES
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD
STREET 60 State Street, Suite 510
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION UNMBER: US/08/661,052
FILING DATE:
                                                                                                                                                                                                                                                                                                               9; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME: Arnold, Beth E.
REGIZFRATION NUMBER: 35,430
REFRENCE/DOCKET NUMBER: MXI-043CP
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)227-7400
TELEPHX: (617)227-7401
INFORMATION FOR SEQ ID NO: 16:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION DATA:
APPLICÂTION NUMBER: US 08/484,172
FILING DATE: 07-JUNE-1995
ATTORNEY/AGENT INFORMATION:
                                       38,777-F
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COUNTRY: USA
ZIP: (02109-1875
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 16 Application US/08661052 Patent No. 5837243
                                REFERENCE/DOCKET NUMBER: 38,7
TELECOMMUNICATION INFORMATION:
TELEPHONE: (517) 636-8104
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 124 amino acids
                   34,941
                                                                                                                                                                                                                                                                      81.18;
77.28;
                                                                                                                                    LENCTH: 124 amino acids
TYPE: amino acids
TOPOLOGY linear
MOLECULE TYPE: protein
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amino acid
                                                                                                                                                                                                                                                                                                             Conservative
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ULMER, DUANE C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Moston
Massachusetts
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Best Local Similarity
Matches 98; Conserva
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GENERAL INFORMATION:
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STATE:
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Patent No. 6395272
GENERAL INFORMATION:
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SS 396
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Yashwant M. Deo, et al.
TITLE OF INVENTION: OF ANTI-FC RECEPTOR ANTIBODIES
NUMBER OF SEQUENCES: 16
CORRESPONDENCE S.S.
ADDRESSEE: LAHIVE & COCKFIELD, LLP
STREET: 28 State Street, 24th Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 4;
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80.3%; Pred. No. 4.1e-44;
iive 6; Mismatches 9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 09/188,082
FILING DATE: UO "JUNE-1996
PRIOR APPLICATION NUMBER: US 08/484,172
FILING DATE: US 08/484,172
FILING DATE: US 08/484,172
FILING DATE: US 07-UNE-1995
ATTORNEY AGENT INFORMATION:
NAME: REMITLARY JANGE:
REFERENCE JOCKET NUMBER: MXI-043CP2
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION INF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: US/09/364,088 FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                               Sequence 16, Application US/09364088 Patent No. 6365161 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 80.3°
Matches 98; Conservative
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MOLECULE TYPE: protein
US-09-364-088-16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STATE: Massachusetts
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       amino acid
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US-09-102-716-16
                                                                                                                                       395 SS 396
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                                                                                                116 SS 117
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62 PKFQGKATMTADSSSNTAYLQLSSLTSEDTAVYYCN-----AYYGDYEGYWGQGTTVTV 115
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        81.1%; Score 511.5; DB 4; Length 553; 80.3%; Pred. No. 4.1e-44; 1ive 6; Mismatches 9; Indels 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 4, Application US/08017570
Patent No. 5472693
GENERAL INPORMATION:
APPLICANT: RIXON, MARK W
APPLICANT: RIXON, MARK W
APPLICANT: RAPLAN, DONALD A
APPLICANT: KAPLAN, DONALD A
APPLICANT: SCHLOM, JEFRERY
TITLE OF INVENTION: A NOVEL FAMILY OF ANTI-CARCINOEMBRYONIC
TITLE OF INVENTION: A NATIGEN CHIMERIC ANTIBODIES
                                                                                                                                                                                                                                                                       COUNTER READABLE FORM:

ZIP: 02109-1875

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: 1BM PC COMPATIBLE

COMPUTER: 1BM PC COMPATIBLE

CORRENT APPLICATION DATA:

APPLICATION DATA:

FILING DATE: 25-Jun-1998

PRIOR APPLICATION DATA:
                                                        TITLE OF INVENTION: THERAPEUTIC COMPOUNDS COMPRISED OF ANTI-FC RECEPTOR ANTIBODIES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REGISTRATION NUMBER: 35,430
REFERENCE/DOCKET NUMBER: MXI-043CP
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)227-7400
TELEPAX: (617)227-5941
INFORMATION FOR SEQ ID NO: 16:
SEQUENCE_CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 16:
                                                                                                                                                                          ADDRESSEE: LAHIVE & COCKFIELD
STREET: 60 State Street, Suite
CITY: Boston
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: 08/661,052
FILING DATE: «UNKNOWN»
ATTORNEY/AGENT INFORMATION:
NAME: Arnold, Beth E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LENGTH: 553 amino acids TYPE: amino acid
APPLICANT: Yashwant M. Deo
                                              Robert Graziano
                      Joel Goldstein
                                                                                                                                                                                                                                                        STATE: Massachusetts
                                                                                                                                                                CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         98; Conservative
                                                                                                                                       NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Best Local Similarity
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FILING DATE: 06-JUN-1995
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/017,570
FILING DATE: 16-FEB-1993
ATTORNEY/AGENT INFORMATION:
NAME: ULMER, DIANE C
REGISTRATION NUMBER: 34,941
REFERENCE/DOCKET NUMBER: C-38,777
TELECOMMUNICATION INFORMATION:
TELEPHONE: (517) 636-8104
INFORMATION FOR SEQ ID NO: 4:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: ULMER, DUANE C 34,941
REFERENCE/DOCKET NUMBER: 38,777-F
TELECOMMUNICATION INFORMATION:
TELEPHONE: (517) 636-8104
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
06-JUN-1995
N: 536
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADDRESSEE: Duane C. Ulmer
STREET: P.O. Box 1967
CITY: Midland
                                                                                                                                                                                                                                                                                                                                                                                           Query Match

Best Local Similarity 76.4%;
Matches 97; Conservative 9
                                                                                                                                                                                                                                                               SEQUENCE CHARACTERISTICS:
LENGTH: 124 amino acids
TYPE: amino acid
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-471-426-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LENGTH: 124 amino acids TYPE: amino acid
                                 APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STATE: MI
COUNTRY: US
ZIP: 48641-1967
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APPLICANT: GOURLIE, BRIAN B
APPLICANT: MEXES, PETER S
APPLICANT: RAPLAN, DONALD A
APPLICANT: RAPLAN, DONALD A
APPLICANT: SCHLOM, JEFREY
TITLE OFFINVENTION: A NOVEL FAMILY OF ANTI-CARCINOEMBRYONIC
TITLE OFFINVENTION: A NIGEN CHIMERIC ANTIBODIES
NUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESS:
ADDRESSE: Duane C. Ulmer
STREET; P.O. BOX 1967
CITY: Midland
STATE: MI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  80.3%; Score 506.5; DB 1; Length 124; 76.4%; Pred. No. 2.1e-44; Live 9; Mismatches 8; Indels 13
                                                                                                 ZIP: 48641-1967

ZIP: 48641-1967

COMPUTER REDABLE FORM:

MEDION TAPE: Floppy disk

COMPUTER FIBER: PC-DOS/MS-DOS

SOFTWARE: PATENTIN Release #1.0, Version #1.25

CURENT APPLICATION DATA:

APPLICATION DATA:

CLASSIFICATION: 424

ATTORNEY/AGENT INFORMATION:

NAME: ULMER. DIANEA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDIUM TYPE: Floppy disk
COMPUPER: IBM PC compatible
OPERATING SYSTEM: PC-005/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                NAME: ULMER, DUANE C
REGISTRATION NUMBER: 34,941
REFERENCE/DOCKET NUMBER: C-38,777
TELEPHONE: (517) 636-8104
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-08-471-426 4 Application US/08471426; Patent No. §808033
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LENGTH: 124 amino acids TYPE: AMINO ACID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                               ADDRESSEE: Duane C. U. STREET: AP.O. Box 1967 CITY: Midland
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MOLECULE PYPE: protein
                                 CORRESPONDÊNCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             READABLE FORM:
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Best Local Similarity
Matches 976 Conserv
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COMPUTER READABLE
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61 APKFQGKATMTADSSSNTAYLQLSSLTSEDTAVYYCNA······YYGDYEGYWGQG 110
                                                                                                                                                                                                                                                                                      61 APKFOGKATMTTDTSSNTAYLOLSSLTSEDTAVYXCNTRGLSTMITTRWFFD---VWGAG 117
                                                                  Indels 13; Gaps
                                                                                                                                                              1 QVKLQQSGAELVGSGASVKLSCTTSGFNIKDFYMHWVKQRPEQGLEWIGWIDPENGDSDY
      Length 124;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 4, Application PC/TUS9401709
APPLICANT: THE DOW CHEMICAL COMPANY
TITLE OF INVENTION: A NOVEL FAMILY OF ANTI-CARCINOEMBRYONIC
TITLE OF INVENTION: ANTIGEN CHIMERIC ANTIBODIES
NUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESS:
Score 506.5; DB 1;
Pred. No. 2.1e-44;
9; Mismatches 8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPOTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/01709
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; FEATURE:
; NAMEZ/KEY: Murine Col-1 VH
; LOCATION: 1..124
US-09-025-403A-1
                                                                                                                                                                                                                                  TYPE: PRT
ORGANISM: Mus musculus
                   TITLE OF INVENTION:
FILE REFERENCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     111 TTVTVSS 117
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                                                                                                                                                                                                                                                                                                                                                                                  Sequence 1, Application US/09672609
Patent No. 6333405
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
M.H. Kerr
APPLICANT: Tempest, Philip R.
APPLICANT: Carr, Frank J.
APPLICANT: Harris, William J.
APPLICANT: Armour, Kathryn
TITLE OF INVENTION: High Affinity Humanized Anti-CEA Monoclonal Antibodies
FILE REFERENCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APKFQGKATMTADSSSNTAYLQLSSLTSEDTAVYYCNA-----YYGDYEGYWGQG 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        61 APKFQGKATMTTDYSSNTAYLQLSSLTSEDTAVYYCNTRGLSTMITTRWFFD---VWGAG 117
                                                                                                                                                                                              61 APKFQGKATMTADSSSNTAYLQLSSLTSEDTAVYYCNA-----YYGDYEGYWGQG 110
                                                                                                                                                                                                                61 APKFQGKATMTTDTSSNTAYLQLSSLTSEDTAVYYCNTRGLSTMITTRWFFD----VWGAG 117
                                                                                          Gaps
                                                                                                                                           1 QVKLQQSGAELVGSGASVKLSCTTSGFNIKDFYMHWVKQRPEQGLEWIGWIDPENGDSDY 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 QVKLQQSGAELVGSGASVKLSCTTSGFNIKDFYMHWVKQRPEQGLEWIGWIDPENGDSDY 60
                                                                                        13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 4; Length 124;
                                                        DB 5; Length 124;
                                                                                        Indels
                                                    80.3%; Score 506.5; DB 5;
76.4%; Pred. No. 2.1e-44;
Live 9; Mismatches 8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 503.5; DB 4;
Pred. No. 4.3e-44;
8; Mismatches 9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CURRENT APPLICATION NUMBER: US/09/672,609
CURRENT FILING DATE: 2000-09-28
PRIOR APPLICATION NUMBER: 09/025,403
PRIOR FILING DATE: 1998-02-18
NUMBER OF SEQ ID NOS: 50
SOFTWARE: Microsoft Word 97 SR-2
SEQ ID NO 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 1, Application US/09025403A Patent No. 6417337
PADELERAL INFORMATION:
APPLICANT: Anderson, W.H. Kerr APPLICANT: Tempest, Philip R. APPLICANT: Carr, Frank J. APPLICANT: Harris, William J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 76.4%;
Matches 97; Conservative
                                         Ouery Match
Best Local Similarity 76.4%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; FEATURE:
; NAME/KEY: Murine Col-1 VH
; LOCATION: 1..124
US-09-672-609-1
; MOLECULE TYPE: protein PCT-US94-01709-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: PRT ORGANISM: Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  118 TTVAVSS 124
                                                                                                                                                                                                                                                                 111 TTVTVSS 117
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US-09-025-403A-1
                                                                                                                                                                                                                                                                                                                                                                       US-09-672-609-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LENGTH: 124
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| APPLICAMY: Armour, Kathryn | TITLE REPERBEL: Armour, Kathryn | TITLE REPERBEL: | CONTREMY PAPLICAMY: Alba Affinity Humanized Anti-CEA Monoclonal Antibodies | FILE REPERBEL: | CONTRART APPLICATION NUMBER: US/09/025,403A | CURRENT FILING DATE: 1998-02-18 | PRIOR FILING DATE: 1998-02-18 | PRIOR FILING DATE: 1998-02-18 | PRIOR FILING DATE: 1996-10-30 | PRIOR FILING DATE: 1996-10-30 | PRIOR FILING DATE: 1996-10-30 | SOFTAME: Microsoft Word 97 SR-2 | SEQ ID NO 1 | CONTAINS: Microsoft Word 97 SR-2 | SEQ ID NO 1 | COATION: 1.124 | CO
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GenCore version 5.1.3
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- protein search, using sw model OM protein December 23, 2002, 07:30:08; Search time 10.8837 Seconds Run on:

(without alignments) 180.208 Million cell updates/sec

US-09-865-198-22 631 Title: Perfect score:

1 QVKLQQSGAELVGSGASVKL......AYYGDYEGYWGQĞTTVTVSS 117 Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

106657 seqs, 16763532 residues Searched:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Total number of hits satisfying chosen parameters:

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

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(cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep:*
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(cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep:*
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(cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep:*
(cgn2_6/ptodata/2/pubpaa/US09_PUBCOMB.pep:*
(cgn2_6/ptodata/2/pubpaa/US09_PUBCOMB.pep:* /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep:* /cgn2_6/ptodata/2/pubpaa/US10_PUBCOMB.pep:* /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep:* /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep:* Published_Applications_AA:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

		dР				
Result		Query		•		
. S	Score	Match	Length DB	DB	ID	Description
7	631	100.0	117	10	US-09-976-787-23	Sequence 23, Appl
7	631	100.0	117	10	US-09-865-198-22	22,
m	631	100.0	238	10	US-09-976-787-29	
4	631	100.0	238	10	US-09-865-198-28	Sequence 28, Appl
വ	624	98.9	117	10	US-09-976-787-7	
ø	624	98.9	117	10	US-09-865-198-7	Sequence 7, Appli
7	624	6.86	240	10	US-09-976-787-28	2
α	624	98.9	240	70	US-09-865-198-27	Sequence 27, Appl
σ	503.5	79.8	124	6	US-09-974-052-1	Sequence 1, Appli
10	503.5	79.8	124	6	US-09-974-051-1	
11	502.5	79.6	120	10	US-09-910-059-11	
. 12	502.5	9.64	255	10	US-09-910-059-19	
13	488.5	77.4	136	10	US-09-564-329A-11	11,
14	488.5	77.4	136	10	US-09-855-153-11	Sequence 11, Appl
15	488.5	77.4	136	10	US-09-854-811-11	Sequence 11, Appl
16	488.5	77.4	136	10	US-09-934-773-11	
17	488.5	77.4	136	10	US-09-963-620-11	Sequence 11, Appl
18	478	75.8	117	10	US-09-158-120A-18	Sequence 18, Appl
19	428.5	67.9	139	10	US-09-809-739-5	Sequence 5, Appli

Sequence 22, Application US/09865198 Patent No. US20020103345A1 GENERAL INFORMATION: APPLICANT: Zhu, Zhenping

US-09-865-198-22

11. 12. 13. 14. 15. 16. 16. 17. 17. 17. 17. 17. 18. 17. 17. 18. 17. 18. 18. 19. 19. 19. 19. 19. 19. 19. 19	Sequence 2, Appli
0.09 - 1158 - 0.09 - 1158 - 0.09 - 0.	12 US-10-025-687-2
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          Sequence 23, Application US/09976787

Patent No. US2002006452841

GENERAL INFORMATION:
APPLICANT: Zhu, Zhenping

APPLICANT: Zhu, Zhenping

TITLE OF INVENTION: Antibodies Specific to KDR and Uses Thereof
FILE REFERENCE: 11245/46505

CURRENT FILING DATE: 2001-10-12

PRIOR APPLICATION NUMBER: US 69/493,539

PRIOR FILING DATE: 2000-1.28

PRIOR FILING DATE: 1099-01-29

NUMBER OF SEQ ID NOS: 40

SOFTWARE: WordPerfect 8.0 for Windows

SEQ ID NO 23
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100.0%; Pred. No. 1.4e-42;
tive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches 117; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                       ) LENGTH: 117

; TYPE: PRT

; ORGANISM: MOUSE

US-09-976-787-23
US-09-976-787-23
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Gaps

Indels

Length 238;

Score 631; DB 10; Pred. No. 2.5e-42;

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1 QVKLQQSGAELVGSGASVKLSCTTSGFNIKDFYMHWVKQRPEQGLEWIGWIDPENGDSDY 60
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                                                                                                                                                                                                                                                                                                                                                                                      100.0%; Scor.
100.0%; Pred. No. 2..
0; Mismatches
CURRENT APPLICATION NUMBER: US/09/865,198
CURRENT FILING DATE: 2001-05-24
PRIOR APPLICATION NUMBER: US 60/206,749
PRIOR FILING DATE: 2000-05-24
NUMBER OF SEQ ID NOS: 34
SOFTWARE: WordPerfect 8.0 for Windows
SEQ ID NO 28
LENGTH: 238
                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 100.
Best Local Similarity 100.
Matches 117; Conservative
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                                                                                                                                                                                                                                                                                          TYPE: PRT
ORGANISM: Mouse
US-09-865-198-28
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US-09-976-787-7
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Patent No. US20020103345A1
GENERAL INFORMATION:
APPLICANT: Zhu, Zhenping
TITLE OF INVENTION: Bispecific Immunoglobulin-Like Antigen Binding Proteins and Methor FILE REFERENCE: 11245/47102
          TITLE OF INVENTION: Bispecific Immunoglobulin-Like Antigen Binding Proteins and Methd
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             11113 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1
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APPLICANT 2 Witte, Larry
TITLE OF INVENTION: Antibodies Specific to KDR and Uses Thereof
FILE REFERENCE: 11245/46505
CURRENT ABPLICATION NUMBER: US/09/976,787
CURRENT FELING DATE: 2001-10-12
PRIOR FILENG DATE: 2000-01-28
PRIOR FILENG DATE: 1999-01-29
PRIOR FILENG DATE: 1999-01-29
NUMBER OF SEQ ID NOS: 40
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1.4e-42;
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100.0%; Pred. No. 2.5e-42;
iive 0; Mismatches 0;
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Best Local Similarity 100.0%; Pred. No. 1.4
Matches 117; Conservative '0; Mismatches
                                              TITLE OF INVENTION: Production
FILE REFERENCE: 1124547102
CURRENT APPLICATION NUMBER: US/09/865,198
CURRENT FILING DATE: 2001-05-24
PRIOR APPLICATION NUMBER: US 60/206,749
PRIOR FILING DATE: 2000-05-24
NUMBER OF SEQ ID NOS: 34
SOFTWARE: WordPerfect 8.0 for Windows
SEQ ID NO 22
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US20020064528A1
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                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: PRT
ORGANISM: Mouse
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US-09-976-787-29
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US-09-865-198-28
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GENERAL INFORMATION:
APPLICANT: Zhu, Zhenping
TITLE OF INVENTION: Bispecific Immunoglobulin-Like Antigen Binding Proteins and Me
TITLE OF INVENTION: Bispecific Immunoglobulin-Like Antigen Binding Proteins and Me
TITLE OF INVENTION: Broduction
FILE REFERENCE: 11245/47102
CURRENT PAPLICATION NUMBER: US,09/865,198
PRIOR APPLICATION NUMBER: US 60/206,749
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61 APKFQGKATMTADSSSNTAYLQLSSLTSEDTAVYXCNAYXGDYEGYWGQGTTVTVSS 117
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                                                                                                                                                           Sequence 7, Application US/09976787
Patent No. US20020064528A1
GENERAL INFORMATION:
APPLICANT: Zhu, Zhenping
APPLICANT: Witte, Larry
TITLE OF INVENTION: Antibodies Specific to KDR and Uses Thereof
FILE REFERENCE: 11245/46505
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                                                                                                                                                                                                                                                                                                                                                         CURRENT APPLICATION NUMBER: US/09/976,787
CURRENT FILING DATE: 2001-10-12
PRIOR APPLICATION NUMBER: US 09/493,539
PRIOR FILING DATE: 2000-01-28
PRIOR FILING DATE: 1999-01-29
NUMBER OF SEQ ID NOS: 40
SEQ ID NO 7
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Matches 116; Conservative
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us-09-865-198-22.rapb

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APPLICANT: Acmypest, Fillip R.
APPLICANT: Harris, William J.
APPLICANT: Harris, William J.
APPLICANT: Harris, William J.
APPLICANT: Armour, Kathryn
TILE OF INVENTION: High Affinity Humanized Anti-CEA Monoclonal Antibodies
FILE REFERENCE:
CURRENT PEPLICATION NUMBER: US/09/974,052
CURRENT FILING DATE: 2001-10-09
PRIOR APPLICATION NUMBER: US 09/025,403
PRIOR FILING DATE: 1998-02-18
PRIOR FILING DATE: 1997-10-30
PRIOR FILING DATE: 1997-10-30
PRIOR FILING DATE: 1997-10-30
PRIOR FILING DATE: 1996-10-31
NUMBER OF SEQ ID NOS: 50
SEOFWARE: Microsoft Word 97 SR-2
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                                                                                                                                                                      Score 624; DB 10;
Pred. No. 8.9e-42;
0; Mismatches 1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 1, Application US/09974052 Patent No. US20020165387A1
                                                                                                                                                                         98.9%;
99.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
APPLICANT: Anderson, W.H. Kerr
APPLICANT: Tempest, Philip R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Anderson, W.H. Kerr
                                                                                                                                                                         Query Match
Best Local Similarity 99.1
Matches 116; Conservative
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Matches 97; Conserva
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US-09-974-052-1
                                                                                 ; ORGANISM: Mouse US-09-865-198-27
SEQ ID NO 27
LENGTH: 240
TYPE: PRT
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US-09-974-052-1
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US-09-865-198-27
Sequence 27, Application US/09865198
Sequence 27, Application US/09865198
Sequence 27, Application US/09865198
Sequence 27, Application US/09865198
Sequence 27, Application:

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Faquence 28, Application US/09976787

Faquence 28, Application US/09976787

GENERAL INFORMATION:

APPLICANT: 2bu, Zhenping

APPLICANT: Witte, Larry

TITLE OF INVENTION: Antibodies Specific to KDR and Uses Thereof

FILE REFERENCE: 1124546505

CURRENT APPLICATION NUMBER: US/09/976,787

CURRENT FILING DATE: 2000-01-28

PRIOR APPLICATION NUMBER: US 09/493,539

PRIOR PRIOR TILING DATE: 1999-01-29

NUMBER OF SEQ ID NOS: 40

SOFTWARE: WordPerfect 8.0 for Windows

SEQ ID NO 28

LENGTH: 240
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                                                                                                                                                                                                                                                          Score 624; DB 10;
Pred. No. 4.7e-42;
0; Mismatches 1;
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Pred. No. 8.9e-42;
0; Mismatches 1;
            NUMBER OF SEQ ID NOS: 34
SOFTWARE: WordPerfect 8.0 for Windows
SEQ ID NO 7
ENGTH: 117
TYPE: PRT
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99.18;
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Best Local Similarity 99.1%;
Matches 116; Conservative
PRIOR FILING DATE: 2000-05-24
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Best Local Similarity
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SERBEAL INFORMATION:

SERBEAL INFORMATION:

APPLICANT: Copley, Clive G

APPLICANT: Copley, Clive G

APPLICANT: Edge, Michael Derk

APPLICANT: Edge, Michael Derk

TITLE OF INVENTION: Monoclonal Antibody to CEA, Conjugates Comprising Said Antibod

TITLE OF INVENTION: Their Therapeutic use in an Adept System

TITLE OF INVENTION: Their Therapeutic use in an Adept System

FILE REPERENCE: 1991-209

CURRENT FILING DATE: 1991-10-29

PRIOR FILING DATE: 1996-10-29

PRIOR FILING DATE: 1997-04-29

PRIOR FILING DATE: 1997-04-29

PRIOR FILING DATE: 1997-04-29

PRIOR FILING DATE: 1997-04-29

PRIOR FILING DATE: 1996-05-04

NUMBER OF SEQ ID NOS: 131

SEQ ID NOS: 131

SEQ ID NOS: 131
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Petent No. US20010055751A1

GENERAL INFORMATION:

APPLICANT: Reiter, Robert E.

APPLICANT: Witte, Owen N.

APPLICANT: Witte, Owen N.

TITLE OF INVENTION: PSCA: PROSTATE STEM CELL ANTIGEN AND USES THEREOF

FILE REFERENCE: 30435, 54US14

CURRENT APPLICATION NUMBER: US/09/564,329A

CURRENT FILING DATE: 1097-07-20

PRIOR FILING DATE: 1997-07-20

PRIOR FILING DATE: 1997-01-10

PRIOR FILING DATE: 1998-01-12

PRIOR APPLICATION NUMBER: 60/071,141
                                                                                                                                                       61 APKFQGKATMTADSSSNTAYLQLSSLTSEDTAVYYCNA-YYGDY--EGYWGQGTTVTVSS 117
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                                                           1 OVKLQOSGAELVGSGASVKLSCTTSGFNIKDFYMHWVKQRPEQGLEWIGWIDPENGDSDY
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                                                                                                                                                                                                                                                                                                        Sequence 19, Application US/09910059
Patent No. US20020142359A1
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ORGANISM: Artificial Sequence
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Best Local Similarity 80.89
Matches 97; Conservative
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US-09-564-329A-11
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US-09-910-059-19
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Patent No. US20020142359A1

GENERAL INFORMATION:

APPLICANT: Copley, Clive G

APPLICANT: Edge, Michael Derek

APPLICANT: Emery, Stephen Charles

TITLE OF INVENTION: Monoclonal Antibody to CEA, Conjugates Comprising Said Antibody,

TITLE OF INVENTION: Monoclonal Antibody to CEA, Conjugates Comprising Said Antibody,

TITLE OF INVENTION: Monoclonal Antibody to CEA, Conjugates Comprising Said Antibody,

TITLE OF INVENTION: Their Therapeutic use in an Adept System

FILE REFERENCE: 1991-209

CURRENT APPLICATION NUMBER: US 09/171,945

PRIOR APPLICATION NUMBER: PCT/GB97/01165

PRIOR FILING DATE: 1997-04-29

PRIOR FILING DATE: 1997-02-14

PRIOR FILING DATE: 1997-03-13

SOFTWARE: Patentin version 3.1

SEQ ID NOS: 131

SEQ ID NOS: 131

SEQ ID NOS: 131
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                                                           APPLICANT: Farmour, Kathryn
TITLE OF INVENTION: High Affinity Humanized Anti-CEA Monoclonal
TITLE OF INVENTION: Antibodies
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 120;
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80.8%; Pred. No. 1.1e-32;
live 8; Mismatches 12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 503.5; DB 9;
Pred. No. 9.5e-33;
8; Mismatches 9;
                                                                                                                                                                       CURRENT APPLICATION NUMBER: US/09/974,051
CURRENT FILMS DATE: 2001-10-09
PRIOR APPLICATION NUMBER: 09/025,403
PRIOR FILLING DATE: 1998-02-18
PRIOR PLING DATE: 1996-10-31
PRIOR FILLING DATE: 1996-10-31
NUMBER OF SED ID NOS: 50
SOFTWARE: Microsoft World 97 SR-2
Tempest, Philip R.
Carr, Frank J.
Harris, William J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     79.8%;
76.4%;
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Best Local Similarity 76.4*
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US-09-910-059-11
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Matches 97; Conserv
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Gaps

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31; 11; Indels

Length 136;

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Sequence 11, Application US/09854811
Fatent No. US20020119157A1
GENERAL INFORMATION:
APPLICANT: Reiter, Robert E.
APPLICANT: Saffran, Douglas C.
TITLE OF INVENTION: PSCA: PROSTATE STEM CELL ANTIGEN AND USES THEREOF
FILE REFERENCE: 30435.54US14
CURRENT APPLICATION NUMBER: US/09/854,811
CURRENT FILING DATE: 2000-05-14
FRIOR PILING DATE: 2000-05-03
FRIOR PILING DATE: 1999-07-20
FRIOR FILING DATE: 1999-07-20
NUMBER OF SEQ ID NOS: 27
SOFTWARE: PatentIn Ver. 2.0
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                                                                                                                                                                                                                                                                                                                                                          14 EVQLQQSGAELVRSGASVKLSCTASGFNIKDYXIHWVNQRPDQGLEWIGWIDPENGDTEF 73
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                14 EVQLQQSGAELVRSGASVKLSCTASGENIKDYXIHWVNQRPDQGLEWIGWIDPENGDTEF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     77.4%; Score 488.5; DB 10;
77.8%; Pred. No. 1.5e-31;
tive 10; Mismatches 11; 1
                                                                                                                                                                                                         DB 10;
                                                                                                                                                                                                      Query Match 77.4%; Score 488.5; DB Best Local Similarity 77.8%; Pred. No. 1.5e-31 Matches 91; Conservative 10; Mismatches 1
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   SOFTWARE: Patentin Ver. 2.0
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Matches 91; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; ORGANISM: SCID Mice US-09-854-811-11
                                                                                                                  ORGANISM: SCID Mice
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 15
US-09-854-811-11
                           SEQ ID NO 11
LENGTH: 136
                                                                                                                                                 US-09-855-153-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQ ID NO 11
LENGTH: 136
                                                                                         TYPE: PRT
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GENERAL INFORMATION:
APPLICANT: Witte, Owen N.
APPLICANT: Witte, Owen N.
APPLICANT: Saffran, Douglas C.
TITLE OF INVENTION: PSCA: PROSTATE STEM CELL ANTIGEN AND USES THEREOF
FILE REFERENCE: 30435.540S14
FILE REFERENCE: 3001-05-14
CURRENT FILING DATE: 2001-05-14
PRIOR APPLICATION NUMBER: 09/564,329
PRIOR APPLICATION NUMBER: 09/564,329
PRIOR APPLICATION NUMBER: 09/564,329
PRIOR PLING DATE: 1999-07-20
PRIOR FILING DATE: 1999-07-20
PRIOR FILING DATE: 1999-07-20
PRIOR PLING DATE: 1999-07-30
PRIOR PLING DATE: 1999-01-12
PRIOR PLING DATE: 1998-01-12
PRIOR PLING DATE: 1998-01-12
PRIOR APPLICATION NUMBER: 60/071,44
PRIOR PLING DATE: 1999-02-17
PRIOR APPLICATION NUMBER: 60/113,230
PRIOR PLING DATE: 1999-02-17
PRIOR APPLICATION NUMBER: 60/120,536
PRIOR PLING DATE: 1999-02-17
PRIOR APPLICATION NUMBER: 09/203,939
PRIOR PLING DATE: 1999-03-16
PRIOR PLING DATE: 1999-03-16
PRIOR APPLICATION NUMBER: 09/203,939
PRIOR PLING DATE: 1999-02-17
PRIOR PLING DATE: 1999-02-17
PRIOR PLING DATE: 1999-02-17
PRIOR PLING DATE: 1999-02-17
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          61 APKFQGKATMTADSSSNTAYLQLSSLTSEDTAVYYCNAYYGDYEGYWGQGTTVTVSS 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 5;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 77.4%; Score 488.5; DB 1 Best Local Similarity 77.8%; Pred. No. 1.5e-31; Matches 91; Conservative 10; Mismatches 11
               PRIOR APPLICATION UNBER: 60/113,230
PRIOR FILING DATE: 1998-12-21
PRIOR PEDFLICATION NUBBER: 60/120,536
PRIOR FILING DATE: 1999-02-17
PRIOR PILING DATE: 1999-03-16
PRIOR APPLICATION NUMBER: 60/124,658
PRIOR PILING DATE: 1998-03-16
PRIOR PILING DATE: 1998-03-10
PRIOR PILING DATE: 1998-03-10
PRIOR APPLICATION NUMBER: 09/203,939
PRIOR FILING DATE: 1998-12-02
PRIOR PILING DATE: 1999-02-17
PRIOR PILING DATE: 1999-02-17
PRIOR FILING DATE: 1909-02-17
PRIOR FILING DATE: 1909-02-17
PRIOR FILING DATE: 1909-02-17
SOFTWARE: PALCHIN UNBER: 09/208,503
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 11, Application US/09855153 Patent No. US20020102666A1
FILING DATE: 1998-02-13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ORGANISM: SCID Mice
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-09-564-329A-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQ ID NO 11
LENGTH: 136
TYPE: PRT
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US-09-855-153-11
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Length 136;

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GenCore version 5.1.3
CApyright (c) 1993 - 2002 Compugen Ltd.
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OM protein - proteiñ search, using sw model

Run on:

December 23, 2002, 07:17:57; Search time 23.1279 Seconds (without alignments) 486.327 Million cell updates/sec

US-09-865-198-22 631 1 QVKLQQSGAELVGSGASVKL......AYYGDYEGYWQQGTTVTVSS 117 Perfect score:

Sedneuce:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283224 seqs, 96134422 residues

Searched:

283224 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

PIR_73:* Database :

pirl:* pir2:* pir3:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Description	Iq heavy chain pre	neavy chain V	chain V	leavy	neavy	Ig heavy chain V r	Ig gamma-1 chain -	Ig heavy chain V-D	gamma	gamma cha	rophen	heavy cha	p53 specific singl	heavy chai	heavy	Ig heavy chain V r	single chain Fv an	Ig heavy chain V r	heavy	heavy	heavy	heavy cha	heavy	Ig heavy chain V r	heavy	ь	ь	ь	Ļ
	ID	804576	A56446	1567	S25174	S52445	S17586	S49220	S03471	S29594	S24289	A47271	806823	JC5322	S03484	S03482	PH1012	S41374	PL0246	PH1403	Η	G37267	PS0024	A54378	S21810	B22769	838950	029	A27646	375
	DB	7	C3	~	7	~	7	7	7	7	7	4	ď	~	~	N	~	N	~	ď	N	~	7	~	7	~	~	~	~	7
		136	268	116	118	137	117	221	120	178	116	114	122	233	120	115	108	249	115	123	107	118	139	115	138	120	246	446	101	116
ФP	Query Match	81.0		8	77.8	9	ú	75.9	'n.	ω.	4	ë.	ë,		72.1	÷	8	9.89	ω.	œ	ζ.	ė.	0.99	ď.	'n	-	4.	٠		63.9
	Score	511	498.5	496.5	491	481.5	480	479	ਯ	473.5		465.5		459	455	454	435		430.5	430	2	420.5	7	410.5	410	406.5	406	406	8	403.5
	Result No.		2	m	4	S	9	7	80	σ	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	56	27	28	29

RESULT 2

To heavy chain V region (3H-3H scFv) - mouse (strain BALB/C)

C; Species: Mus musculus (house mouse)
C; Species: House musculus (house mouse)
C; Species: 19-Jan-1996 #sequence_revision 19-Jan-1996 #text_change 16-Aug-1996
C; Accession: A56446
B; Tang, P.M.; Foltz, L.A.; Mahoney, W.C.; Schueler, P.A.
J; Biol. Chen. 270, 7829-7835, 1995
A; Title: A high affinity digoxin-binding protein displayed on M13 is functionally ide A; Reference number: A56446; MUID:95229583; PMID:7713873
A; Reference number: A56446
A; Status: preliminary
A; Molecule type: mRNA
A; Residues: 1-268 < TAND
A; Cross-references: GB:U20617
C; Keywords: heterotetramer; immunoglobulin

Score 498.5; DB 2; Length 268; Pred. No. 1e-37;

79.0%; 83.1%;

Query Match Best Local Similarity

	pelB leader/Ig hea														
MHMS18	PC4402	S41394	PC1155	F28195	PL0208	D30562	JL0077	JL0076	S37483	S55542	A27472	A24672	G28195	S29690	D37262
-	4	7	~	~	7	~	7	N	~	7	7	7	7	7	7
139	287	120	133	120	136	119	136	141	469	116	131	119	120	288	66
63	63.9	63.5	63.3	63.0	65.9	62.8	62.5	62.5	62.5	62.4	62.4	62.4	62.4	62.4	62.1
403 5	403.5	400.5	399.5	397.5	397	396	394.5	394.5	394.5	394	394	393.5	393.5	393.5	392
30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

ALIGNMENTS

	RESULT 1 S04576
	Ig heavy chain precursor V region (MRL-histone 7H) - mouse (fragment) C;Species: Mus musculus (house mouse)
	C;Date: 04-Dec-1992 #sequence_revision 04-Dec-1992 #text_change 21-Jan-2000 C;Accession: S04576
	R;Kofler, R.; Noonan, D.J.; Strohal, R.; Balderas, R.S.; Moller, N.P.H.; Dixon, F.J.; Eur. J. Immunol. 17, 91-95, 1987
	A; Title: Molecular analysis of the murine lupus-associated anti-self response: involv A; Reference number: S04573; WUID:87133856; PMID:3102255
	A;Accession: S04576 A;Molecule type: mRNA
	A; Residues: 1-136 <kof></kof>
	A;Cross-references: EMBL:X14624; N1D:352029; PIDN:CAA32///.1; P1D:352030 C;Superfamily: immunoqlobulin V reqion; immunoqlobulin homology
	C; Keywords: heterotetramer; immunoglobulin
	F;1-19/Domain: signal sequence #status predicted <sig> F;20-136/Product: Iq heavy chain V region (fragment) #status predicted <mat></mat></sig>
	F;34-117/Domain: immunoglobulin homology <imm></imm>
	Query Match 81.0%; Score 511; DB 2; Length 136; Best Local Similarity 82.9%; Pred. No. 3.7e-39;
	u ,
	Qy 1 QVKLQQSGAELVGSGASVKLSCTTSGFNIKDFYMHWVKQRPEGGLEWIGWIDPENGDSDY 60
	Db 20 EVQLQQSGAELVRPGASVKLSCTASGFNIKDDYMHWVKQRPEQGLEWIGWIDPENGDTQY 79
_	Qy 61 APKFQGKATWTADSSSNTAYLQLSSLTSEDTAVYYCNAYYGDYEGYWGQGTTVTVSS 117
	Db 80 ASKFQGKATMTADTSSNTTYLQLSSLTSEDTAVYYCTTYGAYAMDYWGQGTSVTVSS 136
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Ig heavy chain V region (E8) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 22-Nov-1993 #sequence_revision 26-May-1995 #text_change 21-Jan-2000
C;Accession: S17586
R;Mylvaganam, S.E.; Paterson, Y.; Raiser, K.; Bowdish, K.; Getzoff, E.D.
A;Title: Biol. 221, 455-462, 1991
A;Title: Biochemical implications from the variable gene sequences of an anti-cytochr
                                                                                                                                                                                                                                                                C; Species: Mus musculus (house mouse)
C; Date: 08-May-1995 #sequence_revision 21-Jul-1995 #text_change 21-Jan-2000
C; Date: 08-May-1995 #sequence_revision 21-Jul-1995 #text_change 21-Jan-2000
C; Date: 08-May-1995 #sequence_revision 21-Jul-1995 #text_change 21-Jan-2000
C; Ascassion: 352445
A; Description: Specific amplification by the polymerase chain reaction of rearranged A; Reference number: 552445
A; Accession: 552445
A; Accession: 552445
A; Status: preliminary
A; Molecule type: DNA
A; Coss. references: EMBL:X82690; NID:g673439; PIDN:CAA58011.1; PID:g673440
C; Genetics:
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EIQLQQSGAELVXXGASVKLSCTASGFNIKDDYLHWVKQRPEQGLEWIGWIDPENGDTEY 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    20 EVQLQOSGAELVRPGALVKLSCKASGFNIKDYYMYWKQRPEQGLEWIGWIDPENGNIVY 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 QVKLQQSGAELVGSGASVKLSCTTSGFNIKDFYMHWVKQRPEQGLEWIGWIDPENGDSDY 60
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                                                     61 APKFQGKATMTADSSSNTAYLQLSSLTSEDTAVYYCNAYYGDYE--GYWGQGTTVTVS 116
                                                                              ASKRQCKATITADISSNTAYLQLSSLTSEDTAVYYCSSPLVHLRTFAYWGQGTLVTVS 118
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A;Accession: S17586
A;Accession: S17586
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-117 <MYL>
A;Cross-references: EMBL:X60683; NID:951820; PIDN:CAA43095.1; PI
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;15-98/Domain: immunoglobulin homology <IMM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 117;
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Best Local Similarity 78.8%; Pred. No. 2e-36;
Matches 93; Conservative 12; Mismatches 11; Indels
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78.2%; Pred. No. 1.7e-36;
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C; Superfamily: immunoglobulin V region; immunoc
C; Keywords: heterotetramer; immunoglobulin
F; 34-115/Domain: immunoglobulin homology <IMM>
                                                                                                                                                                                                                                                  - mouse
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Best Local Similarity 78.29
Matches 93; Conservative
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S17586
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A; Title: Reshaping a human monoclonal antibody to inhibit human respiratory syncytial vi A; Reference number: $15672; MUID:91337412; PMID:1367535
A; Accession: $\frac{3}{2}5672
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(S. Species: Mis musculus (house mouse)
(S. Species: Mis musculus (house mouse)
(S. Daces 10-1995 #sequence_revision 20-Feb-1995 #text_change 21-Jan-2000
(S. Accession: E.S. 1913)
(S. Monestier, M.; Fasy, T.M.; Losman, M.J.; Novick, K.E.; Muller, S.
(S. Monestier, M.; Fasy, T.M.; Losman, M.J.; Novick, K.E.; Muller, S.
(A. Description: Structure and binding properties of monoclonal antibodies to core A. Reference fnumber: S.25174
(A. Status: preliminary
(A. Molecule type: mRNA
(A. Residues: 1.118 < MON)
(A. Cession; S.33133
(A. Status: preliminary
(A. Molecule type: mRNA
(A. Residues: 1.118 < MON)
(A. Molecule type: mRNA
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                                                                                                                                                                                                                                                                                                                                                  Ig heavy chain vegion - mouse (fragment)
C;Species: Musmusculus (house mouse)
C;Date: 18-Feb 1994 #sequence_revision 10-Nov-1995 #text_change 21-Jan-2000
C;Accession: Si5672
                                                     1 QVKLOGSGAELVGSGASVKLSCTTSGFNIKDFYMHWVKQRPEQGLEWIGWIDPENGDSDY 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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                                                                                                             62
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C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Status: preliminary; nucleic acid sequence not shown
A; Molecule type: mRNA
A; Residues: 1-116 <-TEM>
A; Residues: 1-116 <-TEM>
A; Cross-references: EMBL:X58835; NID:951978; PIDN:CAA41644.1; PID:951979
C; Superfamily finmunoglobulin V region; immunoglobulin homology
C; Reywords: heterotetramer; immunoglobulin
F;15-98/Domaiñ: immunoglobulin homology <IMM>
                                                                                                                                                                61 APKFQGKATMTADSSSNTAYLQLSSLTSEDTAVYYCNAYY-GDYEGYWGQGTTVTVSS 117
                                                                                                                                                                                            3 QVKLQESGAELVKPGASVKLSCTTSGFNIKDTYMHWVKQRPEQGLEWIGRIAPANGITKY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            62 PKFOGKATMTADSSSNTAYLQLSSLTSEDTAVYYCNAYYGDYEGYWGQGTTVTVSS 117
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     14; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               13; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 77.8%; Score 491; DB 2, Best Local Similarity 78.8%; Pred. No. 2e-37; Matches 93; Conservative 10; Mismatches
     Mismatches
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     5;
     98; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         | Similarity
92; Conserv
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Matches
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Matches
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        Matches
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C;Species: synthetic
A;Note: Mus musculus (house mouse) gene engineered and expressed in Escherichia coli
C;Date: 21.58p-1993 #sequence_revision 11.Aug-1995 #text_change 11.Aug-1995
C;Accession: A47271
S;Lesley, S.A.; Patten, P.A.; Schultz, P.G.
Proc. Natl. Acad. Sci. U.S.A. 90, 1160-1165, 1993
A;Title: A genetic approach to the generation of antibodies with enhanced catalytic a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             nitrophenyl phosphonate-specific antibody 48G7 heavy chain VDJ - synthetic (fragment)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        submitted to the EMBL Data Library, September 1991
A;Description: Cloning and sequencing of the cDNA coding for the variable regions of
A;Reference number: S24287
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                                             Ig gamma chain (WM65) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Species: Mus musculus (house mouse)
C;Accession: S29594
R;Seymour, R.
Submitted to the EMBL Data Library, February 1991
A;Reference number: S29594
A;Accession: S29594
A;Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ig gamma chain V region (JS34/32) - mouse
C;Species: Mus musculus (house mouse)
C;Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 20-Jun-2000
C;Accession: S24289
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Cross-references: EMBL:X62705; NID:951690; PIDN:CAA44584.1; PID:91333963 Cs. Superfamily: immunoglobulin V region; immunoglobulin homology C; Keywords: immunoglobulin F; Reywords: immunoglobulin homology < IMM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   61 APKFQGKATMTADSSSNTAYLQLSSLTSEDTAVYYC---NAYYGDYEGYWGQGTTVTVSS 117
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C;Keywords: immunoglobulin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                62 PKFQGKATMTADSSSNTAYLQLSSLTSEDTAVYYCNAYYGDYEGYWGQGTTVTVSS 117
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Pred. No. 1.2e-35;
9; Mismatches 12;
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ilarity 78.3%;
Conservative
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A; Residues: 1-178 <SEY>
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A, Status: preliminary
A, Molecule type: mRNA
A, Residues: 1-116 < MON>
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S24289
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RESULT 9
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                                       C'Species: Mus musculus (house mouse)
C'Species: Mus musculus (house mouse)
C'Date: 19-Mar-1997 #sequence_revision 01-Aug-1997 #text_change 21-Jan-2000
C'Accession: $49220
R'Kipp, B.; Becker, W.P.; Schlaak, M.M.
Submitted to the EMBL Data Library, September 1994
A'Description: Cloning and expression of a recombinant mouse Fab-fragment recognizing a A'Reference number: $49220
A'Rolecule type: mRNA
A'Residues: 1-221 <KIPA
A'Cross references: EMBL:237502; NID:9541778; PIDN:CAA85732.1; PID:9541779
A'Cross references: EMBL:237502; NID:9541778; PIDN:CAA85732.1; PID:9541779
A'Cross references: EMBL:237502; NID:9541778; PIDN:CAA85732.1; PID:9541779
C'Superfamily: immunoglobulin C region; immunoglobulin homology
C'Keywords: immunoglobulin
F;1-120/Domain: V region #status predicted <VRG>F;121-221/Domain: C region #status predicted <CRG>F;139-203/Domain: immunoglobulin homology <IMM>
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A:Recession: $03471
A:Molecule type: mRNA
A:Molecule type: mRNA
A:Residues: 7-120 <ROCI>
A:Coss.references: EMBL:X01820; NID:951833; FIDN:CAA25962.1; PID:9133983
A:Coss.references: EMBL:X01820; NID:951833; FIDN:CAA25962.1; PID:9133983
A:Coss.references: EMBL:X01820; NID:951833; FIDN:CAA25962.1; PID:9133983
A:Coss.references: EMBL:X01820; NID:951833; FIDN:CAA25962.1; PID:91333983
A:Title: This individed diversity of the mouse gamma-chains anti-GAT repertoire does not se A:Reference number: $07453; MUID:83058021; PMID:6815271
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Title: Analysis of antibody diversity: V-D-J mRNA nucleotide sequence of four anti-GAT hypervariable regions.
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g gamma-1 chain - mouse (fragment)
;Species: Mus musculus (house mouse)
;Date: 19-Mar-1997 #sequence_revision 01-Aug-1997 #text_change 21-Jan-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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Pred. No. 4.6e-36;
8; Mismatches 15; Indels
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Pred. No. 4.7e-36;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           6; Mismatches
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Best Local Similarity 79.0%;
Matches 94; Conservative
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Matches 94; Conservative
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                      Ig gamma-1
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A; Molecule type: mRNA
A; Residues: 10-115 <ROCI>
A; Ross-references: EMBL:X03219
A; Note: this sequence was determined from the differentiated gene
R; Rocca-Serra, J.; Mazie, J.C.; Moinier, D.; Leclercq, L.; Somme, G.; Theze, J.; Foug
                                                                                                                                                                                                                                                                                                                                                                           Ig heavy chain V-D-J region (hybridoma G7 Ab 2.9) - mouse (fragment)
C; Species: Mus musculus (house mouse)
A; Variety: strain BALB/C
C; Date: 26-Feb-1998 #sequence_revision 26-Feb-1998 #text_change 21-Jan-2000
C; Accession: S03484; S07453
B; Rocca-Serra, J; Matthes, H.W.; Kaartinen, M.; Milstein, C.; Theze, J.; Fougereau, EMBO J. 2, 867-872, 1983
A; Title: Analysis of antibody diversity: V-D-J mRNA nucleotide sequence of four anti-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               C;Species: Mus musculus (house mouse)
A;Variety: strain BALB/c
C;Date: 26-Feb-1998 #sequence_revision 26-Feb-1998 #text_change 21-Jan-2000
C;Accession: S03482; S07453
R;Rocca-Serra, J; Matthes, H.W.; Kaartinen, M.; Milstein, C.; Theze, J.; Fougereau, EMBO J. 2, 867-872, 1983
A;Title: Analysis of antibody diversity: V-D-J mRNA nucleotide sequence of four anti-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Note: this sequence was determined from the differentiated gene
KROcca-Serra, J.; Mazie, J.C.; Moinler, D.; Leclercq, L.; Somme, G.; Theze, J.; F.
J. Immunol. 129, 2554-2558, 1982.
A;Title: The limited diversity of the mouse gamma-chains anti-GAT repertoire does A;Reference number: S07453; MUID:83058021; PMID:6815271
                                                                                                            5 QQSGAELVGSGASVKLSCTTSGFNIKDFYMHWVKQRPEQGLEWIGWIDPENGDSDYAPKF 64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 QVKLQQSGAELVGSGASVKLSCTTSGFNIKDFYMHWVKQRPEQGLEWIGWIDPENGDSDY 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ig heavy chain V-D-J region (hybridoma G8 Ad 3.8) - mouse (fragment)
                                                                                                                                                                                        65 QGKATMTADSSSNTAYLQLSSLTSEDTAVYYCNAYYGDYEGYWGQGTTVTVSS 117
                                                                                                                                                                                                                        61 GVKAIMTADTSSNTAYLQLSSLTSEDTAVYYCNAGM----DYWGQGTTVTVSS 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-43 <ROC2>
C;Superfamily: immunoglobulin V region; immunoglobulin homology
F;15-98/Domain: immunoglobulin homology <IMM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 120;
                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Reference number: S03471; MUID:84057768; PMID:6416834
A;Accession: S03484
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A;Reference number: S03471; MUID:84057768; PMID:6416834
A;Accession: S03482
                      13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        72.1%; Score 455; DB 2; 75.6%; Pred. No. 3.6e-34; ive 8; Mismatches 19
  No. 3.2e-34;
                            5; Mismatches
     Pred.
  80.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Molecule trype: mRNA
A; Residues: 10-120 < ROC1>
A; Cross-references: EMBL:X07144
                            91; Conservative
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  Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      hypervariable regions.
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C; Species: Mus musculus (house mouse)

C; Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 21-Jan-2000

C; Accession: $50623

R; Miller III, $A.; Glasel, J.A.

J. Mol. Biol. $209, 763-778, 1989

A; Fitle: Compārative sequence and immunochemical analyses of murine monoclonal anti-morp

A; Reference number: $06815; MUID: 90064531; PMID: 2555519

A; Status: not compared with conceptual translation
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A;Residues; 1-233 <JAN>
A;Experimental source: hydricloma cell
C;Comment: Anhis protein specifically binds the tumor suppressor protein p53. It restores
                                                                                                                                                                                                                                                                        1;
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C; Date: 15-May-1997 #sequence_revision 15-May-1997 #text_change 18-Jul-1997
C; Accession; JG5322
R; Jannot, O(B.; Hynes, N.E.
Biochem. Biophys. Res. Commun. 230, 242-246, 1997
A; Title: Cipiaracterization of scFv-421, a single-chain antibody targeted to B A; Reference number: JG5322; MUID:97168950; PMID:9016757
A; Accession: JG5322
                                             A; Molecule types DNA; protein
A; Residues: 1.114 <LES>
A; Note: sequence extracted from NCBI backbone (NCBIN:124854, NCBIP:124855)
A; Note: parts of this sequence were determined by protein sequencing
F;22-96/Disulfige bonds: #status predicted
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A; Residues: 11-122 <MIL>
C; Superfamily: immunoglobulin V region; immunoglobulin homology
C; Keywords: heteroterramer; immunoglobulin
F; 15-99/Domain: immunoglobulin homology < IMM>
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A; Reference number: A47271; MUID:93165660; PMID:8094556
                                                                                                                                                                                                                  Score 465.5; DB 4;
Pred. No. 3.9e-35;
7; Mismatches 16;
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Pred. No. 9.5e-35;
8; Mismatches 14
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hilarity 77.8%;
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Best Local Similarity 77.9%;
Matches 95; Conservative
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Gaps

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J. Immunol. 129, 2554-2558, 1982
A;Title: The limited diversity of the mouse gamma-chains anti-GAT repertoire does not se A;Title: The limited diversity of the mouse gamma-chains anti-GAT repertoire does not se A;Accession: 807453
A;Reference number: 807453
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-43 <ROC2>
C;Superfamily: immunoglobulin V region; immunoglobulin homology
F;15-98/Domain: immunoglobulin homology <IMM>
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631
1 QVKLQQSGAELVGSGASVKL......AYYGDYEGYWGQGTTVTVSS 117
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P01757
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GenCore version 5.1.3 Copyright (c) 1993 - 2002 Compugen Ltd.
                                                                                                                                                                           Total number of hits satisfying chosen parameters:
                                                                                                                                                          112892 seqs, 41476328 residues
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HV03_MOUSE
HV02_MOUSE
HV12_MOUSE
HV13_MOUSE
HV15_MOUSE
HV15_MOUSE
HV1C_HUMAN
HV1C_HUMAN
HV1C_HUMAN
HV1C_HUMAN
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						ALIGNMENTS	
RE HV	D2.	MOU	STA	STANDARD;		PRT; 139 AA.	
AC DT DT		P01751; P017 21-JUL-1986 21-JUL-1986 15-JUL-1999 Ig heavy cha	らくくく	01, Creat 01, Last 38, Last egion B1-	1-1:4 th	ted) sequence update) annotation update) -8/186-2 precursor.	
8008		Mus musculus (Mou Eukaryota; Metazo Mammalia; Eutheri NCBI_TaxID=10090;	.us (Mouse) Metazoa; Eutheria;	e). ; Chordata ; Rodentia	lata Itia	; Craniata; Vertebrata; E ; Sciurognathi; Muridae;	Euteleostomi; Murinae; Mus.
R R R R		[1] SEQUENCE FROM N.A. STRAIN=C57BL/6; MEDLINE=81234548; Bothwell A.L.M., F	FROM N.A. 57BL/6; 31234548; A.L.M.	PubMed=6788376 Paskind M., Ret	.6788 M.,	1376; Reth M., Imanishi-Kari	T., Rajewsky K.,
RR		Baltimore D.; "Heavy chain antibodies: S	vari omat	ble rec	rion ion	contribution to the NE evident in a gamma 2a	family of Triable regio
		-!- MISCEL MAKING (NPB A	MISCELLANEOUS: THE BI MAKING ANTIBODIES TO (NPB ANTIBODIES).	THE BI	-8 M THE	U CHAIN MRNA WAS CL HAPTEN (4-HYDROXY-3	ONED FROM A HYBRIDOMA -NITROPHENYL)ACETYL
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20 20 20		EMBL; J00529; P	29; AAA381	AAA38170.1;			
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FT		NON_TER SEQUENCE	- 2	139 1541	9 MW;	; 1B57DD4FD0C9F465 CRC64;	54;
	Query Best L	Match	ı Similarity	63.9%;	.; .;	Score 403.5; DB 1; Le Pred. No. 2.4e-33;	Length 139;

mus musculu mus musculu mus musculu

homo sapien mus musculu homo sapien rattus norv

homo sapien mus musculu mus musculu

HV3G_HUMAN HV01_RAT HV1A_HUMAN HV39_MOUSE HV21_MOUSE

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"Heavy chain variable region contribution to the NPb family of antibodies: somatic mutation evident in a gamma 2a variable region."; Cell 24:625-637(1981).
 Bothwell A.L.M., Paskind M., Reth M., Imanishi-Kari T., Rajewsky
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                      1 QVKLQÖSGAELVGSGASVKLSCTTSGFNIKDFYMHWVKQRPEQGLEWIGWIDPENGDSDY 60
                                2 VKŠŽQQSGAELVGSGASVKLSCTTSGFNIKDFYMHWVKQRPEQGLEWIGWIDPENGDSDYA 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      21-JUL-1986 (Rel. 01, Created)
21-JUL-1998 (Rel. 01, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
15-JUL-1999 (Rel. 38, Last annotation update)
16-JUL-1999 (Rel. 38, Last annotation update)
Mus misculus (Mouse).
Bukariota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalua: Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                            Eukaryotaf Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
NCBI_Taxip=10090;
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M
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 120;
                                                                                                                                                                                                                                                                                                                                                                    HSSP; PO0789; IMCP.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003006; Ig_W.
Pfam; PE00047; 1g; 1.
SMART; $M00406; IGv; 1.
Immunoglobulin V region; Antiarsonate antibody; Hybridoma.
   25; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    22; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                            120 AA; 13307 MW; FF04E4A167B654AF CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 390; DB 1;
Pred. No. 4.4e-32;
                                                                                                                                                    21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
19 heavy chain V region 36-65.
Is musculus (Mouse).
Eukaryota Metazoa; Chordata; Craniata; Vertel
   13; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    19; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
MEDLINE-81234548; Pubmed-6788376;
                                                                                                                                                                                                                                                                                                                                                                                                                                                               61.8%;
62.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Local Similarity 62.59 nes 7.5; Conservative
79; Conservative
                                                                                                                                    STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STANDARD;
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                                                                                                                                 HV03_MOUSE
P01747;
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P01755
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                                                                                                                         HV03_MOUSE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ij
-!- MISCELLANEOUS: THE GAMMA-2A CHAIN MRNA WAS CLONED FROM A HYBRIDOMA MAKING ANTIBODIES TO THE HAPTEN (4-HYDROXY-3-NITROPHENYL)ACETYL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 QVKLQQSGAELVGSGASVKLSCTTSGFNIKDFYMHWVKQRPEQGLEWIGWIDPENGDSDY 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              61 APKFQGKATMTADSSSNTAYLQLSSLTSEDTAVYYCNAY-YGDYEGYWGQGTTVTVSS 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    20 QVQLQQPGAEFVKPGASVKLSCKASGYTFTSYLMHWVNQRPGRGLEWIGRIDPNSGGTTY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi;
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1;
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MEDLINE-82152818; PubMed-6801765;
Sims J., Rabbitts T.H., Estess P., Slaughter C., Tucker P.W.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         IG HEAVY CHAIN V REGION S43.
FRAMEWORK-1.
COMPLEMENTARITY-DETERMINING-1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPLEMENTARITY - DETERMINING - 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "Somatic mutation in genes for the variable portion of immunoglobulin heavy chain."; Science 216:309-311(1982).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       15200 MW; ADD5881BF44B8EC9 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 61.1%; Score 385.5; DB 1; Best Local Similarity 63.6%; Pred. No. 1.4e-31; Matches 75; Conservative 12; Mismatches 30;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
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JH2 SEGMENT.
BY SIMILARITY.
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                                                                                                                                                                                                                                                                                   EMBL; J00539; AAA38172.1; -.
PIR; A02038; GZMS43.
HSSP; P01810; ZFBJ.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_V.
Ffam; PF00047; Igj. 1.
SMART; SM00406; IGV. 1.
Immunoglobulin V region; Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STANDARD;
                                                    (NPB ANTIBODIES)
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137 AA;
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                                                                                                                                                                                                                                                                                                 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              heavy chain constant region domains.";
Biochemistry 21:5415-5424(1982).
-!- MISCELLANEOUS: THE SEQUENCE OF THE LIGHT CHAIN OF THIS IGM MYELOMA
                                                                                                                                                                                                                                                                                                                                                                        61 APKFQGKATMTADSSSNTAYLQLSSLTSEDTAVYYC--NAYYG---DYEGYWGQGTTVTV 115
                                                                                                                                                                                                                                                                                                                                                                                     6; Gaps
                                                                                                                                                                                                                                                                                                                                               79
                                                                                                                                                                                                                                                                                                                      1 QVKLQQSGAELVGSGASVKLSCTTSGFNIKDFYMHWVKQRPEQGLEWIGWIDPENGDSDY 60
                                                                                                                                                               Pfam; PF00047; ig; i. SWART; SW00406; IGv; i. Immunoglobulin V region; Antiarsonate antibody; Hybridoma; Signal.
                                                                                                                                                                                                                                                                                                                                      20 EVQLQQSGAELVRAGSSVKMSCKASGYTFTSYGINWVKQRPGQGLEWIGYINPGNGYINY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE, AND CARBOHYDRATE-LINKAGE SITE ASN-55.
BEDLINE-83075344; PubMed-6816276;
Kehry M.R., Fuhrman J.S., Schilling J.W., Rogers J., Sibley C.H., Hood L.E.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         amond
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Hood L.E.; "Complete amino acid sequence of a mouse mu chain: homology
                                                                                                                                                                                                                                                                      Length 140;
                                                                                                                                                                                                                    IG HEAVY CHAIN V REGION 93G7
                                                                                                                                                                                                                                                                  60.4%; Score 381; DB 1; Length 14 60.7%; Pred. No. 4.1e-31; ive 22; Mismatches 20; Indels
                                                                                                                                                                                                                                            140 AA; 15514 MW; 25A4CBBE31DA5CE8 CRC64;
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PROTEIN HAS ALSO BEEN DETERMINED.
-!- MISCELLANEOUS: THIS PROTEIN BINDS DEXTRAN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
21-JUN-2002 (Rel. 41, Last annotation update)
1g heavy chain V region MOPC 104E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              117 AA.
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DISULFID 22 96 BY SIMILARITY.
                                                                                                              PIR; A02028; HVMSG7.
HSSP; P01810; 2FBJ.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_V.
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InterPro; IPR003596; Ig_v.
                                                                                                     EMBL; J00493; AAA38128.1; -
                                                                                                                                                                                                                                                                                             74; Conservative
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SMART; SM00406; IGv; 1.
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HSSP; P01789; IMCP.
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55
117 1
117 AA;
                                                                                                                                                                                                                                                                               Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                         SS 117
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P01756;
                                                                                                                                                                                                                               NON_TER
SEQUENCE
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NON_TER
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HV12_MOUSE
                                                                                                                                                                                                                                                                                                                                                                                                                         116
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                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               20 QVQLQQPGAELVKPGASVQLSCKASGHTFTNYWIHWYKQRPGQGLEWIGEINPNDGRSNY 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Tucker P.W.;
"Illegitimate recombination generates a class switch from C mu to C delta in an IgD-secreting plasmacytoma.";
PIN: A02033; HVMST7.
HSSP, PO1810, 2FBJ.
InterPro; IPR0033006; Ig_MHC.
InterPro; IPR003596; Ig_W.
Pfan: PR0047; Ig_1.
SMART: SM00406; IGV: 1.
Immunoglobulin V region; Signal.
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                                                                                     1 QVKLQQSGAELVGSGASVKLSCTTSGFNIKDFYMHWVKQRPEQGLEWIGWIDPENGDSDY 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gilliam A.C., Shen A., Richards J.E., Blattner F.R., Mushinski J.F.,
                                                                                                                                    61 APKFQGKATMTADSSSNTAYLQLSSLTSEDTAVYYCNAYYGDYEGYWGQGTTVTVSS 117
                                                                                                                                                     61 NQKFKGKATLIYUDKSSSTAYMQLNSLISEDSAVYYCARDYDWYFDVWGAGTITVINSS 117
                                                                                                                                                                                                                                                                                                                                                    Mús musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         HEAVY CHAIN V REGION TEPC 1017.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          59.3%; Score 374; DB 1; Length 138; 61.7%; Pred. No. 2e-30; Live 17; Mismatches 25; Indels
; Score 377; DB 1; Length 117;
; Pred. No. 8.3e-31;
14; Mismatches 30; Indels
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COMPLEMENTARITY-DETERMINING-1.
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15576 MW; 748157E4C6907B8E CRC64;
                                                                                                                                                                                                                                                                                  (Rel. 02, Created)
(Rel. 02, Last sequence update)
(Rel. 38, Last annotation update)
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Last annotation update)
                                                                                                                                                                                                                                                                                  23-OCT-1986 (Rel. 02, Created)
23-OCT-1986 (Rel. 02, Last sequence update)
15-ULL-1999 (Rel. 38, Last annotation update
Ig heavy chain V region TEPC 1017 precursor.
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                                                                                                                                                                                                                                                     138 AA
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BY SIMILARITY.
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   59.7%;
62.4%;
 Query Match
Best Local Similarity 62.4%
Matches 73; Conservative
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                                                                                                                                                                                                                                                      STANDARD;
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138 AA;
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(Rel.
(Rel.
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21-JUL-1986
15-JUL-1999
                                                                                                                                                                                                                                                   HV48_MOUSE
P03980;
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P01757;
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DISULFID
NON_TER
SEQUENCE
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DOMAIN
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HV13_MOUSE
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InterPro; IPR003006; Ig_MHC
                                          IPR003596; Ig_v.
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Best Local Similarity
Matches 69; Conserv
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                                          InterPro;
                                                                                                                                                                                                                                                                                       NON_TER
SEQUENCE
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A Schilling $2. Clevinger B., Davie J.M., Hood L.;

Tamino arigi sequence of homogeneous antibodies to dextran and DNA rearrangements in heavy chain V-region gene segments.";

Nature 283:35-40(1980).

I Mature 283:35-40(1980).

HICHECCELANBOOUS: THE SEQUENCES OF 10 HYBRIDOMA PROTEINS THAT ALSO BIND DEXTRAN DIFFER FROM THAT SHOWN AT 1-7 POSITIONS, MANY OF C. I- MISCELELANBOOUS: THIS PROTEIN BINDS DEXTRAN.

PIR: A26242: MHMSJ5.

HSSP: POLO 89: IMCP.

RICHEPOS: IPREMO3306: Ig_MHC.

RICHEPOS: IPREMO3306: Ig_MHC.

RICHEPOS: IPREMO3596: Ig_V.

RICHERPOS: IGV.

RICHERP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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                                                                         Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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Mammalią; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus
NCBI_TaxID=10090;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              58.3%; Score 368; DB 1;
61.3%; Pred. No. 6.5e-30;
iive 16; Mismatches 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
15-JUL-1999 (Rel. 38, Last annotation update)
Mus musculus (Mouse).
Ig heavy chain V region J558
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nes 73; Conserv
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MEDLINE-84182519; PubMed-6201362;
Dildrop R., Bovens J., Slekevlitz M., Beyreuther K., Rajewsky K.;
Tak V region determinant (idiotope) expressed at high frequency in B
lymphocytes is encoded by a large set of antibody structural genes.";
EMBO J. 3:517-523(1984).
PIR; A02037; MHMS15.
HSSP; P01810; 2FBJ.
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                                                                                                                                                                                                                                                                                                                                                               20 QVQLQQSGPEVVRPGVSVKISCKGSGYTFTDYAMHWVKQSHAKSLEWIGVISTYNGNTSY 79
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
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                                                                                                             IG HEAVY CHAIN V REGION BCL1
                                                                                                                                                                                                                   58.3%; Score 368; DB 1; Length 13
59.0%; Pred. No. 7.7e-30;
tive 17; Mismatches 31; Indels
                                                                                                             20 136 IG HEAVY CHAIN V REGION Bi
136 136 136 WW; 6827CFBC6DB3F35E CRC64;
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01-JAN-1988 (Rel. 06, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
heavy chain V region AC38 15.3.
Mus musculus (Mouse).
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J SEGMENT.
BY SIMILARITY.
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Pfam: PF00047; 1g; 1.
SMART; SM00406; IGv; 1.
Immunoglobulin V region; Signal.
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InterPro; IPR003596; Ig_v.
Pfam; PF00047; Ig_.
SMART; SM00406; IGv; I.
Immunoglobulin V region.
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Matches 71; Conservative
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120 1
120 AA;
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ALCOHEN J., COHEN J., GIVOL D.;
Nucleic Acids Res. 8:4839-4840(1980).
-! MISCELLANBEDUS: THIS SEQUENCE WAS TRANSLATED FROM AN MRNA ISOLATED
FROM A MYELOMA THAT SECRETES IGG2B.
PIR; A02027; GVMS11.
HISSP: P01810; ZFBJ.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR00356; Ig_V.
Pfam; PF00047; ig; 1.
SNART; SM00406; IG; 1.
Imminoglobulin V region.
NON_TER
                                                                                                      MEDLINE-64182519; PubMed-6201362;
Dildrop R., Bovens J., Slekevitz M., Beyreuther K., Rajewsky K.;
Dildrop R., Bovens J., Slekevitz M., Beyreuther K., Rajewsky K.;
A. V region determinant (idiotope) expressed at high frequency in B lymphocytes is encoded by a large set of antibody structural genes.";
EMBO J. 3:517-523(1984).
PIR: A02040; MHMS38
HSSP, P01789; IMCP.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        61 APKFQGKATMTADSSSNTAYLQLSSLTSEDTAVYYCNAYYGDYEGY--WGQGTTVTVSS 117
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus. NCBL_TaxID=10090;
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MEDIINE-81053741; Pubmed-6253904;
Zakut R., Cohen J., Givol D.;
"Cloning and sequence of the cDNA corresponding to the variable region of immunoglobulin heavy chain MPC11.";
Nucleic Acids Res. 8:3591-3601(1980).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                57.4%; Score 362.5; DB 1; Length 118; 59.7%; Pred. No. 2.3e-29; Live 17; Mismatches 28; Indels 3
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99 104 D SEGMENT.

105 118 J SEGMENT.

22 96 BY SIMILARITY.

118 118 AM; 94F7BEE4C762A018 CRC64;
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121 AA; 13135 MW; 227AEF3EC56ED0BF CRC64;
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Pred. No. 6.6e-28;
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21-JUL-1986 (Rel. 01, Last sequence update)
12-JUL-1999 (Rel. 38, Last annotation update)
15 heavy chain V region MPC 11.
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                                                                                                                                                                                                                                                                                         naser, Follows, IMCC.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_v.
Pfam; PR0047; Ig; 1.
SMART; SM00406; IGv. 1.
Immunoglobulin V region.
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56.2%;
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Matches 71; Conserv
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Best Local Similarity
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P01745;
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SEQUENCE.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bennich H.H., Johansson S.G.O., von Bahr-Lindstrom H.; (In) Bach M.K. (eds.); Immediate hypersensitivity: modern concepts and developments, pp.1-36, Marcel Dekker, New York (1978).
-i- MISCELLANEOUS: THIS EPSILON CHAIN WAS ISOLATED FROM A MYELOMA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      61 APKFQGKATMTADSSSNTAYLQLSSLTSEDTAVYYC---NAYYGDYEGY------WGQ 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  11; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 QVKLQQSGAELVGSGASVKLSCTTSGFNIKDFYMHWVKQRPEQGLEWIGWIDPENGDSDY 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE-83065234; PubMed-6815656; MEDLINE-83065234; PubMed-6815656; Menten J.H., Molgaard H.V., Houghton M., Derbyshire R.B., Viney J. Bell L.O., Gould H.J.; "Cloning and sequence determination of the gene for the human immunoglobulin epsilon chain expressed in a myeloma cell line."; Proc. Natl. Acad. Sci. U.S.A. 79:6661-6665(1982).
                                             HVIC_HUMAN STANDARD; PRT; 147 AA.

101744;
21-JUL-1986 (Rel. 01, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
17-OCT-2001 (Rel. 40, Last annotation update)
18-OCT-2001 (Rel. 40, Last annotation upda
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-JAN-1988 (Rel. 06, Created)
01-JAN-1988 (Rel. 06, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
19 heavy chain V region AC38 205.12.
Mus musculus (Mouse).
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              57.8%; Score 364.5; DB 1; Length 147; 51.6%; Pred. No. 1.9e-29; Live 25; Mismatches 26; Indels 11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     IG HEAVY CHAIN V-I REGION ND. PYRROLIDONE CARBOXYLIC ACID.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     T -> V (IN REF. 2).
IH -> HI (IN REF. 2).
VG -> GV (IN REF. 2).
MISSING (IN REF. 2).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pfam; PF00047; ig; 1. SMART; SM00406; IGv; 1. Immunoglobulin V region; Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PIR; A02026; ELHUND.
HSSP; P01789; IMCP.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_V.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       66; Conservative
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                                                                                                                                                                                                                                                                                               NCBI_TaxID=9606;
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P06330;
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HV51_MOUSE
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                            HV1C_HUMAN
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                                                          61 APKRÖGKATMTADSSSNTAYLQLSSLTSEDTAVYYC--NAYYGD--YEGYWGOGTTVTVS 116
[1111:11:11:11:11:11]
61 NDNLKGKATLTADTSSSTAYIQLSSLTSEDSAIYHCARGIYYNSSPYFDSWGOGTTLTVS 120
                                                                                                                                                                                                                                                                                                               "Heavy chain variable region contribution to the NPb family of antibodies: somatic mutation evident in a gamma 2a variable region."; Cell 24:625-637(1981).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                      1 QVKLQQSGAELVGSGASVKLSCTTSGFNIKDFYMHWVKQRPEQGLEWIGWIDPENGDSDY 60
                                Bothwell A.L.M., Paskind M., Reth M., Imanishi-Kari T., Rajewsky K.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              VKLQQSGAELVGSGASVKLSCTTSGFNIKDFYMHWVKQRPEQGLEWIGWIDPENGDSDYA 61
                                                                                                                                                                                                                        Mus muscullus (Mouse).
Eukaryota Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                              -I- MISCELLANEOUS: THIS GENALINE GENE BELONGS TO A SET OF CLOSELY RELATED GENES THAT COULD ENCODE V REGIONS OF NPB ANTIBODIES.
PIR, A02022; HVWNS02.
HSSP, P01810; 2FBJ.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003595; Ig_V.
Pf00047; ig; 1.
SMART; $M00406; IGV; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                           IG HEAVY CHAIN V REGION 102.
FRAMEWORK-1.
COMPLEMENTARITY-DETERMINING-1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         54.7%; Score 345; DB 1; Length 117; 67.4%; Pred. No. 1.3e-27;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPLEMENTARITY - DETERMINING - 2
  28; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           18; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      12867 MW; 740A65DD851FCA8C CRC64;
                                                                                                                                                                                  21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
12-JUL-1999 (Rel. 38, Last annotation update)
19 heavy chain V region 102 precursor.
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   21; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                         Immunoglobulin V region; Signal.
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           64; Conservative
                                                                                                                                                                  STANDARD;
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P01753; P11271;
                                                                                                                                                                                                                                                                                 STRAIN-C57BL/6;
                                                                                                                                                                                                                                                                                                             Baltimore D.;
 . * 89
                                                                                                117 S 117
                                                                                                                                                                  HV06_MOUSE
P01750;
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ID HV09_MG
AC P01753;
  Matches
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"Heavy chain, variable region contribution to the NPb family of antibodies: somatic mutation evident in a gamma 2a variable region."; cell 24:625-637(1981).
-!- MISCELLANEOUS: THIS GERMINE GENE BELONGS TO A SET OF CLOSELY RELATED GENES THAT COULD ENCODE V REGIONS OF NPB ANTIBODIES.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               20 QVQLQQPGAELVKPGASVKLSCKASGYTFTSYWMHWVKQRPGRGLEWIGRIDPNSGGTKY 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE-81234548; PubMed-6788376;
Bothwell A.L.M., Paskind M., Reth M., Imanishi-Kari T., Rajewsky K.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 QVKLQQSGAELVGSGASVKLSCTTSGFNIKDFYMHWVKQRPEQGLEWIGWIDPENGDSDY 60
                                                                                                                                                                                                                                                                                 Bothwell A.L.M., Paskind M., Reth M., Imanishi-Kari T., Rajewsky K.,
                                                                     Ig heavy chain V region 186-1 precursor.
Mus musculus (Mouse).
Bukaryota; Metazoa: Craniata; Vertebrata; Buteleostomi;
Mammalla; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    IG HEAVY CHAIN V REGION 186-1.
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COMPLEMENTARITY-DETERMINING-1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   16191A088CB17F5A CRC64;
21-JUL-1986 (Rel. 01, Created)
01-JUL-1989 (Rel. 11, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        P01748;
21-JUL-1986 (Rel. 01, Created)
1-JUL-1986 (Rel. 01, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
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                                                                                                                                                                                                                                                            MEDLINE-81234548; PubMed-6788376;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pfam; PF00047; ig; 1.
SMART; SM00406; IGv; 1.
Immunoglobulin V region; Signal.
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117 AA;
                                                                                                                                                                                                              SEQUENCE FROM N.A.
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SEQUENCE FROM N.A.
                                                                                                                                                                     NCBI_TaxID=10090;
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                                                                                                                                                                                                                                           STRAIN=C57BL/6;
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SMART; SM0040
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HV04_MOUSE
ID HV04_MOUSE
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SEQUENCE
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    December 23, 2002, 07:17:27; Search time 48.5233 Seconds (without alignments) 496.824 Million cell updates/sec
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631
1 QVKLQQSGABLVGSGASVKL......AYYGDYEGYWGQGTTVTVSS 117
                        GenCore version 5.1.3 (opyright (c) 1993 - 2002 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Total number of hits satisfying chosen parameters:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
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Gapop 10.0 , Gapext 0.5
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Perfect score:
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091v67 mus musculu 09249 mus musculu 09246 mus musculu 09246 mus musculu 09246 mus musculu 09246 mus musculu 09249 mus musculu 09249 mus musculu 09247 mus musculu 09246 mus musculu 09246 mus musculu 09426 mus musculu 09553 mus musculu 09553 mus musculu 09246 mus musculu 09249 mus musculu 09249 mus musculu 09549 mus musculu 09549 mus musculu 095175 mus musculu 09553 mus musculu 095175 mus musculu 091175 mus musculu

091V67 0924P5 0924P6 0924P6 0924P6 09124P8 09124P1 0924P7 0925P7 0925P7 0925P7 0925P7 0925P7 0925P7 0925P7 0925P7

ALIGNMENTS

SPTREMBL_21:*

Database :

Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Mus.

BL/GenBank/DDBJ databases.

	ALIGNMENTS		RESULT 1	11.31	Q99L31;	DT 01-JUN-2001 (TrEMBLrel. 17, Created)	DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)	01-JUN-2002				RP SEQUENCE FROM N.A.	RA Strausberg R.;			_		InterPro; IPR003597;	InterPro; IPR003600;	DR InterPro; IPR003006; Ig_MHC.	DR Pram; PF00047; ig; 3.		SMART;			PS00290; IG_MHC; UNKNC	SQ SEQUENCE 468 AA; SI661 MW; 96352328B3332ADB CRC64		80.88;	11 Similarity 80.7%; Pred. No. 1.3e-44;	Matches 90; Conservative 9; Mismatches 12; Inc	,	QY 1 QVKLQQSGAELVGSGASVKLSCTTSGFNIKDFYMHWVKQRPEQGLEWI	Ċ	DD ZO EVQLQQSGAELVRPGASVKLSCTASGFNIKDSLMHWVKQRPEQGLEWI	_
SPTREMBL_21:*	 Sp_bacteria:*	 	5: sp_invertebrate:*		 				13: sp_vertebrate:*				Pred. No. is the number of results predicted by chance to have a	score greater than or equal to the score of the result being printed,	and is derived by analysis of the total score distribution.		SUMMARIES	- Option ()	Query	Score March Length DB 10 Description	099131 mus	8.78 11 Q9J185 mus	65.2 143 11 Q924P9 Q924p9 mus	64.5 146 II Q924R8 Q924r8 mus	63.9 145 11 0924Q7 mus	63.9 146 11 Q924Q3 Q3	Q9ZIC4 mus	63.3 473 11 Q39L23 IIIIS	03.2 4/3 II 29508L4 03.25	Q924R0 mus	03.2 14.3 11 Q924Q3 mus	63.1 140 11 Q924KZ mus	62.9 142 11 Q924Q1 Q924q1 mus	11 Q924K4 mus	62.5 143 11 Q924KI Q924KI Q924KI	374767 TT 74T 1:70 *
case:													Prec	SCOI	and				, בי		٦ ،)

No. Result

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5;

core 510; DB 11; Length 468; red. No. 1.3e-44; Mismatches 12; Indels

OWN_1. 96352328B3332ADB CRC64;

GENIKDSLMHWVKQRPEQGLEWIGWIDPEDGETKY 79 GFNIKDFYMHWVKQRPEQGLEWIGWIDPENGDSDY 60

1;

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Pfam; PF00047; ig; 1.
                                 143 AA;
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                                 SEQUENCE
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NON_TER
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Q924R8;
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                                                                                                                                                                                                      STRAIN-BALB/C;
WEDLINE-2048942; PubMed=10992488;
Malkiel St. Liao L., Cunningham M.W.; Diamond B.;
"T-Cell dependent antibody response to the dominant epitope of
streptococcal polysaccharide, N-acetyl-glucosamine, is cross-reactive
with cardiac myosin.";
                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
            61 APKFQGKATMTADSSSNTAYLQLSSLTSEDTAVYYC--NAYYGDYEGYWGQGTTVTVSS 117
                                                                                                                                                                                                                                                                                                                                                                                                                        9 AEÜVGSGASVKLSCTTSGFNIKDFYMHWVKORPEQGLEWIGWIDPENGDSDYAPKFQGKA 68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Kozono Y., Kozono H., Azuma T.;
"Direct Estimation of Relative Affinity by Flow Cytometry Reveals
"Direct Estimation of B Cell Antigen Receptors in Response to (4-
Hydroxy-3-Nitrophenyl)Acetyl (NP).";
Submitted (AUG-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AB069916; BAB63932.1;
InterPro; IPR003006; Ig_MHC.
                                                                                                                                   (Fragment).
Mas muscudus (Mouse).
Eukaryotag, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus
NCBL_TāxID=10090;
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                                                                                                                                                                                                                                                                                                                                                                                 DB 11; Length 109;
                                                                                                                                                                                                                                                                                                                                                                                                                                                               69 TMPADSSSNTAYLQLSSLTSEDTAVYYCNAYYGDYEGYWGQGTTVTVSS 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 428; DB 11; Length 1
Pred. No. 7e-37;
5; Mismatches 20; Indels
                                                                                         01-0CT-2000 (TrEMBLrel. 15, Created)
01-0CT-2000 (TrEMBLrel. 15, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
Anti-myosin immunoglobulin heavy chain variable region
                                                                                                                                                                                                                                                                                                                                                            109 AA; 11944 MW; DFE615FE6CED4EDE CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-DEC 2001 (TrEMBLrel. 19, Created)
01-DEC 2001 (TrEMBLrel. 19, Last sequence update)
01-DEC 2002 (TrEMBLrel. 20, Last annotation update)
V303-D5 2 C mu protein (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       143 AA.
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77.1%;
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                                                                        PRELIMINARY;
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es 84; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            E FROM N.A..
                                                                                                                                                                                               FROM N.A.
                                                                                                                                                                            NCBI_TaxID-10090;
                                                                                                                                                                                                                                                                                                                                                 109
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                                                                                                                                                                                               SEQUENCE
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NON_TER
SEQUENCE
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                                                                                   09JL85;
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Q924P9
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                                                                                                                                                                                         1 QVKLQQSGAELVGSGASVKLSCTTSGFNIKDFYMHWVKQRPEQGLEWIGWIDPENGDSDY 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 QVQLQQPGAELVKPGASVKLSCKASGYTFTSYWMHWVKQRPGRGLEWIGKIDPNSGGTKY 60
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                                                                                                                                                                                                                                                                                                                    61 APKFQGKATMTADSSSNTAYLQLSSLTSEDTAVYYC-NAYYGDYECYWGQGTTVTVSS 117
                                                                                                                                                                                                                                                                                                                                                     61 NQKFKGKATLIYDTSSSTAYMQLSSLTSEDSAVYYCASHYYGSSSDYWGQGTTLIVSS 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DEC-2002 (TrEMBLrel. 20, Last annotation update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
VH186.2-D-J-C mu protein (Fragment).
Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
                                                                                                                                                                                                                                 Kozono Y., Kozono H., Azuma T.;
"Direct Estimation of Relative Affinity by Flow Cytometry Reveals "Direct Estimation of B Cell Antigen Receptors in Response to (4-Affinity Maturation of B Cell Antigen Receptors in Response to (4-Hydroxy-3-Nitrophenyl)Acetyl (NP).";
Submitted (Aug-2001) to the EMBL/GenBank/DDBJ databases.
EMBL, AB067781; BAB63266.1;
InterPro; IRR003006; Ig_MHC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
VH186.2-D-J-C mu protein (Fragment).
WHS u.2-Lust (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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                                                               DB 11; Length 143;
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                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
15704 MW; 43CD8C72D52134F6 CRC64;
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                                                           65.2%; Score 411.5; DB 11; 66.9%; Pred. No. 5e-35; tive 15; Mismatches 23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               24;
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Best Local Similarity 65.3%; Pred. No. 1.5e-34;
Matches 79; Conservative 14; Mismatches 24;
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                                                                                                                              Conservative
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                                                                                         Best Local Similarity
Matches 79; Conserv
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63.5%;
66.1%;
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InterPro; IPR003596; Ig_v.
Pfam; PF00047; ig; 1.
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Best Local Similarity 66.18
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                                PRELIMINARY;
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SMARI; SM00406; IGV; 1.
NON_TER 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mus musculus (Mouse).
                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
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                               Q9Z1C4
Q9Z1C4;
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                                                                                                                                                                                                                                                                                                                                                                                                                   61 APKFQGKATMTADSSSNTAYLQLSSLTSEDTAVYYC--NAY-YGDYE-GYWGQGTTVTVS 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                 1 QVKLQQSGAELVGSGASVKLSCTTSGFNIKDFYMHWVKQRPEQGLEWIGWIDPENGDSDY 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 QVKLQQSGAELVGSGASVKLSCTTSGFNIKDFYMHWVKQRPEQGLEWIGWIDPENGDSDY 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Kozono Y., Kozono H., Azuma T.;
"Direct Estimation of Relative Affinity by Flow Cytometry Reveals Affinity Maturation of B Cell Antigen Receptors in Response to (4-Hydroxy-3-Nitrophenyl)Acetyl (NP).";
Submitted (AUG-2001) to the EMBL/GenBank/DDBJ databases.
EMBL, AB067797; BAB63282.1;
InterPro; IPR003006; Ig_MHC.
Pfam; PF00047; ig; 1.
NON_TER 146 146
                                                         Kozono Y., Kozono H., Azuma T.;
Kozono Y., Kozono H., Azuma T.;
Affinity by Flow Cytometry Reveals
Affinity Maturation of Relative Affinity by Flow Cytometry Reveals
Affinity Maturation of B Cell Antigen Receptors in Response to (4-
Hydroxy-3-Nitrophenyl)Acetyl (NP).";
Submitted (AUG-2001) to the EMBL/GenBank/DDBJ databases.
Banel, ABOG7793, Bab63278.1;
InterPro; IPR00047; ig: 1.
NON_TER
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01-DEC-2001 (TrEWBLrel. 19, Last sequence update)
01-MAR-2002 (TrEWBLrel. 20, Last annotation update)
VH186.2-D-JC mu protein (Fragment).
Mus musculus (Mouse).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                  3;
                                                                                                                                                                                                                                                                 DB 11; Length 145;
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                                                                                                                                                                                                                                                              63.9%; Score 403.5; DB 11; Length 65.8%; Pred. No. 3.4e-34; ative 13; Mismatches 25; Indels
                                                                                                                                                                                                                 145 145 145
145 AA; 16141 MW; 55A59A7908B2CD6A CRC64;
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SEQUENCE 146 AA; 16136 MW; CEA8DD6E1955807F CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local Similarity 66.18
les 80; Conservative
                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 65.89
Matches 79; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRELIMINARY;
                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
NCBI_TaxID=10090;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN=C57BL/6;
                                                STRAIN=C57BL/6;
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NON_TER
SEQUENCE
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Matches
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Q924Q3
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AC DOT AC DOT REP REP DE REP D

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STRAIN=BALB/C;
Mueller J.P., Giannoni M.A., Hartman S.L., Elliott E.A., Squinto S.P.,
Matis L.M., Evans M.J.;
                                                                                                                                                                                                                                                                                                      "Humanized porcine VCAM-specific monoclonal antibodies with chimeric IgG2/G4 constant regions block human leukocyte binding to porcine endothelial cells.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 QVKLQQSGAELVGSGASVKLSCTTSGFNIKDFYMHWVKQRPEQGLEWIGWIDPENGDSDY 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       61 APKFQGKAIMTADSSSNTAYLQLSSLTSEDTAVYYC-NAYYGDYEGYWGQGTTVTVSS 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                    01-MAY-1999 (TrEMBLrel. 10, Created)
01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
Anti-porcine VCAM mAb 3F4 heavy chain variable region (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 11; Length 118;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; Score 400.5; DB 11; Length; Pred. No. 5.5e-34; 13; Mismatches 26; Indels
                                                                                                                                                                                                                                                                                                                                                                         Submitted (NOV-1996) to the EMBL/GenBank/DDBJ databases.
EMBL; U78801; AAD00293.1; -.
HSSP; P01810; 2FBJ.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 18
118 18
118 AA, 13036 MW, 90EBC559D31EC4FC CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
similar to RIKEN cDNA 18100660009 gene.
118 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pfan; PF00047; 19; 3.
SMART; SM00409; 1G; 2.
SMART; SM00406; 1Gc1; 3.
SMART; SM00406; 1Gv; 1.
SMART; SM00410; 1G_11ke; 1.
PROSITE; PS00290; 1G_MHC; UNKNOWN_1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Strausberg R.;
Submitted (FEB-2001) to the EMBI
EMBL; BC003888; AAH03888.1;
HSSP; P01842; 7FAB.
InterPro; IPR003599; Ig.
InterPro; IPR003599; Ig.
InterPro; IPR003600; Ig.
InterPro; IPR003606; Ig.like.
InterPro; IPR003606; Ig.like.
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Best Local Similarity 64.79
Matches 77; Conservative
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SEQUENCE
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RA Azakawa M., Shibata K., Konno H., Adachi J., Fukuda S.,
Azakawa M., Nashi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA Azawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
Radota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Kuell P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Schrimid. M., Staubli F., Suvuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Ramiya M., Lee N.H.,
RA Wordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Wanshaw, Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
RA Hayashibaki V.
                                                                                                                                                                                                      61 APKFOGKATMTADSSSNTAYLQLSSLTSEDTAVYYC----NAYYG---DYEGYWGQGTTV 113
                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Craniata; Vertebrata; Euteleostomi;
Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Wylsam with the world of a full-length mouse cDNA collection.";
"Functional annotation of a full-length mouse cDNA collection.";
Nature 409:685-690(2001).
EMBL; %x007918; BAB25349.1; -...
                                                                             7;
                                             Length 473;
                                                                               Indels
       BE9889B7986DA155 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        IG_MHC; UNKNOWN_1.
51699 MW; 9DED57A514475FBB CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                            Last sequence update)
Last annotation update)
                                         63.5%; Score 400.5; DB 11;
63.7%; Pred. No. 3e-33;
tive 16; Mismatches 22;
                                                                                                                                                                                                                                                                                                                                                                                                                             Created)
                                                                                                                                                                                                                                                                                                                                                                                         PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MGD; MGI:96443; IGh-1.
InterPro: IPR003599; Ig.
InterPro: IPR003599; Ig.
InterPro: IPR003600; Ig.like.
InterPro: IPR003006; Ig.MHC.
InterPro: IPR003506; Ig.MHC.
InterPro: IPR003596; Ig.V.
Pro: IPR003596; Ig.V.
SWART; SW00409; IG; 2.
SWART; SW00407; IG; 2.
       52449 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata;
Mammalla; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                        01-JUN-2001 (TrEMBLrel. 17, 01-JUN-2001 (TrEMBLrel. 17, 01-DEC-2001 (TrEMBLrel. 19, 18100600009RIK.
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SM00410; IG_like; 1.
                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                        PRELIMINARY;
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473 AA;
                                                          Local Similarity
es 79% Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         473 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE: FROM
                                                                                                                                                                                                                                                                                     140 TVSS 143
                                                                                                                                                                                                                                                             114 TVSS 117
       SEQUENCE
                                         Query Match
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                                                                             Matches
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Q9D8L4
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DB 11; Length 473;

Score 399;

63.2%;

Query Match

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Gaps
                                                                                QVKLQQSGAELVGSGASVKLSCTTSGFNIKDFYMHWVKQRPEQGLEWIGWIDPENGDSDY 60
                                                                                                                         20 QVQLKQSGAELVKPGASVKISCKASGYTFTDYYINWVKQRPGQGLEWIGKIGPGSGSTYY 79
                                                                                                                                                                                                80 NEKFKGKATLTADKSSSTAYMQLSSLTSEDSAVYFCARSGYDYDWFAYWGQGTLVTVSA 138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1; Gaps
                                                                                                                                                                       61 APKFQGKATMTADSSSNTAYLQLSSLTSEDTAVYYC--NAYYGDYEGYWGQGTTVTVSS 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 QVKLQQSGAELVGSGASVKLSCTTSGFNIKDFYMHWVKQRPEQGLEWIGWIDPENGDSDY 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  61 NEKFKSKATLIYUDKPSSTAYMQLSSLISEDSAVYYCARWDEDYAMDYWGQGTSVIVSS 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       61 APKFQGKATMTADSSSNTAYLQLSSLTSEDTAVYYCNAYYGDYE-GYWGQGTTVTVSS 117
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"Direct Estimation of Relative Affinity by Flow Cytometry Reveals
Affinity Maturation of B Cell Antigen Receptors in Response to (4-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Kozono Y., Kozono H., Azuma T.;
"Direct Estimation of Relative Affinity by Flow Cytometry Reveals
Affinity Maturation of B Cell Antigen Receptors in Response to (4-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                  ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                63.2%; Score 398.5; DB 11; Length 143; 65.3%; Pred. No. 1.1e-33;
                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Hydroxy-3 Nitrophenyl Acetyl (NP).";
Submitted (AUG-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AB067790; BaB63275.1;
InterPro; IPR003598; Ig_c2.
InterPro; IPR003598; Ig_MHC.
Pfam; PF00047; Ig; 1.
Pfam; PR00408; IGc2; 1.
Immunoglobulin domain.
NON_TER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     15868 MW; 139B2E966B81E07F CRC64;
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Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                            Last sequence update)
Last annotation update)
Pred. No. 4.3e-33;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               26;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               14; Mismatches
                                  Mismatches
                                                                                                                                                                                                                                                                                                                                                                                 01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last seq
01-MAR-2002 (TrEMBLrel. 20, Last ann
01-MAR-2002 (TrEMBLrel. 20, Last ann
VH186.2-D-J-C mu protein (Fragment).
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                               18;
         64.78;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-DEC-2001 (TrEMBLrel. 19,
01-DEC-2001 (TrEMBLrel. 19,
01-MAR-2002 (TrEMBLrel. 20,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Dest Local Similaric,
"a+rhes 77; Conservative
                                                                                                                                                                                                                                                                                                                                          PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     143 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=10090;
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62.9%;
65.0%;
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Matches 77; Conservative
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                                                                                                                                                    Pfam; PF00047; ig; 1.
NON_TER 1 1
NON_TER 142 142
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
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Q924R4;
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                                                                                                                                                                                                                                                        Matches
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Q924R1
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0924R4
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                                                                                                                                                                                       61 NEKFKSKATLIVDKPSSTAYMQLSSLTSEDSAVYYCARFY-DYEYFDVWGTGTTVTVSS 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 QVQLQQPGAELVKPGASVKLSCKASGYTFTSYWMHWVKQRPGRGLEWIGRIDPNSGGTKY 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Kozono Y., Kozono H., Azuma T.;
"Direct Estimation of Relative Affinity by Flow Cytometry Reveals
"Direct Estimation of Relative Affinity By Flow Cytometry Reveals
Affinity Maturation of B Cell Antigen Receptors in Response to (4-
Hydroxy-3 Nitrophenyl) Acetyl (NP).";
Submitted (AUG-2001) to the EMBL/GenBank/DDBJ databases.
EMBL, AB067788; BAB63273.1; -
InterPro; IPR003006; Ig_MHC.
Pfam: PF00047; ig: 1.
NON_TER
                                                                                                                                                                                                                                                                                                                                             01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
VH186.2-D-J-C mu protein (Fragment).
Mus musculus (Mouse).
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                               3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       63.1%; Score 398; DB 11; Length 140; 66.1%; Pred. No. 1.2e-33; Live 13; Mismatches 23; Indels
                                                                                                                 Query Match 63.2%; Score 398.5; DB 11; Length Best Local Similarity 65.5%; Pred. No. 1.1e-33; Matches 78; Conservative 14; Mismatches 24; Indels
Hydroxy-3-Nitrophenyl)Acetyl (NP).";
Submitted (AUG-2001) to the EMBL/GenBank/DDBJ databases.
EMBL: AB06795; BAB63280.1;
InterPro; IPR003006; Ig_MHC.
                                                                                         143 AA; 15908 MW; 55A2372870F0D568 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                140 AA; 15361 MW; 60739B790FC6AF24 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
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                                                 Pfam; PF00047; 19; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Best Local Similarity
Matches 78; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=10090;
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SEQUENCE
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61 APKFQGKATMTADSSSNTAYLQLSSLTSEDTAVYYCNAYYGDYE---GYWGQGTTVTVSS 117
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                61 APKFQGKATMTADSSSNTAYLQLSSLTSEDTAVYYCNAYYGDYEGYWGQGTTVTVSS 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Kozono Y., Kozono H., Azuma T.;

*Direct Estimation of Relative Affinity by Flow Cytometry Reveals
Affinity Maturation of B Cell Antigen Receptors in Response to (4-
Hydroxy-3-Nitrophenyl)Acetyl (NP).";
Hydroxy-3-Nitrophenyl)Acetyl (NP).";

EMBL; AB067785; BAB63270.1;
InterPro; IPR003006; Ig_MHC.

InterPro; IPR003006; Ig_MHC.

NOW_TER 145 145
NON_TER 145 145
                                                                                                                                                        Kozono Y., Kozono H., Azuma T.;

"Direct Estimation of Relative Affinity by Flow Cytometry Reveals
"ffinity Maturation of B Cell Antigen Receptors in Response to (4-
Hydroxy-3-Nitrophenyl)Acetyl (NP).";
Submitted (AUG-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AB069913; BAB63929.1; -
Interpro; IPR003006; Ig_MHC.
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
VH186.2-D-J-C mu protein (Fragment).
Was musculus (Mouse).
Eukariyets Metazoa; Chordats, Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               26; Indels
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145 AA; 16081 MW; ECDBIA135E05BBAA CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  142 AA; 15622 MW; 24A265CE4EA4318B CRC64;
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Pred. No. 1.6e-33;
4; Mismatches 27;
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"Direct Eğtimation of Relative Affinity by Flow Cytometry Reveals
"Direct Eğtimation of B Cell Antigen Receptors in Response to (4-
Hydroxy-3-Nitrophenyl)Acetyl (NP).",
SubmittedA.(Aug-2001) to the EMBL/GenBank/DDBJ databases.
EMBL, ABO 7789; BAB 574.1;
InterPro. A. F. BAB 63274.1;
InterPro. A. F. BAB 63274.1;
0924R1; 010-DEC-2001 (TrEMBLrel. 19, Created) 01-DEC-2001 (TrEMBLrel. 19, Last sequence update) 01-DEC-2002 (TrEMBLrel. 20, Last annotation update) 01-MAR-2002 (TrEMBLrel. 20, Last annotation update) VH186.2-Did-C mu protein (Fragment). Whus musculjus (Mouse). Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus. VIDEL_TaxID_10090;
                                                                                                                                                                                                                                                                                                                                                                                 62.5%; Score 394.5; DB 11; Length 145; Ilarity 64.2%; Pred. No. 3e-33; Conservative 13; Mismatches 27; Indels 3;
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NON_TER 145 145

SEQUENCE 145 AA; 15979 MW; 0162D0A26C746C04 CRC64;
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Search completed: December 23, 2002, 07:29:59 Job time : 49 5233 secs

163, App 1, 63, App 1, 63, App 116, App 116, App 11, App 11, App 11, App 11, App 11, App 2, Appl 2, Appl 3, Appl 4, Appl 4, Appl 4, Appl 4, Appl 5, Appl 6, Appl 8, Ap

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US-08-646-360-163 US-08-082-842A-83 US-08-136-899-163 US-09-136-899-163 US-08-484-537-16 US-08-484-537-16 US-08-404-537-16 US-08-279-772A-8 US-08-279-772A-8 US-08-279-772A-8 US-08-279-772A-8 US-08-279-772A-8 US-08-279-772A-8 US-08-279-772A-8 US-08-279-772A-8 US-08-279-172A-8 US-08-933-385B-111 US-08-19-491-2 US-08-619-491-2 US-08-619-491-2

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5516 5516 5516 5516 5516 5516 5516 489 489 4881 4881 4881 4881

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December 23, 2002, 07:20:23 ; Search time 19:1047 Seconds (without alignments) 163.250 Million cell updates/sec
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549
1 DIELTQSPAIMSASPGEKVT.......CQQRSSYPFTFGSGTKLEIK 106
GenCore version 5.1.3
Copyright (c) 1993 - 2002 Compugen Ltd.
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                                                                                                                                                                                                                                                                                                                                                                 262574 segs, 29422922 residues
                                                                                  - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 2000000000
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Perfect score:
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/cgn2_6/ptodata/1/jaa/5A_COMB.pep:*
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/cgn2_6/ptodata/1/jaa/6A_COMB.pep:*
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/cgn2_6/ptodata/1/jaa/PcTUS_COMB.pep:*

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Issued_Patents_AA:*

Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

, Apple 1, Appli 16, Arrival 1, Appii 16, Appl 1, Appli 16, Appl 1, Appli 16, Appli Sequence 17, App] Description Sequence Seq Sequence Sequence Sequence 6 US-08-487-200-16 US-08-488-113B-163 US-08-477-484B-163 US-08-107-669D-49 US-08-477-531B-49 US-08 483-562-2 US-08 483-562-2 US-08 483-558-92 US-08 661-052-16 US-09-188-082-16 US-09-16-088-16 US-09-423-439-44 US-09-423-439-51 US-09-423-439-51 US-09-423-439-16 US-09-312-157-12 US-09-312-157-12 US-07-634-278-16 US-08-477-728-1 US-08-477-728-1 US-08-477-728-1 US-08-477-728-1 US-08-477-728-1 US-08-477-728-1 US-08-477-728-1 US-08-477-728-1 -08-116-778E-2 SUMMARIES DB Length Query Result Š

RESULT 2
US-09-171-945-9
; Sequence 9, Application US/09171945
; Patent No. 6277599
; GENERAL INFORMATION:
; APPLICANT: Emery, Stephen
; APPLICANT: Copley, Clive Graham
; APPLICANT: Edge, Michael Derek

Sequence

RESULT 1 US-09-171-945-17 Sequence 17, Application US/09171945 GENERAL INFORMATION: APPLICANT: Emerry, Stephen APPLICANT: Edge, Michael Derek APPLICANT: Edge, Michael Derek TITLE OF INVENTION: Antibody and Their Therapeutic Use in an Adept System TITLE OF INVENTION: Antibody to CEA TITLE OF INVENTION: Antibody to CEA TITLE OF INVENTION: Antibody to CEA TITLE OF INVENTION: Application UNMBER: US/09/171,945 PRIOR PILING DATE: 1999-10-29 PRIOR FILING DATE: 1999-02-14 PRIOR FILING DATE: 1996-05-04 PRIOR FILING DATE: 1996-05-04 PRIOR FILING DATE: 1997-04-29 NUMBER OF SEQ ID NOS: 131 SOFTWARE: PatentIN Ver: 2.1 SEQ ID NO 177 LENGTH: 2335	TYPE: PRT ORGANISM: Artificial Sequence FEATURE: CORGANISM: Artificial Sequence FEATURE: COHER INFORMATION: Description of Artificial Sequence: humanized US-09-171-945-17 Query Match Usery Match Best Local Similarity 96.2%; Pred. No. 1.7e-40; Matches 102; Conservative 3; Mismatches 1; Indels 0; Gaps 0; Matches 102; Conservative 3; Mismatches 1; Indels 0; Gaps 0; DIELTQSPAIMSASPGEKVTITCSASSSVSYMHWFQQKPGTSPKLWIYSTSNLASGVPAR 60
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24 IVLTQSPAIMSASPGEKVTITCSASSSVSYMHWFQQKPGTSPKLWIXSTSNLASGVPARF 83
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME/KEY: domain

LOCATION: 88.496

IDENTIFICATION METHOD: BY SIMILARITY

IDENTIFICATION METHOD: WITH KNOWN SEQUENCE OR TO AN ESTABLISHED

IDENTIFICATION METHOD: CONSENSUS

OTHER INFORMATION: /product= "HYPERVARIABLE REGION 3"

US-08-116-778E-2
                                                                                                                                             BY SIMILARITY WITH KNOWN SEQUENCE TO TO AN ESTABLISHED
                                                                                                                                                                                                                                                                                        BY SIMILARITY WITH KNOWN SEQUENCE OR TO AN ESTABLISHED
                                                                                                                                                                                                                                                                                                                                                                                                                                                      BY SIMILARITY WITH KNOWN SEQUENCE OR TO AN ESTABLISHED
                                                                                                                                                                                                                                                                                                                                                      /product= "HYPERVARIABLE REGION 1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               OD: CONSENSUS /product= "HYPERVARIABLE REGION 2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       62 SGSGSGTSYSLTISRMEAEDAATYYCQQRSSYPFTFGSGTKLEIK 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               84 SGSGSGTSYSLTISRMEAEDAATYYCQQRSSYPYTFGGGTKLEIK 128
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SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   96.4%; Score 529; DB 2;
97.1%; Pred. No. 2.5e-40;
Live 1; Mismatches 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: KOIKE, MASAMICHI
APPLICANT: SHITARA, KENYA
APPLICANT: HANAI, NOBUO
APPLICANT: KUWANIA, YOSHIHISA
APPLICANT: HASEGAWA, MAMORU
TITLE OF INVENTION: HUMANIZED ANTIBODIES
NUMBER OF SEQUENCES: 49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: US/08/438,562 FILING DATE: 10-MAY-95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          5: NIXON & VANDERHYE P.C. 1100 NORTH GLEBE ROAD
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Patent No. 5874255
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER: IBM PC COMPATIBLE OPERATING SYSTEM: PC-DOS/MS-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: NAKAMURA, KAZUYASU
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CITY: ARLINGTON
STATE: VIRGINIA
COUNTRY: U.S.A.
ZIP: 22201-4714
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                LOCATION: 24..33
IDENTIFICATION METHOD: 1
IDENTIFICATION METHOD: 1
IDENTIFICATION METHOD: 0
OTHER INFORMATION: /prod
                                                                                                                                                                                                                                                                                                                                                                                                                              LOCATION: 49..55
IDENTIFICATION METHOD:
IDENTIFICATION METHOD:
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Best Local Similarity 97.15
Matches 102; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 IDENTIFICATION METHOD: OTHER INFORMATION: /pr
                                                                                                  NAME/KEY: sig_peptide
                                                                                                                                             IDENTIFICATION METHOD:
IDENTIFICATION METHOD:
IDENTIFICATION METHOD:
                                                    MOLECULE TYPE: protein FEATURE:
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         amino acid
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LOCATION:
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                                 TOPOLOGY
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TITLE OF INVENTION: Monoclonal Antibody to CEA, Conjugates Comprising Said TITLE OF INVENTION: Antibody, and Their Therapeutic Use in an Adept System FILE REFERENCE: Monoclonal Antibody to CEA CURRENT APPLICATION NUMBER: U5/09/171,945
PRIOR PELLING DATE: 1998-10-29
PRIOR APPLICATION NUMBER: GB9703103.3
PRIOR APPLICATION NUMBER: GB9703103.3
PRIOR FILING DATE: 1997-02-14
PRIOR PILING DATE: 1997-02-14
PRIOR FILING DATE: 1997-04-29
NUMBER: PERIOR PRIOR FILING DATE: 1997-04-29
NUMBER OF SEQ ID NOS: 131
SSGTURNS: Patentin Ver: 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                    FEATURE: * OTHER INFORMATION: Description of Artificial Sequence: humanized US-09-171-945 $\frac{4}{2}$
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1; Indels
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE PATENTIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
FILING DATE: 07-SEP-93
CLASSIFICATION: 424
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 532; DB 4;
Pred. No. 1.1e-40;
4; Mismatches 1;
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APPLICAÑT: HASEGAMA, MAMORU
TITLE OE: INVENTION: HUMANIZED ANTIBODIES
NUMBER ÔF SEQUENCES: 49
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        E: NIXON & VANDERHYE P.C. 1100 NORTH GLEBE ROAD
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ATTORNEY/AGENT INFORMATION:
NAME: WILSON, MARY J.
REGISTRATION NUMBER: 32,955
REFERENCE/DOCKET NUMBER: 249-59
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 2 Application US/08116778E Patent No. 5830470
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAKAMURA, KAZUYASU
                                                                                                                                                                                                                                                                                                                                                         TYPE: PRT F
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match (96.9%)
Best Local Similarity 95.3%;
Matches 10‡; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    KOIKE, MASAMICHI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 INFORMATION FOR SEO ID NO: 2: SEQUENCE CHARACTERISTICS:
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(703)816-4100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SHITARA, KENYA
HANAI, NOBUO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 129 amino acids
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COUNTRY: U.S. ZIP.
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STREET: 110
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NAME/KEY: domain
LOCATION: 24..33
IDENTIFICATION METHOD:
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LOCATION: -22...1
IDENTIFICATION METHOD:
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Best Local Similarity 97.1
Matches 102; Conservative
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IDENTIFICATION METHOD:
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IDENTIFICATION METHOD:
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IDENTIFICATION METHOD:
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INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MOLECULE TYPE: protein FEATURE:
                                                                                                                                                                                                                                       COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            OTHER INFORMATION:
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LOCATION: 49..55
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                                                                                                                                                                            COUNTRY: U.S.A. ZIP: 22201-4714
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WITH KNOWN SEQUENCE OR TO AN ESTABLISHED
CONSENSUS
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WITH KNOWN SEQUENCE OR TO AN ESTABLISHED
CONSENSUS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /product= "HYPERVARIABLE REGION 1"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; OTHER INFORMATION: /product= "HYPERVARIABLE REGION US-08-438-562-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /product= "HYPERVARIABLE REGION
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Patent No. 5993532
GENERAL INFORMATION:
APPLICANT: NATAMURA, KAZUYASU
APPLICANT: KOIKE, MASAMICHI
APPLICANT: HANAI, NOBUO
APPLICANT: KUWANA, YOSHIHISA
APPLICANT: HARSGAMAN, MAMORU
APPLICANT: HASEGAMAN, MAMORU
TITLE OF INVENTION: HUMANIZED ANTIBODIES
NUMBER OF SEQUENCES: 103
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CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/116,778
FILING DATE: 07-SEP-93
CLASSIFICATION: 424
ATORNEY/AGENT INFORMATION:
ATORNEY/AGENT INFORMATION:
REGISTRATION NUMBER: 32,955
REERRENGE/DOCKET NUMBER: 249-76
TELEPHONE: (703)816-4000
TELEPHONE: (703)816-4100
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CONSENSUS
                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: amino acids TypeLogg: 1.50PoLOGg: 1.
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IDENTIFICATION METHOD:
IDENTIFICATION METHOD:
IDENTIFICATION METHOD:
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LOCATION: 24..33
IDENTIFICATION METHOD:
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LOCATION: 49..55
IDENTIFICATION METHOD:
IDENTIFICATION METHOD:
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Best Local S
Matches 102
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BY SIMILARITY WITH KNOWN SEQUENCE TO TO AN ESTABLISHED CONSENSUS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              IDENTIFICATION METHOD: BY SIMILARITY
IDENTIFICATION METHOD: WITH KNOWN SEQUENCE OR TO AN ESTABLISHED
IDENTIFICATION METHOD: CONSENSUS
OTHER INFORMATION: /product= "HYPERVARIABLE REGION 3"
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WITH KNOWN SEQUENCE OR TO AN ESTABLISHED
CONSENSUS
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Pred. No. 2.5e-40;
1; Mismatches 2; Indels
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COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
CORRENTING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/483,528B
FILING DATE: 07-JUN-95
CLASSIFICATION: 536
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1; Mismatches
  VANDERHYE P.C.
ADDRESSEE: NIXON & VANDERHYE E
STREET: 1100 NORTH GLEBE ROAD
CITY: ARLINGTON
STATE: VIRGINIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 2, Application US/08652507
Patent No. 5876691
GENERAL INFORMATION:
APPLICANT:
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Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 553;
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Patent No. 6270765
GENERAL INFORMATION:
APPLICANT: Vashwant M. Deo
APPLICANT: Joel Goldstein
APPLICANT: Robert Graziano
APPLICANT: Robert Graziano
APPLICANT: Robert Graziano
APPLICANT: ROBERT GRAZIANO
APPLICANT: OF INVENTION: THERRAPEUTIC COMPOUNDS COMPRISED
TITLE OF INVENTION: OF ANTI-FC RECEPTOR ANTIBODIES
NUMBER OF SEQUENCES: 16
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/188,082
                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 523; DB 2;
Pred. No. 4e-39;
2; Mismatches 1.
                PRICE APPLICATION DATA:
APPLICATION NUMBER: US 08/484,172
FILING DATE: U7-UNE-1995
ATTONNEY/AGENT INFORMATION:
NAME: ALTOLA, BELL E.
REGISTRATION NUMBER: 35,430
REFERENCE/DOCKET NUMBER: MXI-043CP
TELEPHONE: (617)227-7400
TELEPHONE: (617)227-7400
TELEPHONE: (617)227-5941
INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
LENGTH: 553 antho acids
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60 State Street, Suite 510
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COUNTRY: USA
ZIP: 02109-1875
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN READABLE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: Arnold, Beth E.
REGISTRATION NUMBER: 35,430
REFERENCE/DOCKET NUMBER: MXI-O
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)227-7400
INFORMATION FOR SEQ. ID NO: 16:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                       95.3%;
97.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE: ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 95.3
Best Local Similarity 97.1
Matches 100; Conservative
                                                                                                                                                                                                                                                                                                                     TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE &
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Massachusetts
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LITY: Boston
STATE: Macon
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-09-188-082-16
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CITY: BC
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TITLE OF INVENTION: ANTIBODY AGAINST CARCINOEMBRYONIC ANTIGEN TITLE OF INVENTION:
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                                                                                                                                                       STATE: Wilding COUNTRY: USA
ZID: 2201-4714
COMPUTER FEADALE FORM:
MEDIUM THE E Floppy disk
COMPUTER: IBM PC COMPALIBLE
OPETATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
APPLICATION UNMER: US/08/652,507
FILING DATE: 02-Jul-1996
CLASSIFȚCATION: 530
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APPLICANT: Joel Goldstein
APPLICANT: Robert Graziano
APPLICANT: Robert Graziano
APPLICANT: Chezian Somasundaram
TITLE OF INVENTION: THERAPEUTIC COMPOUNDS COMPRISED
TITLE OF INVENTION: OF ANTI-FC RECEPTOR ANTIBODIES
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
ADDRESSE: LAHIVE & COCKFIELD
STREET: 60 State Street, Suite 510
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            64 SGSGTSYSLTISRMEAEDAATYYCQQRSSYPFTFGSGTKLEIK 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: Wixon & Vanderhye, P.C.
STREET: 11100 No. 5876691th Glebe Road, 8th Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ZIP: [02109-1875
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
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NAME: Arthur R. Crawford
REGISTRATION NUMBER: 25,327
REFERENGATOOKET NUMBER: 117-211
TELECOMMÜNICATION INFORMATION:
TELEPHONE: 703-816-4000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 16, Application US/08661052
Patent No. 5837243
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            INFORMATION FOR SEQ ID NO: 2: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           270 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEPHONE: 703-816-400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CURRENT APPLICATION DATA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-652-507-72
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STATE Massacl
COUNTRY: USA
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                                                                                Length 553;
                                                                            95.3%; Score 523; DB 4; Length 55 97.1%; Pred. No. 4e-39; 1; Indels 1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Yashwart M. Deo, et al.
TITLE OF INVENTION: THERAPEUTIC COMPOUNDS COMPRISED
TITLE OF INVENTION: OF ANTI-FC RECEPTOR ANTIBODIES
CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                 SGSGTSYSLTISRMEAEDAATYYCQQRSSYPFTFGSGTKLEIK 106
                                                                                                                                                                                                                                                  SOFTWARE: PatentIn Release #1.0, Version #1.25
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APPLICATION NUMBER: US 09/188,082
FILING DATE: US 07-JUNB-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/484,172
FILING DATE: 07-JUNE-1995
ATTONNEY,AGENT INFORMATION:
NAME: Remillard, Jane E.
REGISTRATION NUMBER: 38,872
FEECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)227-7400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADDRESSEE: LAHIVE & COCKFIELD, LLP
STREET: 28 State Street, 24th Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US/09/364,088
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                              Sequence 16, Application US/09364088 Patent No. 6365161 GENERAL INFORMATION:
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amino acid
                                                                          Query Match 95.3
Best Local Similarity 97.1
Matches 100; Conservative
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APPLICATION NUMBER: US
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Matches 100; Conservative
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STATE: Massachusetts
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-364-088-16
       ; TOPOLOGY: linear; MOLECULE TYPE: protein US-09-188-082-16
     linear
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TOPOLOGY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                    TITLE OF INVENTION: THERAPEUTIC COMPOUNDS COMPRISED OF ANTI-FC RECEPTOR ANTIBODIES
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BLAKEY, David Charles
TITLE OF INVENTION: CHEMICAL COMPOUNDS
NUMBER OF SQUENCES: 60
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pillsbury Winthrop, L.L.P.
STREET: 1100 New York Ave., N.W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: US/09/102,716
FILING DATE: 22-Jun-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/661,052
FILING DATE: <UNKNOWN>
ATTORNEY, ACENT INFORMATION:
NAME: ALROID ACET E.
REGISTRATION NUMBER: 35,430
                                                                                                                                                                                                                                          CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD
STREET: 60 State Street, Suite 510
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REFERENCE/DOCKET NUMBER: MXI-043CP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 16:
                                                                                                                                               Chezian Somasundaram
                                                                                                                                                                                                                                                                                                              CITY: Boston
STATE: Massachusetts
COUNTRY: USA
ZIP: 02109-1875
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
Sequence 16, Application US/09102716
Patent No. 6395272
GENERAL INFORMATION:
APPLICANT: Yashwant M. Deo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELECOMMUNICATION INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEPHONE: (617)227-7400
TELEFAX: (617)227-5941
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LENGTH: 553 amino acids
                                                                                               Joel Goldstein
Robert Graziano
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              INFORMATION FOR SEQ ID NO: 16: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                    NUMBER OF SEQUENCES: 16
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Best Local Similarity
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US-09-423-439-44
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Gaps
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GEMERAL INFORMATION:
GEMERAL INFORMATION:
TITLE OF INVENTION: IMMUNOSLOBULINS CONTAINING PROTECTION
TITLE OF INVENTION: PROTEINS IN PLANTS AND THEIR USES
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
STREET: 633 West Lyon
STREET: Suite 4700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 105;
                                                                                                                                                                                                               Length 666;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         216 SGSGSGTSYSLTISRMEAEDAATYYCQQRSTYPLTFGAGTKLEIK 260
                                                                                                                                                                                                               Score 521; DB 4;
Pred. No. 7.4e-39;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CLASSIFICATION: 435
PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
Including application
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER:
08/367,395
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                                                                                                                                                                                                                                                                 3; Mismatches
                                                                                                                                ; SEQUENCE DESCRIPTION: SEQ ID NO: 51:
US-09-423-439-51
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COMPUTER READBLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: storage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/434,000A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       REFERENCE/DOCKET NUMBER: 212/127 TELECOMMUNICATION INFORMATION:
LENGTH: 666 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE: 12/30/94
ATTORNEY/AGENT INFORMATION:
NAME: Guise, Jeffrey W.
REGISTRATION NUMBER: 34,613
                         TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SYSTEM: IBM P.C. Word Perfect 5.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NE: (619) 552-8400
(109) 552-0159
(67-3510)
                                                                                                                                                                                                         Query Match 94.9%;
Best Local Similarity 95.2%;
Matches 100; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER: IBM COMPATIBLE OPERATING SYSTEM: IBM P.C SOFTWARE: Word Perfect 5.
                                                                        TOPOLOGY: linear
MOLECULE TYPE: protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    105 amino acids
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TOPOLOGY: linear
TOPOLOGY: DESCRIPTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CITY: Los Angeles
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEPHONE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEFAX:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       94.9%; Score 521; DB 4; Length 281; 95.2%; Pred. No. 2.9e-39; Live 3; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         62 SGSGSGTSYSLTISRMEAEDAATYYCQQRSSYPFTFGSGTKLEIK 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     219 SGSGSGTSYSLTISRMEAEDAATYXCQQRSTYPLTFGAGTKLEIK 263
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/423,439
FILING DATE: 09-NO. 6339070-1999
CLASSIFICATION NUMBER: US/09/423,439
PRIOR APPLICATION NUMBER: PCT/GB98/01294
FILING DATE: 05-MAY-1998
APPLICATION NUMBER: GB 9709421.3
FILING DATE: 10-MAY-1997
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/GB98/01294
FILING DATE: 05-MAY-1998
APPLICATION NUMBER: GB 9709421.3
FILING DATE: 10-MAY-1997
INFORMATION FOR SEQ ID NO: 44:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: EMERY, Stephen Charles
BLAKEY, David Charles
TITLE OF INVENTION: CHEMICAL COMPOUNDS
                                                                                                                                                                                                                                     CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/423,439
FILING DATE: 09-No. 6339070-1999
CLASSIFICATION: <un><un><un><un><un><un><un><un><un><un><un><un><un><un><un><un><un><un><un><un><un><un><un><un><un><un><un><un><un><un><un><un><un><un><un><un><un><un><un><un><un><un><un><un><un><un><un><un><un><un><un><un><un><un><un><un><un><un><un><un><un><un><un><un><un><un><un><un><un><un><un><un><un><un><un><un><un><un><un><un><un><un><un><un><un><un><un><un><un><un><un><un><un><un><un><un><un><un><un><un><un><un><un><un><un><un><un><un><un><un><un><un><un><un><un><un><un><un><un><un><un><un><un><un><un><un><un><un><un><un><un><un><un><un><un><un><un><un><un><un><un><un><un><un><un><un><un><un><un><un><un><un><un><un><un><un><un><un><un><un><un><un><un><un><un><un><un><un><un><un><un><un><un><un><un><un><un><un><un><un><un><un><un><un><un><un><un><un><un><un><un><un><un><un><un><un><un><un><un><un><un><un><un><un><un><un><un><un><un><un><un><un><un><un><un><un><un><un><un><un><un><un><un><un><un><un><un><un><un><un><un><un><un><un><l><un><un><l><un><l><un><l><un><l><un><l><un><l><un><l><un><l><u
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STREET: 1100 New York Ave., N.W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER: IBM PC COMPATIBLE OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: MS Word
                                                                                                                                                            COMPUTER: IBM PC COMPATIBLE OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE DESCRIPTION: SEQ ID NO: 44:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 51, Application US/09423439 Patent No. 6339070 GENERAL INFORMATION:
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                                                                                                                                   MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE CHARACTERISTICS:
LENGTH: 281 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQUENCES: 60 CORRESPONDENCE ADDRESS:
                                                                                                          COMPUTER READABLE FORM:
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                                                                                                                                                                                                                    SOFTWARE: MS Word
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20005
  CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Best Local Similarity 95.2
Matches 100; Conservative
                           STATE: D.C. COUNTRY: U.S.A. ZIP: 20005
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93.3%;

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2 IELTQSPAIMSASPGEKVTITCSASSSVSYMHWFQQKPGTSPKLWIYSTSNLASGVPARF 61
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Pred. No. 2.9e-39;
4; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note= "Variable region of the mouse
anti-Tac antibody light chain."
                                                                                                                                                                                                                                                                TITLE OF INVENTION: IMPROVED HUMANIZED IMMUNGLOBLINS NUMBER OF SEQUENCES: 113
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SGSGSGTSYSLTISRMEAEDAATYYCQQRSSYPFTFGSGTKLEIK 106
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                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/634,278
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION UNBER: US 07/590,274
FILING DATE: 28-SEP-1990
FILING APPLICATION DATA:
APPLICATION NUMBER: US 07/310,252
FILING DATE: 13-FEB-1989
FILING DATE: 13-FEB-1989
APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US 07/290,975
FILING DATE: 28-DEC-1988
ATTONNEY/AGENT INFORMATION:
NAME: Smith, William M
REGISTRATION NUMBER: 30,223
RESTERNEY/CDOCKET NUMBER: 11823-002600
TELEPPHONE: (415) 326-2400:
TELEPHONE: (415) 326-2400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         19-DEC-1990
                                                                                                                                                 APPLICANT: QUEEN, Cary L.
APPLICANT: CO, Man Sung
APPLICANT: SCHNETDER, William P.
APPLICANT: LANDOLFI, Nicholas F.
APPLICANT: SELIKH, Kathleen L.
APPLICANT: SELIKH, Harold E.
                                                                                            Sequence 1, Application US/07634278 Patent No. 5530101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEPHONE: (415) 326-2400
TELEFAX: (415) 326-2422
INFORMATION FOR SEQ ID NO: 1:
                                                                                                                                                                                                                                                                                                                                       379 Lytton Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    94.08;
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amino acid
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Best Local Similarity 93.3
Matches 98; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE CHARACTERISTICS:
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OTHER INFORMATION:
OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                            CITY: Palo Alto
STATE: California
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                                                                                                                                     GENERAL INFORMATION:
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CLASSIFICATION:
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MOLECULE TYPE:
HYPOTHETICAL:
                                                                                                                                                                                                                                                                                                                                                                                                                   9430
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                                                                            US-07-634-278-1
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                                                                        DIELTQSPAIMSASPGEKVTITCSASSSVSYMHWFQQKPGTSPKLWIYSTSNLASGVPAR 60
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                                                                                                                                                                                                                                                                                                                                 APPLICANT: ANDREW C. HIATT, JULIAN
R.-C. MA, THOMAS LEHNER
TITLE OF INVENTION: IMMUNOGLOBULINS CONTAINING PROTECTION
PROTEINS IN PLANTS AND THEIR USES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 105;
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                                       Indels
                                                                                                                                               61 FSGSGGTSYSLTISRMEAEDAATYYCHQRTSYPYTFGGGTKLEI 105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FSGSGSGTSYSLTISRMEAEDAATYYCQQRSSYPFTFGSGTKLEI 105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; SEQUENCE DESCRIPTION: Guy's 13 Kappa
US-09-312-157-12
Pred. No. 1.9e-39;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              94.4%; Score 518; DB 4; L6 93.3%; Pred. No. 1.9e-39; Live 4; Mismatches 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER: IBM COMPATIBLE
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: Word Perfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/312,157
FILING DATE: 14-May-1999
CLASSIFICATION: <Unknown>
                                     4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME: Guise, Jeffrey W.
REGISTRATION NUMBER: 34,613
REFERENCE/DOCKET NUMBER: 212/127
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 552-8400
TELEPAX: (619) 552-0159
TELEX: 67-351
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: 08/434,000 FILING DATE: <UNKNOWN> ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                   CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
Suite 4700
                                                                                                                                                                                                                                           RESULT 14
US-09-312-157-12
Sequence 12, Application US/09312157
Patent No. 6303341
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE LISTING INFORMATION FOR SEQ ID NO: 12: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LENGTH: 105 amino acids TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             storage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
ZIP: 90071
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION DATA:
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Best Local Similarity 93.33
Matches 98; Conservative
                 Best Local Similarity 93.3
Matches 98; Conservative
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Gaps

Search completed: December 23, 2002, 07:33:20 Job time : 20.1047 secs

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December 23, 2002, 07:30:08 ; Search time 9.86047 Seconds (without alignments) 180.208 Million cell updates/sec
                                                                                                                                                                                                                 US-09-865-198-23
549
1 DIELTQSPAIMSASPGEKVT......CQQRSSYPFTFGSGTKLEIK 106
GenCore version 5.1.3
Copyright (c) 1993 - 2002 Compugen Ltd.
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                                                                                   OM protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 200000000
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Perfect score:
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Cgga2_6/prodata/2/pubpaa/USOB_NEW_PUB.pep:*
(cgn2_6/prodata/2/pubpaa/PCT_NEW_PUB.pep:*
(cgn2_6/prodata/2/pubpaa/USO6_NEW_PUB.pep:*
(cgn2_6/prodata/2/pubpaa/USO6_NEW_PUB.pep:*
(cgn2_6/prodata/2/pubpaa/USO7_NEW_PUB.pep:*
(cgn2_6/prodata/2/pubpaa/USO7_NEW_PUB.pep:*
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(cgn2_6/prodata/2/pubpaa/USO0_NEW_PUB.pep:*
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(cgn2_6/prodata/2/pubpaa/USO0_NEW_PUB.pep:*
(cgn2_6/prodata/2/pubpaa/USO0_NEW_PUB.pep:* Published_Applications_AA:* Database:

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Description	Sequence 24, Appl		8,	ω,	29,	Sequence 28, Appl	Sequence 28, Appl	Sequence 27, Appl	17,	9, A	Sequence 12, Appl	Ø		Sequence 28, Appl	Sequence 6, Appli	-		Sequence 75, Appl	Sequence 78, Appl
	ID	US-09-976-787-24	US-09-865-198-23	US-09-976-787-8	US-09-865-198-8	US-09-976-787-29	US-09-865-198-28	US-09-976-787-28	US-09-865-198-27	US-09-910-059-17	US-09-910-059-9	US-09-982-107-12	US-09-807-721-2	US-09-144-886-88	US-09-808-037-28	0 US-09-808-037-6	US-09-144-886-76	US-09-144-886-90	US-09-144-886-75	US-09-144-886-78
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	Query Match Length DB	106	106	108	108	238	238	240	240	235	108	105	699	107	119	239	107	107	107	107
æ	Query Match	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	97.3	6.96	94.4	94.4	92.7	92.2	92.2	91.1	90.5	88.2	88.2
	Score	549	549	549	549	549	549	549	549	534	532	518	518	509	206	206	200	495	484	484
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Sequence 82, Appl Sequence 91, Appl Sequence 6, Appl Sequence 6, Appl Sequence 96, Appl Sequence 105, Appl Sequence 105, Appl Sequence 105, Appl Sequence 107, Appl Sequence 103, Appl Sequence 103, Appl Sequence 103, Appl Sequence 97, Appl Sequence 97, Appl Sequence 97, Appl Sequence 98, Appl Sequence 98, Appl Sequence 89, Appl Sequence 61, Appl Sequence 52, Appl Sequence 61, Appl Sequence 61, Appl Sequence 52, Appl Sequence 52, Appl Sequence 52, Appl Sequence 65, Appl Sequenc
9 US-09-144-886-82 9 US-09-144-886-83 9 US-09-144-886-91 0 US-09-144-886-96 9 US-09-144-886-96 10 US-09-158-120A-35 10 US-09-158-120A-35 10 US-09-158-120A-35 10 US-09-165-099-105 10 US-09-95-099-11 10 US-09-95-099-11 10 US-09-144-886-79 10 US-09-144-886-97 10 US-09-144-886-97 10 US-09-144-886-97 10 US-09-144-886-98 10 US-09-144-886-98 10 US-09-144-886-98 10 US-09-144-886-98 10 US-09-144-886-98 10 US-09-144-886-98 10 US-09-144-886-98 10 US-09-144-886-98 10 US-09-144-886-98 10 US-09-910-059-61 10 US-09-910-059-61 10 US-09-910-059-50 10 US-09-910-059-50 10 US-09-910-059-50
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ALIGNMENTS

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Gaps
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                                                    GENERAL INFORMATION:
APPLICANT: Zhu, Zhenping
APPLICANT: Air, Zhenping
TITLE OF INVENTION: Antibodies Specific to KDR and Uses Thereof
FILE REFERENCE: 11245/46505
CURRENT APPLICATION NUMBER: US/09/976,787
CURRENT FILING DATE: 2000-10-02
PRIOR FILING DATE: 2000-10-08
PRIOR FILING DATE: 1090-01-29
NUMBER OF SEQ ID NUMBER: US 60/117,726
NUMBER OF SEQ ID NOS: 40
SOFTWARE: WordPerfect 8.0 for Windows
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Best Local Similarity 100.0%; Pred. No. 5.3e-31;
Matches 106; Conservative 0; Mismatches 0;
                      Sequence 24, Application US/09976787 Patent No. US20020064528A1
                                                                                                                                                                                                                                                                                                                                                                                                        ; ORGANISM: Mouse US-09-976-787-24
US-09-976-787-24
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RESULT 2
US-09-865-198-23
Sequence 23, Application US/09865198
Patent No. US20020103345A1
GENERAL INFORMATION:
APPLICANT: Zhu, Zhenping

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Gaps

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Indels

Length 108;

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61 FSGSGSGTSYSLTISRMEAEDAATYYCQQRSSYPFTFGSGTKLEIK 106
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100.0%; Pred. No. 5.4e-31;
iive 0; Mismatches 0;
         CURRENT APPLICATION NUMBER: US/09/865,198 CURRENT FILING DATE: 2001-05-24 PRIOR APPLICATION NUMBER: US 60/206,749 PRIOR FILING DATE: 2000-05-24
                                                                               NUMBER OF SEQ ID NOS: 34
SOFTWARE: WordPerfect 8.0 for Windows
SEQ ID NO 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 29, Application US/09976787 Patent No. US20020064528A1 GENERAL INFORMATION:
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Best Local Similarity 100.0
Matches 106; Conservative
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Best Local Similarity 100.
Matches 106; Conservative
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US-09-865-198-28
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TITLE OF INVENTION: Bispecific Immunoglobulin-Like Antigen Binding Proteins and Methory TITLE OF INVENTION: Production FILE REFERENCE: 11245/47102
CURRENT APPLAGATION NUMBER: US/09/865,198
CURRENT APPLAGATION NUMBER: US 60/206,749
PRIOR FILING DATE: 2001-05-24
NUMBER OF SEQ ID NOS: 34
SOFTWARE: WordPerfect 8.0 for Windows
SEQ ID NO 23.
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APPLICANT ZAU, Zhenping
TITLE OF INVENTION: Bispecific Immunoglobulin-Like Antigen Binding Proteins and MethorITLE OF INVENTION: Production
FILE REFERENCE: 11245/47102
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Sequence 8, Application US/09976787

Patent No. USZ002006452841

GENERAL INFORMATION:

APPLICANT: Zhu, Zhenping

APPLICANT: Zhu, Zhenping

TITLE OF INVENTION: Antibodies Specific to KDR and Uses Thereof

FILE REPRENCE: 11245/46505

CURRENT APPLICATION NUMBER: US/09/976,787

CURRENT FIGUR DATE: 2001-10-12

PRIOR RPLING DATE: 2001-01-28

PRIOR PLLING DATE: 1999-01-29

NUMBER OF SEQ ID NOS: 40

SOFTWARE: WordPerfect 8.0 for Windows

SEQ ID NO 86
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nilarity 100.0%; Pred. No. 5.4e-31;
Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                               0; Mismatches
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US20020103345A1
                                                                                                                                                                                                                                                                                                                                             Conservative
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Best Local Similarity
Matches 106; Conserv
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Matches 106ぎ Conserv
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ORGANISM: Mouse
US-09-865-198-23
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Sequence 28, Application US/09865198
Patent No. US2020103345A1
Patent No. US202020103345A1
APPLICANT: Zhu, Zhenping
TITLE OF INVENTION: Bispecific Immunoglobulin-Like Antigen Binding Proteins and Me
TITLE OF INVENTION: Production
FILE REFERENCE: 11245/47102
CURRENT APPLICATION NUMBER: US/09/865,198
CURRENT PILING DATE: 2001-05-24
PRIOR APPLICATION NUMBER: US 60/206,749
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y depticant: Zhu, Zhenping
APPLICANT: Witte, Larry
APPLICANT: Witte, Larry
TTILE OF INVENTION: Antibodies Specific to KDR and Uses Thereof
FILE REFERENCE: 11245/46505
CURRENT APPLICATION NUMBER: US/09/976,787
CURRENT FILING DATE: 2001-10-12
PRIOR APPLICATION NUMBER: US 09/493,539
PRIOR FILING DATE: 1909-01-28
PRIOR APPLICATION NUMBER: US 60/117,726
PRIOR APPLICATION NUMBER: US 60/117,726
PRIOR PRIOR SEQ ID NOS: 40
SOFTWARE: WordPerfect 8.0 for Windows
SOFTWARE: WordPerfect 8.0 for Windows
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 238;
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Pred. No. 9.8e-31;
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0; Mismatches
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Sequence 17, Application US/09910059

Sequence 17, Application US/09910059

Patent No. US2002014235941

GENERAL INFORMATION:
APPLICANT: Copley, Clive 6

APPLICANT: Edge, Michael Derek
FILE REFERENCE: 1991-209

CURRENT FILING DATE: 1998-10-29

PRIOR FILING DATE: 1997-04-29

PRIOR FILING DATE: 1997-04-29

PRIOR FILING DATE: 1996-05-04

NUMBER OF SEQ ID NOS: 131

SEQ ID NO 17

LEAGTH: 235

LEAGTH: 235

LEAGTH: 235
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Patent No. US20020142359A1
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Copley, Clive G
APPLICANT: Edge, Michael Derek
APPLICANT: Emery, Stephen Charles
APPLICANT: Emery, Stephen Charles
APPLICANT: Emery, Stephen Charles
APPLICANT: TITLE OF INVENTION: Monoclonal Antibody to CEA, Conjugates Comprising Said Antibod
TITLE OF INVENTION: Their Therapeutic use in an Adept System
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100.0%; Pred. No. 9.9e-31;
tive 0; Mismatches 0;
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                                                                                                                                                                                                         Query Match 100.
Best Local Similarity 100.
Matches 106; Conservative
                                                                                                    ; ORGANISM: Mouse US-09-865-198-27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-09-910-059-17
                                      LENGTH: 240
TYPE: PRT
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Patent No. US20020103345a1
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Zhu, Zhenping
TITLE OF INVENTION: Bispecific Immunoglobulin-Like Antigen Binding Proteins and Methor FILE REFERENCE: 11245/47102
CURRENT APPLICATION NUMBER: US/09/865,198
CURRENT APPLICATION NUMBER: US 60/206,749
PRIOR APPLICATION NUMBER: US 60/206,749
PRIOR PELLING DATE: 2000-05-24
NUMBER OF SEQ ID NOS: 34
SOFTWARE: WordPerfect 8.0 for Windows
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APPLICANT: Zhu, Zhenping
APPLICANT: Witter, Larry
TILE OF INVENTION: Antibodies Specific to KDR and Uses Thereof
FILE REFERENCE: 11245/46505
CURRENT APPLICATION NUMBER: US/09/976,787
CURRENT FILING DATE: 2001-10-12
PRIOR APPLICATION NUMBER: US 09/493,539
PRIOR FILING DATE: 2000-01-28
PRIOR FILING DATE: 1999-01-29
NUMBER OF SEQ ID NOS: 40
SOUTHWARE OF SEQ ID NOS: 40
SOUTHWARE: WORDERFEE WORDER
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Pred. No. 9.8e-31;
Mismatches 0;
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Pred. No. 9.9e-31;
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100.0%; Score 549; D
Best Local Similarity 100.0%; Pred. No. 9.9
Matches 106; Conservative 0; Mismatches
PRIOR FILING DATE: 2000-05-24
NUMBER OF SEQ ID NOS: 34
SOFTWARE: WordPerfect 8.0 for Windows
SEQ ID NO 28
LENGTH: 238
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Patent No. US20020064528A1
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100.0%;
                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 100.
Matches 106; Conservative
                                                                                                                                                               ; TYPE: PRT
; ORGANISM: Mouse
US-09-865-198-28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; ORGANISM: Mouse US-09-976-787-28
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US-09-865-198-27
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LENGTH: 240
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TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR THE TREATMENT AND/OR DIAGNOSIS OF TITLE OF INVENTION: NEUROLOGICAL DISEASES AND DISORDERS
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Patent No. US20020155114A1
GENERAL INFORMATION:
APPLICANT: Marks, James D
APPLICANT: Marks, James D
APPLICANT: Marks James D
APPLICANT: Marks James D
APPLICANT: Marks James D
APPLICANTON: Therapeutic Monoclonal Antibodies That Neutralize TITLE OF INVENTION: Botulinum Neurotoxins FILE OF INVENTION: Botulinum Neurotoxins
FILE REPERENCE: 2500.11708
CURRENT FILING DATE: 1998-08-31
NUMBER OF SEQ ID NOS: 98
SOFTWARE: Patentin Ver. 2.0
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         TITLE OF INVENTION: PRODUCTION OF ANTIBODIES IN TRANSGENIC PLASTIDS FILE REFERENCE: 1463-PCT-US-00 FANTIBODIES IN TRANSGENIC PLASTIDS CURRENT APPLICATION NUMBER: US/09/807,721 PRIOR APPLICATION NUMBER: PCT/US01/06274 PRIOR FILING DATE: 2001-12-21 PRIOR FILING DATE: 2001-02-28 NUMBER OF SEC ID NOS: 6 SOFTWARE: Patentin Ver. 2.1
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92.7%; Score 509; DB 9;
Best Local Similarity 97.0%; Pred. No. 2.5e-28;
Matches 97; Conservative 1; Mismatches 2
                                                                                                                                                                                                                                                                                                                                 Score 518; DB 9;
Pred. No. 2.5e-28;
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UNIVERSITY OF CENTRAL FLORIDA
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; Sequence 28, Application US/09808037
; Patent No. US20020052311A1
; GENERAL INFORMATION:
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92.58;
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Matches 98; Conservative
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                                                                                                                                                                                                                                                                 ; ORGANISM; Homo sapiens
US-09-807-721-2
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                                                                                                                                                                                                   SEO ID NO 2
                                                                                                                                                                                                                                              TYPE: PRT
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Patent No. US20020159958a1
GENERAL INFORMATION:
APPLICANT: HIATT, ANDREW C.
TITLE OF INVENTION: PROTECTION PROTEINS IN PLANTS AND THEIR USE
FILE REPRENENCE: EP13002E
CURRENT APPLICATION NUMBER: US/09/982,107
CURRENT APPLICATION NUMBER: US/09/982,107
CURRENT FIFTING DATE: 201-10-16
NUMBER OF SEQ ID NOS: 19
SOFTWARE: PATENT VET. 2.1
SEQ ID NO 12.
SEQ ID NO 12.
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US-09-982-107-12
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Pred. No. 7.4e-30;
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Pred. No. 6.3e-29;
4; Mismatches 3;
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             CURRENT APPLICATION NUMBER: US/09/910,059
CURRENT FILING DATE: 2001-07-23
PRIOR PILING DATE: 1090-10-29
PRIOR FILING DATE: 1998-10-29
PRIOR FILING DATE: 1997-04-29
PRIOR PILING DATE: 1997-04-29
PRIOR FILING DATE: 1997-04-29
PRIOR FILING DATE: 1997-02-14
PRIOR FILING DATE: 1996-05-04
NUMBER OF SEG ID NOS: 131
SEQ ID NO 9
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95.3%;
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Best Local Similarity 93.3%;
Matches 98; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
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US-09-910-059-9ี้
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Matches 101∯ Conserva
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                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
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Sequence 6, Application US/09808037

Patent No. US20020052311A1

GENERAL INFORMATION:

APPLICANT: SOLOWON, Beka

APPLICANT: HANAN, Eilat

TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR THE TREATMENT AND/OR DIAGNOSIS OF

TITLE OF INVENTION: METHODS AND DISORDERS

FILE REFRENCE: SOLOMON-2D

CURRENT PELLIAG DATE: 2001-03-15

PRIOR APPLICATION NUMBER: 09/629,971

PRIOR APPLICATION NUMBER: 09/629,971

PRIOR FILING DATE: 1999-12-29

PRIOR APPLICATION NUMBER: 05 00/473,653

PRIOR FILING DATE: 1999-09-03

NUMBER OF SEQ ID NOS: 33

SOFTWARE: PATENT VESTOR NOS: 33

LENGTH: 239

LENGTH: 239
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                14 DIELTQSPAIMSASPGEKVTMTCSASSSISYMHWYQQKPGTSPKRWIYDTSKLASGVPAR 73
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                                                                                                                                                                                                                                                                                                                                                              Length 119;
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                                                                                                                                                                                                                                                                                                                                                                                                      7; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  61 FSGSGSGTSYSLTISRMEAEDAATYYCQQRSSYPFTFGSGTKLEIK 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               61 FSGSGSGTSYSLTISRMEAEDAATYYCQQRSSYPFTFGSGTKLEIK 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ouery Match 92.2%; Score 506; DB 10;
Best Local Similarity 90.6%; Pred. No. 7.4e-28;
Matches 96; Conservative 3; Mismatches 7;
                                                                                                                                                                                                                                                                                                                                                          Score 506; DB 10;
Pred. No. 4.4e-28;
3; Mismatches 7;
                 CURRENT APPLICATION NUMBER: US/09/808,037
CURRENT FILING DATE: 2001-03-15
PRIOR APPLICATION NUMBER: 09/629,971
PRIOR FILING DATE: 2000-07-31
PRIOR FILING DATE: 1999-12-29
PRIOR FILING DATE: 1999-12-29
PRIOR FILING DATE: 1999-09-03
NUMBER OF SEQ ID NOS: 33
SOFTWARE: PATCH NOS: 33
LENGTH: 119
                                                                                                                                                                                                                                                                                             ; ORGANISM: synthetic construct US-09-808-037-28
                                                                                                                                                                                                                                                                                                                                                          Query Match 92.2%;
Best Local Similarity 90.6%;
Matches 96; Conservative
FILE REFERENCE: SOLOMON=2D
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CORGANISM: Homo sapiens US-09-808-037-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 15
US-09-808-037-6
                                                                                                                                                                                                                                                                            TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: PRT
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Search completed: December 23, 2002, 07:58:22 Job time: 10.8605 secs

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GenCore version 5.1.3

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OM protein - protein search, using sw model

Run on: December 23, 2002, 07:17:57; Search time 20.9535 Seconds

(without alignments)

486.327 Million cell updates/sec

1 US-09-865-198-23

Sequence: 549

Sequence: 1 DIELTQSPAIMSASPGEKVT...................COORSSYPFTFGSGTKLEIK 106

Scoring table: BLOSUM62

Gapop 10.0, Gapext 0.5

Searched: 283224 seqs, 96134422 residues
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
Database : PIR_73:*

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

: PIR_73:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	kappa chain	kappa chain	light chain		kappa chain	kappa chain	kappa chain	light chain	kappa chain	light	light	kappa chain	light	light	
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ALIGNMENTS

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Gaps

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us-09-865-198-23.rpr

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Ig Kappa chain V region (F3, anti-AFP) - mouse (fragment)
C; Species: Mus musculus (house mouse)
C; Decies: Mus musculus (house mouse)
C; Decies: No-Nov-1997 #sequence_revision 23-Jan-1998 #text_change 21-Jan-2000
C; Accession: PC4405
R; Deng, J.B.; Han, H.; Su, C.Z.; Chen, C.Q.
Chinese Biochem. J. 12, 648-653, 1996
A; Title: Generation of a phage display library of the immunoglobulin repertoire from A; Reference number: PC4405
A; Reference number: PC4405
A; Recience number: PC4405
A; Residues: 1-107 CDEN>
A; Residues: 1-107 CDEN>
A; Experimental source: spleen cell
C; Superfamily: immunoglobulin V region; immunoglobulin homology <IMM>
F; 16-89/Domain: immunoglobulin homology <IMM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       J. Biol. Chem. 266, 2134-2142, 1991
A;Title: Common structural features among monoclonal antibodies binding the same anti
A;Reference number: A38601; MUID:91115823; PMID:1703527
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ig kappa chain V region (6A7) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Species: 30-Aug-1991 #sequence_revision 30-Aug-1991 #text_change 21-Jan-2000
C;Accession: D36601
R;Goshorn, S.C.; Retzel, E.; Jemmerson, R.
                                                                                                                                                                                                                                                                                                                                 DIELTQSPAIMSASPGEKVTITCSASSSVSYMHWFQQKPGTSPKLWIYSTSNLASGVPAR 60
                                                                                                                                                                                                                                                                                                                                                               DIELTQSPAIMSASPGEKVTITCSASSSVSYMHWFQQKPGTSPKLWIYSTSNLASGVPAR 60
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A;Molecule type: mRNA
A;Molecule type; mRNA
A;Residues: 1-99 cGOS>
A;Cross-references: GB:M57981; NID:g196408; PIDN:AAA63362.1; PID:g196409
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;8-81/Domain: immunoglobulin homology <IMM>
                                        C; Keywords: heterotetramer; immunoglobuln
F;1-14/Domain: signal sequence (fragment) #status predicted <SIG>F;15-132/Product: Ig kappa chain (fragment) #status predicted <MAT>F;15-108/Domain: V region (V-kappa-1) <VRE>F;30-103/Domain: immunoglobulin homology <IMM>F;109-132/Domain: J region (J-kappa-4) (fragment) <JRE>
                                                                                                                                                                                                                                    Length 132;
                   immunoglobulin V region; immunoglobulin homology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 99;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            FSGSGSGTSFSFTINSMEAEDVATYCQQRSSYPFTFGSGTKLEIK 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FSGSGSGTSYSLTISRMEAEDAATYYCQQRSSYPFTFGSGTKLEIK 106
                                                                                                                                                                                 pa-4, Score 483; DB 2; Len Score 483; DB 2; Len 6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 87.8%; Score 482; DB 2; I Best Local Similarity 87.7%; Pred. No. 2.1e-32; Matches 93; Conservative 4; Mismatches 9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           87.6%; Score 481; DB 2;
ilarity 94.9%; Pred. No. 2.3e-32;
Conservative 1; Mismatches 4;
                                                                                                                                                                                                                                                       Pred. No. 2.16
9; Mismatches
                                                                                                                                                                                                                               ch 88.0%;
1 Similarity 85.8%;
91; Conservative
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Best Local Similarity
Matches 93; Conserv
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                   C; Superfamily:
                                                                                                                                                                                                                            Query Match
Best Local S
Matches 91
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C; Species: Mus musculus (house mouse)
C; Species: Mus musculus (house mouse)
C; Date: 21-May-1990 #sequence_revision 31-Dec-1990 #text_change 21-Jan-2000
C; Date: 21-May-1990 #sequence_revision 31-Dec-1990 #text_change 21-Jan-2000
C; Accession: A32513
R; Kofler: R: Strohal, R: Balderas, R.S.; Johnson, M.E.; Noonan, D.J.; Duchosal, M.A.; J. Clin. Invest. 82, 852-860, 1988
A; Title: Immunoglobulin kappa 11ght chain variable region gene complex organization and A: Reference number: A94689; MUID:88331394; PMID:3138286
A; Accession: A32513
A; Molecule type: DNA
A; Residues: If:130 < KNF>
A; Residues: If:130 < KNF>
A; Cross-references: GB:M20834; NID:9196943; PIDN:AAA38846.1; PID:9196944
C; Superfamily: immunoglobulin V region; immunoglobulin homology
C; Keywords: heterotetramer; immunoglobulin
E; 38-113/Domagn: immunoglobulin homology < IMM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A Molecule type: mRNA
A; Residues: A-132 <LEV>
A; Residues: A-132 <LEV>
A; Residues: A-132 <LEV>
A; Cross-references: EMBL:X14098; NID:952562; PIDN:CAA32260.1; PID:9736261
B; Carroll, W.L.; Starnes, C.O.; Levy, R.; Levy, S.
J. Exp. Med. 168, 1607-1620, 1988
A; Title: Atternative V kappa gene rearrangements in a murine B cell lymphoma. An explana
A; Reference fuumber: JL0061; MUID:89035985; PMID:3141553
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C;Species: Wig musculus (house mouse)
C;Date: 30-Sèp-1991 #sequence_revision 30-Sep-1991 #text_change 21-Jan-2000
C;Accession: $505268; Ju0062; S03846
                                                                                                                                                                                                                                                                           Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          <MAT>
                                                                                                                                                                                                                                                                           ö
                                #status predicted
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                                                                         F;46-55/Region complementarity-determining 1
F;71-77/Region; complementarity-determining 2
F;110-118/Region: complementarity-determining 3
F;130-140/Domaffin: constant region (fragment) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 130;
                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 483; DB 2; Length 13
Pred. No. 2.1e-32;
7; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 60 RESGSGSSTSYSLTISRMEAEDAATYYCQORSSYPFTEGSGTKLEIK 106
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 SGSGSGTSYSLTISRMEAEDAATYYCQORSSYPPTFGGGTKLEMK 128
             <SIG>
                                                                                                                                                                                                               Score 508; DB 2; L
Pred. No. 2.1e-34;
1; Mismatches 5;
F:1-22/Domain: signal sequence #status predicted F:23-129/Product: Ig heavy chain V region (4C11) F:38-111/Domain: immunoglobulin homology <IMM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          R; Levy, S. submitted to the EMBL Data Library, February 1989 A; Reference number: S05267 A; Accession: S05268
                                                                                                                                                                                                               92.5%;
ilarity 94.3%;
Conservative
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87.9%;
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Best Local Similarity
Matches 997 Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity
Matches 94; Conserv
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A; Molecule type: mRNA
A; Residues: 1-120 <CAR>
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S05268
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19 Kappa chain V region (27.10.2) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 23-Mar-1989 #sequence_revision 23-Mar-1989 #text_change 21-Jan-2000
C:Date: 23-Mar-1989 #sequence_revision 23-Mar-1989 #text_change 21-Jan-2000
C:Date: 23-Mar-1989 #text_change 21-Jan-2000
C:Date: 23-Mar-1989 #text_change 21-Jan-2000
A:Stider, S.K.; Borden, P.; Gruezo, F.; Akolkar, P.N.; Bhattacharya, S.B.; Morrison, I. Imminol. 142, 888-893; 1989
A;Title: Amino acid substitutions in V-H CDR2 change the idiotype but not the antigen A;Reference number: A30562; MUID:89110066; PMID:2464031
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               C; Accession: $26338
R; Stark, S.E.; Caton, A.J.
Exp. Med. 174, 613-624, 1991
A; Title: Antibodies that are specific for a single amino acid interchange in a protei
A; Reference number: $26309; MUID:91341421; PMID:1908510
                                                                                                                                                                                           J. Exp. Med. 170, 1-13, 1989
A;Title: Functional immunoglobulin light chain genes are replaced by ongoing rearrang A;Reference number: A92781; MUID:89310348; PMID:2501443
A;Accession: PS0070
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                                             Ig kappa chain V region (38C13.V6.1) - mouse C;Species: Mus musculus (house mouse) C;Species: Mus musculus (house mouse) C;Date: 31-Mar-1990 #sequence_revision 31-Mar-1990 #text_change 21-Jan-2000 C;Accession: PS0070 R;Levy, S.; Campbell, M.J.; Levy, R. J. Exp. Med. 170, 1-13, 1989
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C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 20-Jun-2000
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                                                                                                                                                                                                                                                                                                                        A; Molecule type: DNA
A; Residues: 1-106 < LEV>
C; Superfamily: immunoglobulin V region; immunoglobulin homology
C; Keywords: heteroterramer; immunoglobulin
F;16-89/Domain: immunoglobulin homology < IMM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     C;Superfamily: immunoglobulin V region; immunoglobulin homology C;Keywords: heterotetramer; immunoglobulin F:16-89/Domain: immunoglobulin homology <IMM>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; DB 2; Let 1.3e-31;
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Pred. No. 1.6e-31;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            86.0%; Score
83.0%; Pred. No. 1.3e .
-+ive 11; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              85.8%; Score 471; DE ilarity 86.7%; Pred. No. 1.6e Conservative 4; Mismatches
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                                                                                                                                                                                                                                                                                                    A; Status: translation not shown
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Matches 88; Conserv
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Matches 91; Conserv
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A; Molecule type: mRNA
A; Residues: 1-107 <SIK>
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                               2 IVLTQSPAIMSASPGEKVTMTCSVSSISYMHWYQQKPGTSPKRWIYDTSKLASGVPTRF
9 AIMSASPGEKVTITCSASSSVSYMHWFQQKPGTSPKLWIYSTSNLASGVPARFSGSGSGT
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C; Superfamily: immunoglobulin V region; immunoglobulin homology C; Keywords: heterotetramer; immunoglobulin F; 16-89/Domain: immunoglobulin homology <IMM>
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6.4e-32;
                                                                                                         SYSLTISRMEAEDAATYYCQQRSSYPFTFGSGTKLEIK 106
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                                                                                                                                        Pred. No. 6.4e
3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 476;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ch 86.7%;
1 Similarity 88.6%;
93; Conservative
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Best Local Similarity 84.8%;
Matches 89; Conservative
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Matches 93; Conserv
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A; Status: preliminary
A; Molecule type: mRNA
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G27887
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complementarity-determining 3
                                            framework 4
F;58-89/Region: framework 3
F;90-98/Region: complementar
F;99-108/Region: framework 4
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C;Species: Mus musculus (house mouse)
C;Species: Mus musculus (house mouse)
C;Date: 16-Sgp-1992 #sequence_revision 16-Sep-1992 #text_change 21-Jan-2000
C;Accession: PL0278
R;Shlomchik. M.; Mascelli, M.; Shan, H.; Radic, M.Z.; Pisetsky, D.; Marshak-Rothstein, P. B. Exp. Med. 171, 265-297, 1990
A;Title: Anti-DNA antibodies from autoimmune mice arise by clonal expansion and somatic A;Reference number: PL0278
A;Accession PL0278
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 19 Kappa chaint v region - mouse
C;Species: Mus musculus (house mouse)
C;Species: Mus musculus (house mouse)
C;Date: 06.Jan_1995 #sequence_revision 06.Jan-1995 #text_change 21-Jan-2000
C;Accession: $29591
R;Kavaler, J.
Submitted to the EMBL Data Library, April 1991
A;Reference number: $26459
A;Status: pregiminary
A;Molecule type: mRNA
A;Residues: 1,103 <KAV
A;Cross-references: EMBL:X59094; NID:952227; PIDN:CAA41820.1; PID:952228
C;Superfamily: Immunoglobulin V region; Immunoglobulin homology
C;Keyvords: heterotetramer; immunoglobulin
F;15-88/Domain: immunoglobulin homology <IMM>
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                                                               A Residues: 1-105 <STA>
A CROSs-references: EMBL:X59197, NID:952328, PIDN:CAA41907.1; PID:91334069
A CROSs-references: EMBL:X59197, NID:952328, PIDN:CAA41907.1; PID:91334069
C:Superfamily: Ammunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:16-89/Domain: immunoglobulin homology <IMM>
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                                                                                                                                                                                                                                                                                             61
                                                                                                                                                                                                                                                                                                                  2 IVLT@SPAIMSASPGEKVTISCSASSSVSYMYWYQQKPGSSPKPWIYRTSNLASGVPARF 61
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A;Residues: 1-108 <SHL>
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: Ahretoretramer; immunoglobulin
F;1-23/Region: framework 1
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Pred. No. 4.8e-31;
3; Mismatches 9; Indels
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                                                                                                                                                                                                    Score 470; DB 2;
Pred. No. 1.9e-31;
4; Mismatches 8;
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F:24-35/Region: complementarity-determining
F:36-50/Region: framework 2
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imilarity 88.3%;
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ilarity 88.5%;
Conservative
                     A; Molecule type: mRNA
7-14/mes: 1-105 <STA>
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Matches 91; Conserv
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92; Conserv
  A; Accession: S26338
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Best Local S
Matches 92
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C;Complex: An immunoglobulin heterotetramer subunit consists of two identical light (hain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;1-22/Domain: signal sequence #status predicted <SIG>F;23-130/Product: Ig kappa chain V region (6F6) #status predicted <MAT>
F;38-111/Domain: immunoglobulin homology <IMM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Cross-references: GB:M27792; NID:g197159
A;Experimental source: mRNA clones for anti-phenyloxazolone antibody 6F6
A;Note: the authors translated the codon TTC for residue 8 as Pro and TTC for residue A;Note: the codon given for 1-Met (AGT) is inconsistent with the authors' translation R;Milstein, C.; Even, J.; Jarvis, J.M.; Gonzalez-Fernandez, A.; Gherardi, E. Eur. J. Immunol. 22, 1677-1634, 1992
Eur. J. Immunol. 22, 1677-1634, 1992
A;Title: Non-random features of the repetitoire expressed by the members of one V kapp A;Reference number: A49044; MUID:92289826; PMID:1601044
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Mol. Immunol. 25, 859-865, 1988
A;Title: Combinatorial association of V genes: one VH gene codes for three non-cross-
A;Reference number: JL0076; MUID:89096973; PMID:3211160
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A;Note: sequences extracted from NCBI backbone; partial nucleotide sequences
A;Note: sequence extracted from NCBI backbone (NCBIN:106807, NCBIP:106822)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ig kappa chain precursor V region (anti-phenyloxazolone 6F6) - mouse C;Species: Was musculus (house mouse) C;Date: 31-Dec-1991 #sequence_revision 09-Aug-1996 #text_change 16-Jul-1999 C;Accession: JL0079; A49044; B49044
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Accession: A49044
A; Molecule type: DNA
A; Residues: 1-25 <MIL>
A; Cross-references: GB:S37663; NID:9250214; PIDN:AAB22331.1; PID:9250217
A; Note: sequence extracted from NCBI backbone (NCBIN:106802, NCBIP:106809)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                       Gaps
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A;Residues: 114-116 <MIL2>
A;Cross-references: GB:S37664; NID:9250215; PIDN:AAB22332.1; PID:9250218
                                                                                                                                                                      4 LIQSPAIMAASPGEKVTMTCSADSSVSSGNFHWYQQKPGTSPKLMIYRTSNLASGVPARF
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                                                                                                                                   4 LTQSPAIMSASPGEKVTITCSASSSVS-.YMHWFQQKPGTSPKLWIYSTSNLASGVPARF
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Length 108
                                                                   Indels
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                                                                                                                                                                                                                                                                      62 SGSGSGTSYSLTISRMEAEDAATYYCOORSSYPFTFGSGTKLEIK 106
                                                                                                                                                                                                                                                                                                             64 SGSGSGTSYSLTISSMEAEDAATYYCQQWCGYPFTFGTGTKLEIK 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                84 SGSGSGXSYSLTISSMEAEDAATYYCQQWSSNPLTFGAGTKLEXK 128
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                                                               ..
8
DB 2;
Score 465; DB 2
Pred. No. 5e-31;
                                                            4; Mismatches
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84.7%;
86.7%;
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Best Local Similarity 86.77
Watches 91; Conservative
                        Best Local Similarity 86.7
Matches 91; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Molecule type: mRNA
A; Residues: 1-130 <KAA>
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Ig Kappa chain V region (38C13.V8) - mouse
C; Species: Mus musculus (house mouse)
C; Species: Mus musculus (house mouse)
C; Obate: 31-Mar-1990 #sequence_revision 31-Mar-1990 #text_change 21-Jan-2000
C; Accession: PS0071
R; Levy, S.; Campbell, M.J.; Levy, R. .
B; Levy, Med. 170, 1-13, 1989
A; Title: Functional immunoglobulin light chain genes are replaced by ongoing rearrangeme A; Reference number: A92781; MUD:89310348; PMID:2501443
A; Accession: PS0071
A; Accession: PS0071
A; Status: translation not shown
A; Molecule type: DNA
A; Residues: 1-106 < LEVA
C; Superfamily: immunoglobulin V region; immunoglobulin homology
C; Keywords: heterotetramer; immunoglobulin
F; 16-89/Domain: immunoglobulin homology <IMM>
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Search completed: December 23, 2002, 07:31:40 Job time: 21.9535 secs

THE PACE BLANK METON

us-09-865-198-23.rsp

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(without alignments)
419.643 Million cell updates/sec
                                                                                                                             December 23, 2002, 07:16:17; Search time 10.4767 Seconds
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549
1 DIELTQSPAIMSASPGEKVT.......CQQRSSYPFTFGSGTKLEIK 106
                                                                                                                                                                                                                                                                                                                                                                                                                         112892
GenCore version 5.1.3
Copyright (c) 1993 - 2002 Compugen Ltd.
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 200000000
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Perfect score:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution. SwissProt_40:* Database :

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

		Description	940 mus	PO4943 mus musculu	mus	P04942 mus musculu	P04941 mus musculu	mns	snu 9	P01675 mus musculu	P01678 mus musculu	P01677 mus musculu	P01679 mus musculu	P01680 mus musculu	PO1665 mus musculu	P01667 mus musculu	P01664 mus musculu	P04430 homo sapien	mus m	mns		homo	mns	mus	P01661 mus musculu	P01670 mus musculu		homo	P04431 homo sapien	. P01672 mus musculu	mus	3 mus	snw	ō	P01654 mus musculu
SUMMARIES		ΩI	KV6F_MOUSE	KV61_MOUSE	KV6J_MOUSE	KV6H_MOUSE	KV6G_MOUSE	KV6K_MOUSE	KV6B_MOUSE	KV6A_MOUSE	KV6D_MOUSE	KV6C_MOUSE	KV6E_MOUSE	KV4A_MOUSE	KV3M_MOUSE	KV30_MOUSE	KV3L_MOUSE	KV1V_HUMAN	KV3H_MOUSE	KV3J_MOUSE	KV3N_MOUSE	KV10_HUMAN	KV3Q_MOUSE	KV3S_MOUSE	KV3I_MOUSE	KV3R_MOUSE	KV3K_MOUSE	KV1B_HUMAN	KV1W_HUMAN	KV3T_MOUSE	KV3P_MOUSE	KV3U_MOUSE	KV5J_MOUSE	KV1H_HUMAN	KV3A_MOUSE
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Gaps

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Ouery Match 83.2%; Score 457; DB 1; Length 107; Best Local Similarity 83.8%; Pred. No. 4.7e-39; Matches 88; Conservative 7; Mismatches 10; Indels

FRAMEWORK-2.
COMPLEMENTARITY-DETERMINING-2.
FRAMEWORK-3.
COMPLEMENTARITY-DETERMINING-3.
FRAMEWORK-4.
BY SIMILARITY.

23 FRAMEWORK-1.
23 COMPLEMENTARITY-DETERMINING48 FRAMEWORK-2.
55 COMPLEMENTARITY-DETERMINING87 FRAMEWORK-3.
96 COMPLEMENTARITY-DETERMINING106 FRAMEWORK-4.
107 BY SIMILARITY.
107
A; 11561 MW; 6F694284ECFA68E6 CRC64;

24 34 49 56 88 97 107 107 AA;

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COMPLEMENTARITY - DETERMINING - 1.

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62 SGSGSGTSYSLTISRMEAEDAATYYCOORSSYPFTFGSGTKLEIK 106

## 349.5 63.7 111 1 KV3C_MOUSE P01656 mus musculu KV3E_MOUSE P01655 mus musculu P01604 homo sapien P01605 mos sapien P01606 mos sapien P0160406 mos	idoma. FRAMEWORK-1. COMPIEMENTARTIV-DETERMINING-1
C_MOUSE M_HUMAN M_HUMAN N_HUMAN N_HUMAN N_HUMAN X_HUMAN X_HUMAN X_HUMAN N_HUMAN N_HUMAN E_HUMAN E_HUMAN S_MIGNENTS ALIGNMENTS ALIGNMENTS ALIGNMENTS ALIGNMENTS ALIGNMENTS ALIGNMENTS ALIGNMENTS ALIGNMENTS S_HUMAN T_A 1.1 T_A 1.1 OF T_A 1.1 T_A 1	PORK
4 349.5 63.7 111 1 KV3C_MOUSE 349 63.6 129 1 KV3M_HUMAN 8 348.5 63.5 108 1 KVJM_HUMAN 9 348.5 63.5 108 1 KVJM_HUMAN 9 348.5 63.5 108 1 KVJM_HUMAN 148.5 63.5 111 1 KV3Z_MOUSE 1346.5 63.1 108 1 KVJL_HUMAN 1346.5 63.1 108 1 KVJL_HUMAN 1345.5 62.9 108 1 KVJM_HUMAN 1345.5 62.9 108 1 KVJN_HUMAN 1345.5 62.9 108 1 KVJN_HUMAN 13-AUG_1997 (Rel. 05, Last sequence updat. 11-AUG_1999 (Rel. 06, Last sequence updat. 12-AUG_1999 (Rel. 06, Last sequence updat. 13-AUG_1999 (Rel. 06, Last sequence updat. 13-AUG_1999 (Rel. 06, Last sequence updat. 13-AUG_	idoma. FRAMEWORK-1 COMPLEMENTA
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111 1 KV 29 1 KV 008 1 KV 009	, H
4 349.5 63.7 111 1 KV3C. 348.5 63.6 129 1 KV1L. 6 348.5 63.5 108 1 KV1L. 6 348.5 63.5 108 1 KV1L. 6 348.5 63.5 108 1 KV1L. 1 1 KV3D. 1 1 1 KV3D. 1 1 1 KV3D. 1 KV3	Pfam; PF00047; ig; i. SMART; SM00406; IGv; 1. Immunoglobulin V region; DOMAIN 24 33
37 AN MAN MAN MAN MAN MAN MAN MAN MAN MAN	IGV IGV / re
63.7 63.6 63.5 63.5 63.5 63.1 63.1 63.1 62.9 62.9 62.9 62.9 62.9 62.9 62.9 62.9	17; 106; in
349.5 63.7 348.5 63.5 348.5 63.5 348.5 63.5 348.5 63.5 348.5 63.5 348.5 63.5 348.5 63.5 346.5 63.1 346.5 63.1 346.5 63.1 346.5 62.9 345.5 62.9 345.5 62.9 345.5 62.9 345.5 62.9 345.5 62.9 345.5 62.9 346.5 62.9 347.5 62.9 347.5 62.9 348.5 63.1 13-AUG-1999 (Rel. 11-AUG-1999 (Rel. 11-A	Pfam; PF00047; ig; i. SMART; SM00406; IGv; Immunoglobulin V regi DOMAIN 1 2
349.5 349.5 348.5 34	TT; PE
34 349.5 63.7 111 1 KV3C MOUSE 35 349 63.6 129 1 KV3M_HUMAN 37 348.5 63.5 108 1 KV1M_HUMAN 38 348.5 63.5 108 1 KV1M_HUMAN 39 348.5 63.5 108 1 KV1M_HUMAN 41 346.5 63.1 108 1 KV3L_HUMAN 42 346.5 63.1 108 1 KV3L_HUMAN 44 345.5 62.9 108 1 KV1Y_HUMAN 44 345.5 62.9 108 1 KV1Y_HUMAN 45 344.5 62.9 108 1 KV1Y_HUMAN 47 345.5 62.9 108 1 KV1Y_HUMAN 48 345.5 62.9 108 1 KV1Y_HUMAN 49 345.5 62.9 108 1 KV1Y_HUMAN 50	Pfam; SMART; Immuno DOMAIN
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This SWISS-PROT entry is copyright. It is produced through a collaboration
  Sukaryota; Metazoa;
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Best Local Simi
Matches 88;
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SEQUENCE
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KV6H_MOUSE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    13-806-1987 (Rel. 05, Created)
13-806-1987 (Rel. 05, Last sequence update)
15-70L-1989 (Rel. 38, Last annotation update)
15-70L-1989 (All 138, Last annotation update)
16 kappa Čhain V-VI region NG6-8.3.1.
Mus musculus (Mouse).
Eukaryotek Metazoa; Chordata; Cranlata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus.
                                                                                                                                                                               SEQUENCE FROM N.A.
MEDLINE-89271467; PubMed-6877353;
Kaartinen M., Griffiths G.M., Markham A.F., Milstein C.;
Marky Sequences define an unusually restricted IgG response to 2-phenyloxažolone and its early diversification.";
Nature 304:320-324(1983).
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COMPLEMENTARITY-DETERMINING-1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 107;
                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPLEMENTARITY - DETERMINING - 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPLEMENTARITY-DETERMINING-3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      11; Indels
62 SÖSGSGTSYSLTISRMEAEDAATYYCQQRSSYPFTFGSGTKLEIK 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -!- FUNCTION: ANTI-2-PHENYL OXAZOLONE (PHOX) ANTIBODY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           11572 MW; 6F694824ECF0C8E6 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 452; DB 1;
Pred. No. 1.5e-38;
7; Mismatches 11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          KV67_MOUSE STANDARD; PRT; 107 AA. p04944; 13-AUG-1987 (Rel. 05, Created) 13-AUG-1987 (Rel. 05, Last sequence update) 15-AUG-1999 (Rel. 38, Last annotation update) 15-AUG-1999 (Rel. 38, Last annotation update) 19 kappa chain V-VI region NO5-78.2.6. Mus musculus (Mouse).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      BY SIMILARITY
                                                               107
                                                                                                                                                                                                                                                                                                                                                                                                                                                   FRAMEWORK-2
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InterProf. IPR003596; Ig_v.
Pfam. PR00047; ig. 1.
SMART: SM00406; IGv; 1.
Immunoglobulin V region; Hybridoma.
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HSSP; PO1679; 2FBJ.
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82.9%;
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                                                              STANDARD;
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48
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                                                                                                                                                            NCBI_TaxID-10090;
                                                            KV6I_MOUSE
P04943;
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Chordata; Craniata; Vertebrata; Euteleostomi;
Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2 IELTQSPAIMSASPGEKVTITCSASSSVSYMHWFQQKPGTSPKLWIYSTSNLASGVPARF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2 ILLTQSPAIMSASPGQKVTMTCSASSSVSYMHWYQQKSGTSPKRWIYDTSKLASGVPARF
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                       SEQUENCE FROM N.A.
MEDLINE-83271467; PubMed-6877353;
Raartinen M., Griffiths G.M., Markham A.F., Milstein C.;
"mRNA sequences define an unusually restricted IgG response to phenyloxazolone and its early diversification.";
Nature 304:320-324(1983).
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COMPLEMENTARITY-DETERMINING-1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPLEMENTARITY-DETERMINING-2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           12; Indels
                                                                                                                                                                                                                                                                         11 FUNCTION: ANTI-2-PHENYL OXAZOLONE (PHOX) ANTIBODY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    11611 MW; A38290781F3C30D3 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                62 SGSGSGTSYSLTISRMEAEDAATYYCQQRSSYPFTFGSGTKLEIK 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 452; DB 1;
Pred. No. 1.5e-38;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                13-AUG-1987 (Rel. 05, Created)
13-AUG-1987 (Rel. 05, Last sequence update)
13-UUL-1999 (Rel. 38, Last annotation update)
1g kappa chain V-VI region NQ5-61.1.2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            107 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           5; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                BY SIMILARITY.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; K00744; AAA38689.1; -. HSSP; P01679; 2FBJ.
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83.8%;
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Interpro; IPR003596; Ig_v.
Pfam; PF00047; ig; 1.
SMART; SM00406; IGv; 1.
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                         Mammalia; Eutheria;
NCBI_TaxID=10090;
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107 AA;
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us-09-865-198-23.rsp

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87;
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P04945;
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the European Bioinformatics Institute. There are no restrictions on its
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modified and this statement is not removed. Usage by and for commercial
entities requires a license agreement (see http://www.isb-sib.ch/announce/
or send an email to license@isb-sib.ch).
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE-83271467; PubMed-6877353;
Kaartinen M., Griffiths G.M., Markham A.F., Milstein C.;
mRNA sequences define an unusually restricted IgG response to 2-
phenyloxazolone and its early diversification.";
Nature 304:320-324(1983).
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COMPLEMENTARITY-DETERMINING-1.
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FRAMEWORK-4.
BY SIMILARITY.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        11; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            11605 MW; CA6C4284ECFCB550 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                !- FUNCTION: ANTI-2-PHENYL OXAZOLONE (PHOX) ANTIBODY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 451; DB 1;
Pred. No. 1.9e-38;
7; Mismatches 11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     13.AUG-1987 (Rel. 05, Last sequence update)
15.JUL-1999 (Rel. 38, Last annotation update)
15 kappa chain V-VI region NQ2-48.2.2
Mus musculus (Mouse).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               107 AA.
                                                                                                                                                                                                                                                                                                                                                             FRAMEWORK-3.
                                                                                                                                                                                                                                                                                                                    FRAMEWORK-2
                                                                                                                                                                                                                                                         Immunoglobulin V region; Hybridoma
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             82.1%;
82.9%;
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InterPro; IPR003596; Ig_v.
Pfam; PF00047; Ig; 1.
SMART; SM00406; IGv; 1.
                                                                                                                                                                          InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_v.
Pfam; PF00047; ig; 1.
SMART; SM00406; IGv; 1.
                                                                                                                                   EMBL; K00739; AAA38684.1; -. HSSP; P01679; 2FBJ.
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NCBL_Taxib=10090;
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Kaartinen M., Griffiths G.M., Markham A.F., Milstein C.;
"mRNA sequences define an unusually restricted IgG response to phenyloxazolone and its early diversification.";
Nature 304:320-324(1983).
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                  FRAMEWORK-1.
COMPLEMENTARITY-DETERMINING-1.
                                                                                                                                                                                                                                                          Length 107;
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                                                                                COMPLEMENTARITY - DETERMINING - 2.
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                                                                                                                            COMPLEMENTARITY - DETERMINING - 3
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COMPLEMENTARITY-DETERMINING-
FRAMEWORK-2.

COMPLEMENTARITY-DETERMINING-
FRAMEWORK-3.

PRAMEWORK-3.

COMPLEMENTARITY-DETERMINING-
FRAMEWORK-3.

BY SIMILARITY.

BY SIMILARITY.

BY SIMILARITY.

108

LOBER STAN
                                                                                                                                                                                                                                                                                                        11; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           11556 MW; 72488DA9EF354934 CRC64;
                                                                                                                                                                                                                                                          Score 450; DB 1;
Pred. No. 2.4e-38;
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Pred. No. 2.4e-38;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       13-AUG-1987 (Rel. 05, Created)
13-AUG-1987 (Rel. 05, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                108 AA
                                                                                                                                                                                                                                                                                                   7; Mismatches
                                                                                                                                                                     BY SIMILARITY.
                                                                                                       FRAMEWORK-3
                                                                                                                                                  FRAMEWORK-4
                                                              FRAMEWORK-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ig kappa chain V-VI region NQ2-6.1. Mus musculus (Mouse).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Immunoglobulin V region; Hybridoma.
DOMAIN 1 23
[mmunoglobulin V region; Hybridoma
                                                                                                                                                                                                                                                          82.0%;
82.9%;
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82.2%;
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InterPro: IPR003006; Ig_MHC.
InterPro: IPR003596; Ig_v.
Pfam; PF00047; ig; 1.
SMART; SM00406; IGv; 1.
                                                                                                                                                                                                                                                                                                          Conservative
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Best Local Similarity
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Best Local Similarity
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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PIR; A01941; KVMSX4.
HSSP, P01679; 2FBJ.
InterPro; IPR003306; Ig_MHC.
InterPro; IPR003596; Ig_V.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pfam; PF00047; ig; 1.
SMART; SM00406; IGv; 1.
Immunoglobulin V region.
DOMAIN 24 33
DOMAIN 34 48
                                                                                                                                                                                                                                                                                                                                                                     Conservative
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                                                                                                                                                                                                                                                                                                                                                       Local Similarity
Les 87; Conserv
             NCBI_TaxID=10090;
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P01678;
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SEQUENCE
                                                                                   proteins.
                                  SEQUENCE.
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-1- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM A MYELOMA PROTEIN THAT
BIND GALACTAN.
 Gaps
                       61
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus
NCBL_TaxID=10090;
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 5
                                                                                                                                                                                                                                                                                           MEDIINE-79082830; Pubmed-103573;
Rao D.N., Rudikoff S., Potter M.;
"k Chain variable regions from three galactan binding myeloma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPLEMENTARITY - DETERMINING - 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPLEMENTARITY - DETERMINING - 2.
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 7; Indels
                                                                              SGSGSGTSYSLTISRMEAEDAATYYCQQRSSYP--FTFGSGTKLEIK 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    61 FSGSGSGTSYSLTISSMEAEDAAIYYCQQ-WNYPLITFGSGTKLEIK 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        61 FSGSGSGTSYSLTISRMEAEDAATYYCQQRSSYP-FTFGSGTKLEIK 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      36E6D022A5EC34D7 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          78.0%; Score 428; DB 1;
ilarity 82.2%; Pred. No. 3.7e-36;
Conservative 5; Mismatches 12;
                                                                                                                                                  KYGB_MOUSE STANDARD; PRT; 107 AA. P01676; 21-JUL-1986 (Rel. 01, Created) 15-JUL-1986 (Rel. 01, bast sequence update) 15-JUL-1999 (Rel. 38, Last annotation update) 19 kappa chain V-VI region XRPC 24.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
18 Appa chain V-VI region XRPC 44.
10; Mismatches
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HSSP; P01679; 2FBJ.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_V.
88; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STANDARD;
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SMART; SM00406; IGv; 1.
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les 88; Conserv
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P01675;
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Elochemistry 17:5555-559(1978).
-!- MISCELLANBOUS: THIS CHAIN WAS ISOLATED FROM A MYELOMA PROTEIN THAT BIND GALACTAN.
PIR, A01941; KVMSX4.
HSRP; P01679; 2FBJ.
Interpro; IPR003006; Ig_MHC.
Interpro; IPR003596; Ig_V.
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Proc. Natl. Acad. Sci. U.S.A. 77:4270-4274(1980).
-1- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM A MYELOMA PROTEIN THAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 DIELTQSPAIMSASPGEKVTITCSASSSVSYMHWFQQKPGTSPXLWIYSTSNLASGVPAR 60
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"Kappa Chain joining segments and structural diversity of antibody
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Musinae; NCBI_TaxID=10090;
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MEDLINE-79082830; PubMed-103573;
Rao D.N., Rudikoff S., Potter M.;
"K Chain variable regions from three galactan binding myeloma
                                                                                                                                                                                                                                                                                                                                                                                                                                                FRAMEWORK-2.
COMPLEMENTARITY-DETERMINING-2.
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FRAMEWORK-2.
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COMPLEMENTARITY - DETERMINING - 3.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               27A2D022BC0A34D7 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                77.4%; Score 425; DB 1;
81.3%; Pred. No. 7.4e-36;
live 6; Mismatches 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
18 Appa chain V-VI region SAPC 10.
Mus musculus (Mouse).
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MEDLINE-81054757; PubMed-6776525;
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FSGSGSGTSYSLTISRMEAEDAATYYCQQRSSYP-FTFGSGTKLEIK
                                                                                            STANDARD;
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P01679;
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KV6E_MOUSE
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                                                                                                             1 DIELTQSPAIMSASPGEKVTITCSASSSVSYMHWFQQKPGTSPKLWIYSTSNLASGVPAR 60
                                                                                                                        Proc. Natl. Acad. Sci. U.S.A. 77:4270-4274(1980).
-!- MISCELLANEOUS: THE TWO SEQUENCES ARE IDENTICAL.
-!- MISCELLANEOUS: THESE CHAINS WERE ISOLATED FROM MYELOMA PROTEINS
                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE (TEPC 191).
MEDLINE-81054757; PubMed-6776525;
Rudikoff S., Rao D.N., Glaudemans C.P.J., Potter M.;
"Rappa Chain joining segments and structural diversity of antibody combining sites.";
                                                                                                                                                                                                                                                                       Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2;
                                                                                                                                                                                                                                                                                                                    SEQUENCE (TEPC 601).
MEDLINE-79082830, PlubMed-103573,
RAO D.N., Rudikoff S., Potter M.;
"k Chain variable regions from three galactan binding myeloma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPLEMENTARITY - DETERMINING - 1.
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COMPLEMENTARITY-DETERMINING-2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            77.0%; Score 423; DB 1; Length 107; 80.4%; Pred. No. 1.2e-35;
 COMPLEMENTARITY - DETERMINING - 2.
         FRAMEWORK-3.
COMPLEMENTARITY-DETERMINING-3.
FRAMEWORK-4.
BY SIMILARITY.
                                                                        Length 107;
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                                                       27A2D022A5EC34D7 CRC64;
                                                                        Score 424; DB 1;
Pred. No. 9.3e-36;
                                                                                                                                                                                                                                 21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
1-JUL-1999 (Rel. 38, Last annotation update)
1g kappa chain V-VI region TEPC 601/TEPC 191.
                                                                                                                                                                                                                 107 AA
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5; Mismatches
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BY SIMILARITY.
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                                                      11554 MW;
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PIR; A01941; KWBX4.
HSSP; P01679; 2FB.
InterPro; IPR003306; Ig_MHC.
InterPro; IPR003596; Ig_V.
                                                                        77.2%;
ilarity 81.3%;
Conservative
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les 86; Conserv
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                                                                                  Similarity
                                                                                                                                                                                                                                                                                                   NCBI_TaxID=10090;
                                                                           Local Single 87;
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KV6C_MOUSE
ID KV6C_MOUSE
AC P01677;
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1 DIELTQSPAIMSASPGEKVTITCSASSSVSYMHWFQQKPGTSPKLWIYSTSNLASGVPAR 60

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study at 2.6-A resolution.";
Proteins 1:74-80(1986).
-!- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM A MYELOMA PROTEIN THAT
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Suh S.W., Bhat T.N., Navia M.A., Cohen G.H., Rao D.N., Rudikoff S.,
Davies D.R.;
                                                                                                                                                                                                                  The galactan-binding immunoglobulin Fab J539: an X-ray diffraction
                                                                                                                 MEDIINE-81054757; PubMed-6776525; Medikivoff S., Rao D.N., Glaudemans C.P.J., Potter M.; RAppa Chain joining segments and structural diversity of antibody combining sites.";
                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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COMPLEMENTARITY - DETERMINING - 3 .
FRAMEWORK - 4 .
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                                                                                                                                                       Proc. Natl. Acad. Sci. U.S.A. 77:4270-4274(1980)
                 21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
Mus musculus (Mouse).
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107
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PDB; 2FBJ; 15-OCT-90.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_v.
Pfam; PF00047; Ig; 1.
SMART; SM00406; IGv; 1.
Immunoglobulin V region; 3D-structure.
                                                                                                                                                                            X-RAY CRYSTALLOGRAPHY (2.6 ANGSTROMS)
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107
107 AA;
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26 LTQSPAIMAASLGQKVTMTCSASSSVSSSYLHWYQQKSGASPKPLIHRTSNLASGVPARF

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MEDLINE—82115300; PubMed-6799208;
Mean S.-P., Max B.E., Seidman J.G., Leder P., Scharff M.D.;
Two kappa immunoglobulin genes are expressed in the myeloma S107.";
Cell 26:[57-66(1981).
-! MISCELLANEOUS; THE PROTEIN, IN WHICH THERE IS A DELETION OF TWO AMING ACIDS AT THE V-J RECOMBINATION SITE (AFTER POSITION 118), IS SYNTHESIZED BUT NOT SECRETED IN CELLS THAT EXPRESS AND SECRETE THE NORMAL KAPPA CHAIN S107.
                                                             Gaps
                                                                                                                  1 DIELĮĮQSPAIMSASPGEKVTITCSASSSVSYMHWFQQKPGTSPKLWIYSTSNLASGVPAR 60
                                                                                                                                                Gaps
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_Taxip=10090;
                                                             2;
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  Length 107;
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COMPLEMENTARITY-DETERMINING-3.
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                                                             13; Indels
                                                                                                                                                                                                                                                             61 FSGSGSGTSYSLTISRMEAEDAATYYCQQRSSYP-FTFGSGTKLEIK 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       E4BB73072DCF6BE4 CRC64;
74.3%; Score 408; DB 1;
77.6%; Pred. No. 3.7e-34;
iive 9; Mismatches 13;
                                                                                                                                                                                                                                                                                                                                                                                                                      PO1680: STANDARD; PRT: 129 AA. PO1680: STANDARD; PRT: 129 AA. 21-JUL-1986 (Rel. 01, Created) Po101-1986 (Rel. 01, Last sequence update) PolyUL-1999 (Rel. 38, Last annotation update) PolyUL-1999 (Rel. 38, La
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EMBL; VQ0780; CAA4157.1; --
FIR. AQ1943; KVMS7B.
HSSP; PQ1679; ZFBJ.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003006; Ig_MHC.
Pfam; PG00047; 19; 1.
SMART; $M00406; IGV; 1.
SIGNAL.
SIGNAL
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                                                          83; Conservative
                                Best Local Similarity
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     Query Match
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LTOSPALMSASPGEKVTITCSASSSV--SYMHWFQOKPGTSPKLMIYSTSNLASGVPARF 61

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Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                              MEDIINE-79073152; PubMed-103003;
Weigert M., Gatmaitan L., Loh E., Schilling J., Hood L.E.;
"Rearrangement of genetic information may produce immunoglobulin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                68.0%; Score 373.5; DB 1; Length 111; 65.8%; Pred. No. 1.1e-30; ive 13; Mismatches 20; Indels 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            56 GVPARFSGSGSGTSYSLTISRMEAEDAATYYCQQRSSYPFTFGSGTKLEIK 106
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Weigert M., Gatmaitan L., Loh E., Schilling J., Hood L.E.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                      12002 MW; 7A5FCB586C306D29 CRC64;
                        21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     P01667;
21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
19 kappa chain V-III region PC 6308.
 111 AA
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                                                                  Ig kappa chain V-III region PC 7043.
 PRT;
                                                                                                                                                                                                                                                          InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_v.
Pfam; PF00047; ig; 1.
SMART; SM00406; IGv; 1.
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Nature 276:785-790(1978).
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 STANDARD;
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HSSP; P80362; 1WTL.
                                                                                 Mus musculus (Mouse)
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Best Local Simi
Matches 73;
 KV3M_MOUSE
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MCKean D.J., Bell M., Potter M.;
McKean D.J., Bell M., Potter M.;
Machanisms of antibody diversity: multiple genes encode structurally related mouse kappa variable regions.";
Proc. Natl. Acad. Sci. U.S.A. 75:3913-3917(1978).
-!- MISCELLANBOUS: THIS CHAIN WAS ISOLATED FROM A MYELOMA PROTEIN.
PIR; A01936; KVMSCI.
INTERPRO; IPRO03006; Ig_MHC.
InterPro; IPRO03006; Ig_WC.
InterPro; IPRO03006; Ig_V.
SMART; SMO0405; ig. 1.
Immunoglobulin V region.
                                                                                                                                                                                                                                                                                          Gaps
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                                                                                                                                                                                                                                                                                                                             Mus musculus (Mouse).

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
"Rearrangement of genetic information may produce immunoglobulin
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COMPLEMENTARITY-DETERMINING-1.
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COMPLEMENTARITY-DETERMINING-2.
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COMPLEMENTARITY-DETERMINING-3.
PRAMEWORK-4.
BY SIMILARITY.
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                                                                                                                                                                                                                                        12071 MW; 7A4ADE4D6C256D29 CRC64;
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21-JUL-1986 (Rel. 01, Last sequence update)
12-JUL-1999 (Rel. 38, Last annotation update)
1g kappa chain V-III region CBPC 101.
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                    Auture 276;785-790(1978).
PIR; C01937; KVMSOB.
HSSP; P80362; 1MTL.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_V.
Pfam; PF00047; ig; 1.
SMART; SMO0406; IGV; 1.
Immunoglobulin V region.
POMAIN
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Best Local Similarity
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P01664;
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KV3L_MOUSE
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DB 1; Length 111;

66.8%; Score 366.5;

Query Match

Search completed: December 23, 2002, 07:26:14 Job time: 11.4767 secs

 Q920e6 mus musculu Q9u186 homo sapien Q8vij0 mus musculu Q9u185 homo sapien

Q99m37 mus musculu Q925s9 mus musculu Q96pf6 homo sapien

Q9j184 mus musculu Q9qyf0 mus musculu Q9u183 homo sapien

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                        GenCore version 5.1.3
Copyright (c) 1993 - 2002 Compugen Ltd.
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Gapop 10.0 , Gapext 0.5
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ALIGNMENTS

134 AA

PRT;

Q9ers9 mus musculu Q9j182 mus musculu Q9j174 mus musculu Q9u180 homo sapien Q921a6 mus musculu Q8wtu6 homo sapien

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OBr028 mus musculu O8wuk4 homo sapien

Q8vci6 mus musculu Q9j180 mus musculu Q8vc55 mus musculu Q8tcd0 homo sapien

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2 IELTQSPAIMSASPGEKVTITCSASSSVSYMHWFQQKPGTSPKLWIYSTSNLASGVPARF 61
                                                                                                                                                                                                            Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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SEQUENCE PROM N.A.
SCALAIN-BALB/C;
SUBMILLOG T Cells to the CNS.";
Submitted (JAN-2002) to the EMBL/GenBank/DDBJ databases.
REMEL; AJ416331; CAC34866.1;
RINTEPPRO; IPR003599; IG.
RINTEPPRO; IPR003596; IG.
RINTEPPRO; IPR003596; IG.
REPPRO; IPR003596; IG.
REPPRO; IPR003596; IG.
REPPRO; IPR0047; IG; 1.
REPART; SM00409; IG; 1.
REPART; SM00406; IGV; 1.
REPROS IGV; 1.
                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
STRARIM-BALBA/C;
Chernajovsky Y.;
Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                134 AA; 14525 MW; CFDF8E2236E2D0CF CRC64;
                                                                                                      01-WAR-2002 (TrEMBLrel. 20, Created)
01-WAR-2002 (TrEMBLrel. 20, Last sequence update)
01-UNN-2002 (TrEMBLrel. 21, Last annotation update)
Anti-WOG 212 variable light chain (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 89.8%; Score 493; DB 11; Best Local Similarity 89.5%; Pred. No. 2.4e-44; Matches 94; Conservative 4; Mismatches 7;
                                                                 PRELIMINARY;
                                                                                                                                                                                                                                                                         NCBI_TaxID=10090;
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Q8VDD0;
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Q91W12
Q9JL78
Q8R062
Q9Z0E9
Q9R1A5
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sp_human:*
sp_invertebrate:*
sp_mammal:*
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sp_vertebrate:*
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sp_organelle:*
sp_phage:*
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sp_bacteriap:*
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EMBL; AF206030; AAF69328.1; -. HSSP; P01679; 2FBJ.
InterPro; IPR003006; Ig_MRC.
InterPro; IPR003596; Ig_V.
Pfam; PF00047; Ig; 1.
SMART; SMO0406; IGV; 1.
NON_TER
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97 AA; 10542 MW;
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86.68;
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Matches 84; Conservative
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TISSUE-BREAST TUMOR;
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SEQUENCE
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Q91W12;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        variable region (Fragment).
Schistosoma japonicum (Blood fluke).
Bukaryotag, Metazoa; Platyhelminthes; Trematoda; Digenea; Strigeldida; Schistosomatoidea; Schistosom
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE-20448942; PubMed-10992488;
Malkiel S., Liao L., Cunningham M.W., Diamond B.;
"T-Ceil-dependent antibody response to the dominant epitope of
streptococcal polysaccharide, N-acetyl-glucosamine, is cross-reactive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
SONG X.T. FENG 2.O., Qiu Z.N., Li Y.O., Huang H.L., Guan X.H.;
Song X.T. Feng 2.O., Qiu Z.N., Li Y.O., Huang H.L., Guan X.H.;
"Amplification, cloning and sequence analysis of the light chain
variable region gene of monoclonal anti-idiotypic antibody NP30 of
Schistosoma japonicum."
Submitted (NOV-1999) to the EMBL/GenBank/DDBJ databases.
EMBL ARZO(5620; AAF19434.1; -.
EMBL ARZO(5620
                                                                                                                                                                                                                                                                                                                                                                                                                                           01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
Monoclonal anti-idiotypic antibody NP30 immunoglobulin light chain
   24 IVLTQSPAIMSASPGEKVTMTCSASSSISYMHWYQQKPGTSPKRWIYDTSKLASGVPARF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    4 LTÖSPAIMSASPGEKVTITCSASSSVSYMHWFQQKPGTSPKLWIYSTSNLASGVPARFSG
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Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
NCBL_TaxID=10090;
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Pred. No. 4.8e-42;
                                                                                                          SGSGSGTSYSLTISRWEAEDAATYVCQQRSSYPFTFGSGTKLEIK 106
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01-OCT+2000 (TrEMBLrel. 15, Last sequence update)
01-OCT+2001 (TrEMBLrel. 19, Last sannotation update)
Anti-myosin immunoglobulin light chain variable region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          106 AA; 11478 MW; F20F544426BAE63E CRC64;
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Infect. Immun. 68:5803-5808(2000).
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| Similarity 87.4%;
90; Conservative
                                                                                                                                                                                                                                                                                                                                                                          PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mus musculus (Mouse).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A. STRAIN-DBA/2;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NON_TER
NON_TER
SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local
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                                                                                                              62
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Q9JL76
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2 IELTQSPAIMSASPGEKVTITCSASSSVSYMHWFQQKPGTSPKLWIYSTSNLASGVPARF 61
                                                                                                                                                            11 MSASPGEKVTITCSASSSVSYMHWFQQKPGTSPKLWIYSTSNLASGVPARFSGSGSGTSY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-DEC-2001 (TrEWBLrel. 19, Created)
01-DEC-2001 (TrEWBLrel. 19, Last sequence update)
01-DEC-2002 (TrEWBLrel. 20, Last annotation update)
01-MAR-2002 (TrEWBLrel. 20, Last annotation update)
Unknown (protein MGC:6582).
Mus musculus (Mouse).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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                                                     97;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 235;
                                                     DB 11; Length
                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Strausberg R.;
Strausberg R.;
Strausberg R.;
Submitted (ARR-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; BC006643; AAH06643.1; -.
InterPro; IPR003006; Ig_MHC.
Pfam; PF00047; ig; 2.
PROSITE; PS00290; IG_MHC; UNKNOWN_1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-00T-2000 (TrEMBLrel. 15, Created)
01-00T-2000 (TrEMBLrel. 15, Last sequence update)
01-0EC-2001 (TrEMBLrel. 19, Last annotation update)
Anti-myosin immunoglobulin light chain variable region (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              62 SGSGSGTSYSLTISRMEAEDAATYYCQQRSSYPFTFGSGTKLEIK 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             C9EE1FFE1F49DA1C CRC64;
                                               Score 434.5; DB 11;
Pred. No. 2.3e-38;
7; Mismatches 5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         78.9%; Score 433; DB 11;
81.0%; Pred. No. 9.7e-38;
iive 5; Mismatches 15;
                                                                                                                                                                                                                                                                       71 SLTISRMEAEDAATYYCQQRSS-YPFTFGSGTKLEIK 106
                                                                                                                                                                                                                                                                                                61 SLTISRVEAEDAATYYCQQWSSKYMYTFGGGTKLEIK 97
                                                                                                                                                                                                                                                                                                                                                                                                                                                          235 AA.
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Gaps

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Wilder K. W. W. Wisra S.;

REGURNCE FROM N.A. Exramoddoullah A.K.M., Misra S.;

REGURNCE FROM N.A. Exramoddoullah A.K.M., Misra S.;

RT "Cloning of cDNAs encoding for anti-white pine blister rust monoclonal wilde K.G., Yu X., Exramoddoullah A.K.M., Misra S.;

RT "Cloning of cDNAs encoding for anti-white pine blister rust monoclonal rantibody (AsrV).";

RT single chain antibody (ScFV).";

RE Submitted (MAY-1999) to the EMBL/GenBank/DDBJ databases.

BE EMBL. AFILSAJJ1; AAD40242.1;

BE EMBL. AFILSAJJ1; AAD40242.1;

BE EMBL. FROWORSON IG_11ke.

DR RICHPRO; IPRO03060; Ig_HKC.

DR InterPro; IPRO03060; Ig_HC.

DR FAMT; SMO0410; IG_11ke;

DR SWART; SWART; SMO0410; IG_11ke;

DR SWART; SWAR
                                                                                                                                            Atkin J.D., Tape A., Jennings I.G., Horaitis O., Cotton R.G.H.; "Definition of the Idiotope of Pterin-Mimicking Antibodies Expressed in Mammalian Cells.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 DIELTQSPAIMSASPGEKVTITCSASSSV----SYMHWFQQKPGTSPKLWIYSTSNLAS 55
(Fragment).
Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mus musculus (Mouse).

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.

NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                         66.6%; Score 365.5; DB 11; Length 111; 64.9%; Pred. No. 5.1e-31; 7ative 10; Mismatches 24; Indels 5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   56 GVPARFSGSGSGTSYSLTISRMEAEDAATYYCQQRSSYPFTFGSGTKLEIK 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Submitted (SEP-2000) to the EMBL/GenBank/DDBJ databases. EMBL; AF307935; AAL09419.1; -. InterPro; IPR003006; Ig_MHC. Pfam; PF00047; ig; 1. NON_TER.
                                                                                                                                                                                                                                                                                                                            111 111
111 AA; 12046 MW; 1E46988AA6858526 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
Kappa light chain of Mab7 (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      66.48;
                                                                                                                                                                                                                                                                                                                                                                                                                                      72; Conservative
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Best Local Similarity
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Best Local Similarity
Matches 71; Conserv
                                                                                                                                SEQUENCE FROM N.A.
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NON_TER
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                                                             Malkiel S., Liao L., Cunningham M.W., Diamond B.; "T-Cell-dependent antibody response to the dominant epitope of streptococcal polysaccharide, N-acetyl-glucosamine, is cross-reactive
                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 DIELTQSPAIMSASPGEKVTITCSASSSVS-YMHWFQQKPGTSPKLWIYSTSNLASGVPA 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              11 MSASPGEKVTITCSASSSVS--YMHWFQQKPGTSPKLWIYSTSNLASGVPARFSGSGGT 68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-JUN-2002 (TrEMBLrel. 21, Created)
01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Hypothetical 25-9 kDa protein.
Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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                                                                                                                                                                                                                                                                                                                                                                                           DB 11; Length 101;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0920E9;
0-1-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
Pterin-mimicking anti-idiotope kappa chain variable region
                                                                                                                                                                                                                                                                                                                                                                                       73.5%; Score 403.5; DB 11; Length
80.8%; Pred. No. 4.5e-35;
Live 6; Mismatches 10; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           60 RFSGSGSGTSYSLTISRMEAEDAATYYCQQRSSYPFTFGSGTKLEIK 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Submitted (APR-2002) to the EMBL/GenBank/DDBJ databases. EMBL, BC027418; AAH27418.1; ... Hypothetical protein. SEQUENCE 234 AA; 25857 MW; 4EB08C81426AEABI CRC64;
                                                                                                                                                                                                                                                                                                                                              101 AA; 10778 MW; 0A7F65E6A7E6F14D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SYSLTISRMEAEDAATYYCQQRSSYP-FTFGSGTKLEIK 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       111 AA
                                                                                                                       with cardiac myosin.";
Infect. Immun. 68:5803-5808(2000).
EMBL. AF205028, AAF69326.1;
HSSP, P01679; ZFBJ.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_V.
Pfam; PF00047; Ig; 1.
SMART; SM00406; IGY; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRT;
                                      MEDLINE-20448942; PubMed-10992488;
                                                                                                                                                                                                                                                                                                                                                                                                              Best_Local Similarity 80.8
Matches 80; Conservative
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                                                                                                                                                                                                                                                                                                                            101
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TISSUE=COLON;
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NON_TER
SEQUENCE
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Q8R062;
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Q920E9
ID Q9201
AC Q9201
DT 01-D1
DT 01-D1
DT 01-M
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ä 1; Gaps 1 DIELTQSPAIMSASPGEKVTITCSASSSV-SYMHWFQQKPGTSPKLWIYSTSNLASGVPA 59 66.0%; Score 362.5; DB 11; Length 214; 66.4%; Pred. No. 2.3e-30; ive 9; Mismatches 26; Indels 1; RFSGSGSGTSYSLTISRMEAEDAATYYCQQRSSYPFTFGSGTKLEIK 106 214 AA; 23922 MW; 52BA205FDE995E2A CRC64; 7

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Length 107;

09UL77

RESULT 9 **090L77**

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1 DIELTQSPAIMSASPGEKVTITCSASSSV-SYMHWFQQKPGTSPKLWIYSTSNLASGVPA 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 DIELTQSPAIMSASPGEKVTITCSASSSV--SYMHWFQQKPGTSPKLWIYSTSNLASGVP 58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 'Myosin-reactive autoantibodies in rheumatic carditis and normal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M., Young D.C.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      QUILTO:
01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
Myosin-reactive immunoglobulin light chain variable region
                                                                                                                                                                                                                                                                                                                                                                         01-MAY-2000 (TrEMBLrel. 13, Created)
1-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
Myosin-reactive immunoglobulin light chain variable region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      59 ARFSGSGSGTSYSLTISRMEAEDAATYYCQQRSSYPFTFGSGTKLEIK 106
                                                                                                                                                                                                 60 RFSGSGSGTSYSLTISRMEAEDAATYYCQQRSSYPFTFGSGTKLEIK 106
                                                                                                                                                                                                                   61 RFSGSGSGTDFTLTISSLQPEDFATYYCQQSYS-TLTFGGGTKVEIK 106
    11520 MW; 4BB43E9C5B577F16 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     11646 MW; 5F675C52EC7EE197 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       64.8%; Score 356; DB 4; L. 62.0%; Pred. No. 5e-30; Live 16; Mismatches 23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                fells.";
Clin. Immunol. Immunopathol. 87:184-192(1998).
EMBL, AP035036, AA556272.1; -.
HSSP; P80362: 1WTL.
InterPro: IPR003006; Ig_MHC.
InterPro: IPR003596; Ig_v.
R Pfam; PF00047; ig; 1.
                                      64.8%; Score 356; DB 4; 64.5%; Pred. No. 4.9e-30;
                                                                                                                                                                                                                                                                                                                                     109 AA
                                                                               19; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE=98277139; PubMed=9614934;
                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Best Local Similarity 62.0%
Matches 67; Conservative
                                                                                                                                                                                                                                                                                                                                       PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (Fragment).
Homo sapiens (Human)
  107 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     109 AA;
                                                          Local Similarity
nes 69; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=9606
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Q9UL70
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                                                                                                                                                                                                               (Fragment).
Momo sapiëns (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryǧta; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammal∯a; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                         Young D.C.; Myosin-geactive autoantibodies in rheumatic carditis and normal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0965A9 PRELIMINARY; PRT, 107 AA.
0965A934
01-DEC 2001 (TrEMBLrel. 19, Created)
01-DEC 2001 (TrEMBLrel. 19, Last sequence update)
01-MAR 2002 (TrEMBLrel. 20, Last annotation update)
Anti-séreptococcal/anti-myosin immunoglobulin kappa light chain variable region (Fragment).
Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1;
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MEDLINE-98375893; PubMed=9712075;
Adderson E.E., Shikhman A.R., Ward K.E., Cunningham M.W.;
Molecular analysis of polyreactive monoclonal antibodies from rheumatic carditis; human anti-N-acetylglucosamine/anti-myosin antibody V region genes.";
J. Immunol. 161:2020-2031(1998).
EMBL; "U96396; AAB68785.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 4; Length 108;
                                                                                                                                                                                                                                                                                                                               SEQUENCE PROM N.A.
MEDLINE-98277139; Pubmed-9614934;
Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
                                                                                                                                                        01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
Myosin-reactive immunoglobulin light chain variable region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  65.7%; Score 360.5; DB 4; Length 363.6%; Pred. No. 1.7e-30; 1.7e- 20; Mismatches 18; Indels
61 RFSGSGSGODYSLTISSLEYEDMGIYYCLOYDEFPFTFGSGTKLEIK 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            60 RFSGSGSGTSYSLTISRMEAEDAATYYCQQRSSYPFTFGSGTKLEIK 106
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  Clin. Immunol. Immunopathol. 87:184-192(1998).
EMBL; AF035037; AAD56273.1; -.
HSSP; P01607; IREI.
InterProf: IPR003006; Ig_MHC.
InterProf: IPR003596; Ig_V.
                                                                                                                                        Created)
                                                                                                 PRT;
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Pfam; PF00047; ig; 1.
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NON_TER 107 107
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SMART; SM00406; IGv; 1.
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                                                                                                                                                                                                              1 DIELTQSPAIMSASPGEKVTITCSASSSVS-YMHWFQQKPGTSPKLWIYSTSNLASGVPA 59
                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens (Human).

Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.

NCBI_TaxID=9606;
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                                       'Myosin-reactive autoantibodies in rheumatic carditis and normal
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MEDLINE-98277139; PubMed-9614934;
Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
               Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M., Young D.C.;
                                                                                                                                                                                                                                                                                                                                             01-MAY-2000 (TrEMBLrel. 13, Created)
1-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-DEC-2001 (TEMBLrel. 19, Last annotation update)
Myosin-reactive immunoglobulin light chain variable region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      / Match 64.2%; Score 352.5; DB 4; Length Local Similarity 61.7%; Pred. No. 1.2e-29; les 66; Conservative 21; Mismatches 19; Indels
                                                                                                                                                                     64.6%; Score 354.5; DB 4; Length 63.6%; Pred. No. 7.1e-30; ive 17; Mismatches 21; Indels
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                                                                                                                                                                                                                                                                  108 AA; 11787 MW; DB5845F19724FB4E CRC64;
                                                                                                                                                   108 AA; 11633 MW; B7BEDC3E41FCCA37 CRC64;
                                               fetus.";
Clin. Immunol. Immunopathol. 87:184-192(1998).
MBML: AF035044; AAD56280.1; --
HSSP; P01607; 1REI.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_V.
Pfam; PF00047; Ig. 1.
SMART: SM00406; IGV; 1.
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EMBL; AR035035, AAD56271.1; -.
INTESP: PO1607; IREI.
INTERPRO; IPRO03006; Ig_MHC.
INTERPRO; IRRO03556; Ig_V.
FRO047; ig; 1.
SMART; SMO0406; IGV: 1.
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           PubMed=9614934;
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           MEDLINE=98277139;
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01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
Hypothetical 25.9 kDa protein.
Hypothetical 25.9 kDa protein.
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostoml; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                    Homo sapiens (Human).
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                                                                Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M., Young D.C.;
                                                 01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
Myosin-reactive immunoglobulin light chain variable region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   63.4%; Score 348; DB 4; Length 10
62.6%; Pred. No. 3.4e-29;
iive 21; Mismatches 17; Indels
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Strausberg R.;
Strausberg R.;
Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; BCD12902.1; -.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR001865; Ribosomal_S2.
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SEQUENCE 234 AA; 25929 MW; BODOBOEGEB7812D2 CRC64;
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Clin. Immunol. Immunopathol. 87:184-192(1998).
EMBL. APO33; AAD56269.1; ...
HSSP. PO1607; 1REI.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR00356; Ig_V.
Pfam; PF00047; ig; 1.
SMART; SM00406; IGV; 1.
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PROSITE; PS00290; IG_MHC; UNKNOWN_1.
PROSITE; PS00962; RIBOSOMAL_S2_1; UNKNOWN_1.
107 AA.
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MEDLINE=98277139; PubMed=9614934;
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Mat	Matches		Conse	rvative	19;	67 Conservative 19; Mismatches	20;	20; Indels	1;	1; Gaps	1;
Qy	1	DIELTO	SPAIMS	ASPGEKVT	TCSAS	DIELEGOSPAIMSASPGEKVTITCSASSSVS-YMHWFQQKPGTSPKLWIYSTSNLASGVPA 59	PGTSP	KLWIYSTSNL	ASGV	PA 59	
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οy	9	RFSGSG	SGTSYS	LTISRMEAF	DAATY	60 RPSGSGGTSYSLTISRMEAEDAATYYCQQRSSYPFTFGSGTKLEIK 106	SGTKLI	SIK 106			
QQ	81	RFSGSG	SGTDYS	LTISNLEQ	DIATY	81 RFSGSGSGTDYSLTISNLEQEDIATYFCQQGNTPPFTFGSGTKLEVK 127	SGTKL	SVK 127			
Searc	h Co	Search completed: December 1.1.	l: Dece	mber 23,	2002,	Search completed December 23, 2002, 07:29:59					

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December 23, 2002, 07:16:08; Search time 4.8314 Seconds (without alignments) 248.221 Million cell updates/sec
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GenCore version 5.1.3
Copyright (c) 1993 - 2002 Compugen Ltd.
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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7	48	100.0	6	22	AAE13142	Humanised antibody
٣	48	100.0	σ	22	AAB82708	VEGF antagonist an
4	48	100.0	6	22	AAG63993	Complementarity de
2	48	100.0	σ	23	AAU74411	Light chain comple
9	48	100.0	106	22	AAE13144	Humanised antibody
7	48	100.0	106	23	AAU74418	Antigen-binding pr
80	48	100.0	107	22	AAG63987	Amino acid sequenc
σ	48	100.0	108	21	AAY97236	Variable light cha
10	48	100.0	108	22	AAB82710	VEGF antagonist an

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ALIGNMENTS

28-JAN-2000; 2000WO-US02180.

99US-0117726. 99US-0240736. 29-JAN-1999; 29-JAN-1999;

(IMCL-) IMCLONE SYSTEMS INC.

Zhu Z, Witte L;

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                                                                                                                 New immunoglobulin molecules are described that bind kinase insert domain-confeaining receptor (KDR) with a comparable affinity to human vascular endothelial growth factor (VEGF). The antibodies neutralise KDR activacion. The immunoglobulin may be a multivalent single chain antibody, a monovalent single chain antibody, a diabody, a chimarised antibody, a diabody, a crimabody, a humanised antibody a chimarised antibody. The immunoglobulin molecules bind specifically to an extracellular domain of the KDR receptor with the same affinity as carracellular domain of the KDR receptor with the same affinity as them number cell lines including glioblastoma multiforme, human tumour cell lines including glioblastoma multiforme, human tumour cell lines including glioblastoma and AIDS associated karposi's sarcoma. The antibodies therefore have applications in treating these conditions. This sequence encodes a conference of immunoglobulins of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Vasculas endothelial growth factor receptor; VEGFR; antagonist; tumour; cytostafelc, light chain hypervariable region; VL; myelocytic leukaemia; lymphocytic; erythrocytic; monocytic; moliphe monocytic; moliphe myeloma; lymphod cell; Hodgkings disease; complementarity determining region-3; CDR-3; mouse.
                                             Novel immunoglobulin molecules binding kinase insert domain-containing receptor with the same affinity as vascular endothelial growth factor, used to reguce tumour growth
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Inhibiting growth of non-solid tumor cells useful to treat bone marrow
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   tumors'such as leukemias or multiple myeloma comprises treatment with an antagonist of a vascular endothelial growth factor receptor -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Humanised antibody murine light chain hypervariable region (VL) CDR3.
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                                                                                                                                                                                                                                                                                                                                                               0; Mismatches
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                                                                                              Claim 3; Páge 50; 55pp; English.
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                                                                                                                                                                                                                                                                                                                                                                  Conservative
          2000-505966/45.
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                                                                                                                                                                                                                                                                                                                                                    Local Similarity
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                         N-PSDB; AAA53766
                                                                                                                                                                                                                                                                                                                  9 AA;
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The invention relates to a method for inhibiting the growth of non-solid tumour cells that are stimulated by a ligand of vascular endothelial growth factor receptor (VEGFR) in mammals particularly humans. The method involves treating the mammals with humanised VEGFR monoclonal antibodies (antagonists). Humanised monoclonal antibody comprises humanised mouse variable region joined to human constant region, where the humanised mouse variable region orntains mouse complementarity determining region (CDR) grafted into human variable region. The method is useful for treating leakemias such as acute or chronic myelocytic leukaemia, extraoric lymphocytic leukaemia, erythrocytic or monocytic leukaemia, multiple myelomas and lymphoid cells, particularly those related to non-Hodgkin's and Hodgkin's disease. The present sequence is humanised antibody murine light chalm hypervariable region (VL) CDR-3 used in the exemplification of the invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             IMC-1C11; chimeric antibody; mouse; human; antagonist; VEGF; vascular endothelial growth factor; antiogenesis; antianglogenic; antitumour; neoplasm; collagen vascular disease; autoimmune diseast tumour; breast carcinoma; lung carcinoma; prostate carcinoma; oon carcinoma; prostate carcinoma; glioblastoma multiforme; melanoma; therapy; light chain; CDR; complementarity determining region.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ;
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Claim 8; Page 15; 68pp; English.
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Matches 9; Conservative
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The present sequence is that of complementarity determining region (see also AAB82702) of IMC-1C11, a mouse-human chimeric antibody that has vascular endothelial growth factor (VEGF) antagonist activity. The antibody, or a fragment of it, can be used as an anti-anglogenic molecule, together with a chemotherapeutic acid, for the treatment of an anglogenic dependent condition in a mammal, especially a human. The invention relates generally to a method of treating or controlling an anglogenic dependent condition by administering an anti-anglogenic molecule and a chemotherapeutic agent. The preventing significant toxicity of the chemotherapeutic agent. The anti-anglogenic molecule inhibits or blocks the action of a vascular endothelium survival factor such as VEGF or its receptor, and is especially IMC-1C11. Conditions that can be treated include a neoplasm, a collagent wascular disease or an autoimmune disease,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                    especially a solid tumour, including breast carcinoma, lung carcinoma, prostate carcinoma, colon carcinoma, prostate carcinoma, ovarian carcinoma, neuroblastoma, central nervous system tumour,
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                                                                                                                                                                                                                                                                                                                                                             neuroblastoma, glioblastoma multiforme or melanoma (all claimed).
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100.0%; Pred. No. 7.8e+05;
ilve 0; Mismatches 0;
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New bispecific immunoglobulin-like antigen-binding protein for reducing tumour growth and for inhibiting angiogenesis, comprises a complex of two polypeptides and two second polypeptides
This antibody binds to human sialoadhesin factor-2 (SAF-2). The antibody is useful for treating or preventing allergic rhinitis, allergies, asthma, anemia, eccema or diseases such as lymphoma, leukemia or systemic mastocytosis in a mammal. It is also useful for detecting the presence of a cell, especially eosinophil in a sample, by detecting binding of the antibody to SAF-2. The antibody can be coupled to toxins, antiproliferative drugs or radionuclides to kill cells in areas of excessive SAF-2 expression.
                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  anglogenesis inhibitor; vascular endothelial growth factor receptor; VEGF; tumour; leukaemia; antibody; cell proliferation inhibitor; antibody light chain variable domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Complementarity determining region; CDR; CDRL3; antigen; cytostatic;
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100.0%; Pred. No. 7.8e+05;
ive 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAU74411 standard; peptide; 9 AA.
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Best Local Similarity
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                                                                                                                                                                                      9 AA;
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Query Match Best Local Similarity

106 AA;

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and in tetrameric form. The heavy chain constant domains which constitute the Fc region (e.g., CH2 and CH3 for an IgG molecule) of a natural antibody and which provide other antibody functions can be present. There is no requirement for processing in virro to obtain the complete product. This peptide sequence represents the light chain variable domain complementarity determining region L3 (CDRL3) incorporated into an antigen-binding protein described in the method of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                              cytostatic; light chain; myelocytic leukaemia; lymphocytic; erythrocytic; monocytic; multiple myeloma; lymphoid cell; Hodgkin's disease; mouse;
                                                                                                                                                                                                                                                                                                                                                                                                  Vascular endothelial growth factor receptor; VEGFR; antagonist; tumour;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Inhibiting growth of non-solid tumor cells useful to treat bone marrow tumors such as leukemias or multiple myeloma comprises treatment with an antigonist of a vascular endothelial growth factor receptor -
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illarity 100.0%; Pred. No. 7.8e+05;
Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                       Humanised antibody light chain fragment.
                                                                                                                                                                                                                                                                                        AAE13144 standard; Protein; 106 AA.
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Chimeric - Mus sp.
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The invention describes an antigen-binding protein (I) comprising a complex of two polypeptides (P1) and two second polypeptides (P2) which care stably associated in an immunoglobulin like complex. Pl has an antigen-binding site located to the N terminus of immunoglobulin (Ig) in the complex of the Culture of immunoglobulin (Ig) is useful for: cartiforth to the N terminus of the CH1 domain. (I) is useful for: cartiforth to the N terminus of the CH1 domain. (I) is useful for: cartiforth to the N terminus of the CH1 domain. (I) is useful for: cartiforth to activation of a vascular endothelial growth factor (VEGF) receptor; reducing tumour growth; inhibiting vEGF induced migration of human leukaemia cells; blocking interaction of a protein and intransity and invitro for investigative, diagnostic or treatment cand in vivo and in vitro for investigative, diagnostic or treatment cand in vitro for investigative, diagnostic or treatment complexed configuration. (I) is bivalent and bispecific, homogeneous on the testime of configuration. (I) is bivalent and bispecific, homogeneous and in tetrameric form. The heavy chain constant domains which constitute the FC region (e.g., CH2 and CH3 for an IgG molecule) of a natural cantibody and which provide other antibody functions can be present. There is no requirement for processing in vitro to obtain the complete product. This sequence represents a light chain variable domain (will incorporated in the method of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New bispecific immunoglobulin-like antigen-binding protein for reducing tumour growth and for inhibiting angiogenesis, comprises a complex of two polypeptides and two second polypeptides .
                                                                                                                                                                                                            Antigen-binding protein; antibody light chain variable domain; cytostatic; angiogenesis inhibitor; tumour; leukaemia; antibody; vascular endothelial growth factor receptor; VEGF; cell proliferation inhibitor.
                                                                                                                                                                      Antigen-binding protein light chain variable domain (VH) #2.
                                        AAU74418 standard; peptide; 106 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 61; Page 61; 64pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                          24-MAY-2001; 2001WO-US16924.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    24-MAY-2000; 2000US-206749P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (IMCL-) IMCLONE SYSTEMS INC.
                                                                                                                               (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 2002-106189/14.
N-PSDB; AAU20289.
                                                                                                                                                                                                                                                                                                                                                                    WO200190192-A2
                                                                                                                             26-MAR-2002
                                                                                                                                                                                                                                                                                                                                                                                                               29-NOV-2001
                                                                                   AAU74418;
                                                                                                                                                                                                                                                                                                                              Mus sp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       z pn z;
RESULT 7
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The invention relates to a method for inhibiting the growth of non-solid tumour cells that are stimulated by a ligand of vascular endothelial growth factor receptor (VEGFR) in mammals particularly humans. The method involves treating the mammals with humanised VEGFR monoclonal antibodies (antagonists). Humanised monoclonal antibody comprises humanised mouse (variable region foined to human constant region, where the humanised mouse action for human constant region, where the humanised mouse ariable region forman variable region. The method is useful for treating leukaemias such as acute or chronic myelocytic leukaemia, acute or chionic lymphocytic leukaemia, erythrocytic or monocytic leukaemia, multiple myelomas and lymphoid cells, particularly those related to non-Hoddkin's and Hodgkin's disease. The present sequence is humanised antibody light chain fragment used in the exemplification of the

invention.

S

Sequence

X S

Matches

pp

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26-NOV-2001

AAG63987;

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New immunoglobulin molecules are described that bind kinase insert domain-containing receptor (KDR) with a comparable affinity to human execular endothelial growth factor (VEGF). The antibodies neutralise CRB activation. The immunoglobulin may be a multivalent single chain antibody, a monovalent single chain antibody, a diabody, a climerised antibody, a diabody, a crimerised antibody, a diabody, a crimerised antibody. The immunoglobulin molecules bind specifically to an extracellular domain of the KDR receptor with the same affinity as CREF. Overexpression of VEGF has been implicated in a number of human tumour cell lines including glioblastoma multiforme, human tumour cell lines including glioblastoma multiforme, cassociated Karposi's sarcoma. The antibodies therefore have applications in treating these conditions. This sequence encodes a preferred heavy chain complementary determining region of the immunoglobulins of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Novel immunoglobulin molecules binding kinase insert domain-containing receptor with the same affinity as vascular endothelial growth factor, used to reduce tumour growth
                                                                                                                                                                                                                                                                                         humanised antibody; chimeric antibody; tumour; diabody; triabody; glioblastoma multiforme; hemangloblastoma; AIDS; central nervous system neoplasms; AIDS associated Karposi's sarcoma; acquired immune deficiency syndrome; AIDS; human.
                                                                                                                                                                                                                       Immunoglobulin; antibody; complementary determing region; CDR; VEGF; vascular endothelial growth factor; KDR; kinase insert domain containing receptor; multivalent; monovalent; humanised antibody; chimeric antibody; tumour; diabody; triabody;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    100.0%; Score 48; DB 21; Length 108; 100.0%; Pred. No. 0.075; 1.ve 0; Mismatches 0; Indels (
                                                                                                                                                                               Variable light chain fragment of anti-SI(KDR) antibody.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAB82710 standard; Protein; 108 AA.
                                          AAY97236 standard; Protein; 108 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 4; Page 51; 55pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       99US-0117726.
99US-0240736.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            28-JAN-2000; 2000WO-US02180.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            IMCL-) IMCLONE SYSTEMS INC
                                                                                                                                  19-DEC-2000 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 2000-505966/45.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            108 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 QQRSSYPFT 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           N-PSDB; AAA53768
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Witte L;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WO200044777-A1
                                                                                                                                                                                                                                                                                                                                                                                                                  sapiens.
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29-JAN-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                     Synthetic
                                                                                       AAY97236;
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ID AAB8
RESULT 9
                  AAY97236
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Monoclonal antibody 2C4; sialoadhesin factor-2; SAF-2; allergic rhinitis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Novel monoclonal antibody specific for human sialoadhesin factor-2 for diagnosis, prevention, treatment of allergy, asthma, eczema or diseases such as lymphoma, leukemia or systemic mastocytosis, in a mammal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Amino acid sequence of light chain variable region of antibody 2C4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               allergy; asthma; anemia; eczema; lymphoma; systemic mastocytosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ;
0
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                                                           100.0%; Score 48; DB 23; Tength 106; 100.0%; Pred. No. 0.073; O. Indels (ive 0; Mismatches 0; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 100.0%; Score 48; DB 22; Length 107; Best Local Similarity 100.0%; Pred. No. 0.074; Matches 9; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Abrahamson JA, Bochner B, Erickson-Miller CL, Kikly KK;
                                                                                                                                                                                                                                                                                                                 AAG63987 standard; Protein; 107 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (SMIK) SMITHKLINE BEECHAM CORP. (SMIK) SMITHKLINE BEECHAM PLC. (UYJO) UNIV JOHNS HOPKINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 11; Fig 2; 35pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    05-MAR-2001; 2001WO-US07193.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 07-MAR-2000; 2000US-0187595.
                                                                                                                                                                                                                                                                                                                                                                                                              (first entry)
                                                                                                          9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Leukemia; eosinophil.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 2001-570749/64.
                                                             Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           107 AA;
                  106 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 QQRSSYPFT 9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WO200166126-A1.
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Schleimer R;

13-SEP-2001

Mus sp.

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Gaps

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Sequence

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IMC-1C11; Chimeric antibody; mouse; human; antagonist; VEGF; vascular endothelial growth factor; angiogenesis; antiangiogenic; antitumout; neoplasm; collagen-vascular disease; autoimmune disease; tumour; byfeast carcinoma; lung carcinoma; prostate carcinoma; colon carcinoma; ovarian carcinoma; neuroblastoma; ovarian carcinoma; neuroblastoma; glioblastoma; melanoma; therapy; light chain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                Treating or controlling an angiogenic dependent condition (e.g. neoplasm, collagen-vascular or autoimmune disease) in mammal by administering a combination of an antiangiogenic molecule and a chemotherapeutic agent
                                               VEGF antagónist antibody IMC-1C11 light chain variable region.
                                                                                                                                                                                      /label= CDR-L1
/note= "complementarity determining region 1"
                                                                                                                                                                                                                              "complementarity determining region 2"
                                                                                                                                                                                                                                                          /note= "complementarity determining region 3"
                                                                                                                                                                    Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                    SUNNYBROOK HEALTH SCI CENT. TMCLONE SYSTEMS INC.
                                                                                                                                                                                                                             /note= "complem
88..96
/label= CDR-L3
                                                                                                                                                                                                         49..55
/label= CDR-L2
                                                                                                                                                                                                                                                                                                                   29-JAN-2001; 2001WO-US02839.
                                                                                                                                                                                                                                                                                                                                         2000US-0178791
                                                                                                                                                                                                                                                                                                                                                  2000US-0539692
                            (first entry)
                                                                                                                                    Mus sp.
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N-PSDB; AAH26406.
                                                                                                                                                                                                                                                                              WO200154723-A1.
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                                                                                                                                                                                                                                                                                                                                      28-JAN-2000;
                           15-0CT-2001
                                                                                                                                                                                                                                                                                                 02-AUG-2001
                                                                                                                                       Chimeric
Chimeric
         AAB82710;
                                                                                                                                                                                                                                                                                                                                                                   (SUNN-)
                                                                                                                                                                                                                                                                                                                                                                                                  Kerbel
                                                                                                                                                                                                          Region
                                                                                                                                                                                                                                       Region
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preventing significant toxicity of the chemotherapeutic agent. The anti-angiogenic molecule inhibits or blocks the action of a vascular endothelium survival factor such as VEGF or its receptor, and is especially INC-1C11. Conditions that can be treated include a neoplasm, a collagen vascular disease or an autoimmune disease, especially a solid tumour, including breast carcinoma, lung The antibody, The présent sequence is that of the light chain variable region of IMC-1CI, a mouse-human chimeric antibody that has vascular endothélial growth factor (VECF) antagonist activity. The antibody or a fragment of it, can be used as an anti-angiogenic molecule, together with a chemotherapeutic acid, for the treatment of an angiogenic dependent condition in a mammal, especially a human. The invention relates generally to a method of treating or controlling an angiogenic dependent condition by administering an anti-angiogenic molecule and a chemotherapeutic agent, to produce a regression or arrest of the condition while minimising or carcinoma, prostate carcinoma, colon carcinoma, prostate carcinoma, ovarián carcinoma, neuroblastoma, central nervous system tumour, neuroblastoma, glioblastoma multiforme or melanoma (all claimed). Disclosure; Page 38-39; 42pp; English.

108 AA; ej Sequence

108 AA;

Sequence

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The invention describes an antigen-binding protein (I) comprising a complex of two polypeptides (P1) and two second polypeptides (P2) which are stably associated in an immunoglobulin like complex. Pl has an antigen-binding site located to the N terminus of immunoglobulin (Ig) light chain constant domain (CL domain), and P2 has an antigen-binding site located to the N terminus of the CH1 domain. (I) is useful for: neutralising the activation of a vascular endothelial growth factor (VEGF) receptor; reducing tumour growth; inhibiting vEGF induced ingration of human leutance cells; blocking interaction of a protein and its ligand; promoting interactions between immune cells and target cells; and in vivo and in vitro for investigative, diagnostic or treatment the design of (I) provides for efficient productions of that substantially all of the antigen-binding proteins produced are assembled in the design of (I) provides for efficient productions of the region (e.g., CH2 and CH3 for an IgG molecule) of a natural cand in vivo much down which provide other antibody functions can be present. There is no requirement for processing in vitro to obtain the complete product. This sequence represents a light chain variable domain (YH) incorporated into FV, an engineered protein containing a heavy chain variable domain and a light chain variable domain in one polypeptide chain, described in the method of the invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New bispecific immunoglobulin-like antigen-binding protein for reducing tumour growth and for inhibiting angiogenesis, comprises a complex of two polypeptides and two second polypeptides
                                       Gaps
                                                                                                                                                                                                                                                                                                                                                        Antigen-binding protein; antibody light chain variable domain; cytostatic; anglogenesis inhibitor; tumour; leukaemia; antibody; vascular endothelial growth factor receptor; VEGF; cell proliferation inhibitor.
                                     ö
100.0%; Score 48; DB 22; Length 108; 100.0%; Pred. No. 0.075;
                                                                                                                                                                                                                                                                                                                      Antigen-binding protein light chain variable domain (VH) #1.
                                     Indels
                                     ö
                                   0; Mismatches
                                                                                                                                                                                                          AAU74413 standard; peptide; 108 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    24-MAY-2001; 2001WO-US16924.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              24-MAY-2000; 2000US-206749P.
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                                                                                                                                                                                                                                                                                   (first entry)
                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 2002-106189/14.
                 Best Local Similarity
Matches 9; Conserv
                                                                                                QORSSYPFT 96
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                                                                        1 QORSSYPFT 9
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 Query Match
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                                                                                                                                                                                                                                                                               Vascular endothelial growth factor receptor; VEGFR; antagonist; tumour; cytostatic; light chain; myelocytic leukaemia; lymphocytic; erythrocytic; monocytic; multiple myeloma; lymphoid cell; Hodgkin's disease; chimeric;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Inhibiting growth of non-solid tumor cells useful to treat bone marrow tumors such as leukemias or multiple myeloma comprises treatment with an antagonist of a vascular endothelial growth factor receptor -
                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                      "Mature chimeric plC11 light chain fragment"
                                       ;
0
          Score 48; DB 23; Length 108; Pred. No. 0.075;
                                       Indels
                                       ö
                                       Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                           1..19
/label- Leader_peptide
                                                                                                                                                                                                                                                    Chimeric plC11 light chain fragment.
                                                                                                                                                                                                                                                                                                                                                                                               Location/Qualifiers
                                                                                                                                                                  AAE13146 standard; Protein; 125 AA.
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/label- CDR_L2
107..115
          100.0%;
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/label= CDR_L1
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/label= CDR_L3
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                                                                                                                                                                                                                          (first entry)
                                       9; Conservative
                                                                                                                                                                                                                                                                                                                                                   Chimeric - Homo sapiens.
Chimeric - Unidentified.
                                                                                                                                                                                                                                                                                                                                                                                                                                                      'note=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 2001-662942/76.
N-PSDB; AAD21683.
                                                                                                                                                                                                                                                                                                                        human; plC11 vector.
                       Best Local Similarity
Matches 9; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Rafii S;
                                                                                  11111111
88 QQRSSYPFT 96
                                                                  1 QQRSSYPFT 9
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                                                                                                                                                                                              AAE13146;
           Query Match
                                                                                                                                                                                                                                                                                                                                                                                                         Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                        Protein
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                                                                                                                                       RESULT 12
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non-Hodgkin's and Hodgkin's disease. The present sequence is chimeric plC11 light chain fragment which is used for the construction of chimeric plC11 IgG expression vector. Chimeric plC11 light chain contains cloned variable light chain (VL) and human kappa light chain constant region
                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                  IMC-1C11; chimeric antibody; mouse; human; antagonist; VEGF; vascular endothelial growth factor; angiogenesis; antianglogenic; antitumour; neoplasm; collagen-vascular disease; autoimmune disease; tumour; breast carcinoma; lung carcinoma; prostate carcinoma; colon carcinoma; ovarian carcinoma; neuroblastoma; glioblastoma multiforme; melanoma; therapy; light chain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Treating or controlling an angiogenic dependent condition (e.g. neoplasm, collagen-vascular or autoimmune disease) in mammal by administering a combination of an antiangiogenic molecule and a chemotherapeutic agent
                                                                                                                                                   ;
0
                                                                                                                                                                                                                                                                                                                                                                        VEGF antagonist antibody IMC-1C11 light chain variable region.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note= "complementarity determining region 1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note= "complementarity determining region 2"
107..115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note= "complementarity determining region 3"
                                                                                                                      Length 125;
                                                                                                                                                 0; Indels
                                                                                                                    100.0%; Score 48; DB 22;
Similarity 100.0%; Pred. No. 0.086;
9; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1..19
/label= Signal_peptide
20..125
/label= Mature_protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SUNN-) SUNNYBROOK HEALTH SCI CENT.
                                                                                                                                                                                                                                                                                  AAB82702 standard; Protein; 125 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             43..52
/label= CDR-L1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       68..74
/label= CDR-L2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               107..115
/label= CDR-L3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             28-JAN-2000; 2000US-0178791
31-MAR-2000; 2000US-0539692
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   29-JAN-2001; 2001WO-US02839
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (IMCL-) IMCLONE SYSTEMS INC
                                                                                                                                                                                                                                                                                                                                            15-OCT-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         - Mus sp.
- Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 2001-514531/56.
                                                                                                                                                                                               107 QQRSSYPFT 115
                                                                                                                      Query Match
Best Local Similarity
                                                                                          125 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   N-PSDB; AAH26414.
                                                                                                                                                                              1 QQRSSYPFT 9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Chimeric
Chimeric
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Kerbel R;
                                                                                            Sequence
                                                                                                                                                                                                                                                                                                               AAB82702;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Region
                                                                                                                                                 Matches
                                                                                                                                                                                                                                                       RESULT 13
AAB82702
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The invention describes an antigen-binding protein (I) comprising a complex of two polypeptides (Pl) and two second polypeptides (P2) which are stably associated in an immunoglobulin like complex. Pl has an antigen-binding site located to the N terminus of immunoglobulin (Ig) [1] is useful for: Ingit chain constant domain (CL domain), and P2 has an antigen-binding site located to the N terminus of the CH1 domain. (I) is useful for: neutralising the activation of a vascular endothelial growth factor (VEF) receptor; reducing tumour growth; inhibiting angiogenesis; reducing endothelial cell proliferation; inhibiting vEGF induced ingration of human leutwaemla cells; blocking interaction of a protein and in vivo and in vitro for investigative, diagnostic or treatment and notice of investigative, diagnostic or treatment substantially all of the antigen-binding produced are assembled in the desired configuration. (I) is bivalent and bispecific, homogeneous the Fc region (e.g., CH2 and CH3 for an IgG molecule) of a natural antibody and which provide other antibody functions can be present. There is the antipon and in vitro to obtain the complete product. This is the annotation contain variable fragment.
                                                                                                                                                                                   New bispecific immunoglobulin-like antigen-binding protein for reducing tumour growth and for inhibiting angiogenesis, comprises a complex of two polypeptides and two second polypeptides
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Antigen-binding protein; single chain variable fragment; scFv; antigen; cytostatic; angiogenesis inhibitor; tumour; leukaemia; antibody; vascular endothelial growth factor receptor; VEGF; cell proliferation inhibitor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (scFv), an engineered protein containing a variable light and variable heavy domain on one polypeptide, described in the method of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Antigen-binding protein, single chain variable fragment version #1.
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/note= "Heavy chain variable domain. Specifically
claimed in claim 57"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              100.0%; Score 48; DB 23; Length 238; 100.0%; Pred. No. 0.16; 1.tve 0; Mismatches 0; Indels 0
                                                                                                                                                                                                                                                                          Claim 63; Page 62-63; 64pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Location/Qualifiers
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24-MAY-2000; 2000US-206749P.
                                             (IMCL-) IMCLONE SYSTEMS INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              26-MAR-2002 (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 2002-106189/14
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     238 AA;
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Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     nvention.
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Region
                                                                                           Zhu Z;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Antigen bid and protein; single chain variable fragment; svFv; antigen; cytostatic; anglogenesis inhibitor; tumour; leukaemia; antibody; vascular, endothelial growth factor receptor; VEGF; cell proliferation inhibitor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /label- Linker
/note= "15 amino acid linker joins the VH and VL
regions of the single chain variable fragment
protein. Encoded by AAS20285"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                        preventing significant toxicity of the chemotherapeutic agent. The anti-angiogenic molecule inhibits or blocks the action of a vascular anotherlum survival factor such as VEGF or its receptor, and is especially IMC-101. Conditions that can be treated include a neoplasm, a collagen-vascular disease or an autoimmune disease, especially a solid tumour, including breast carcinoma, lung carcinoma, prostate carcinoma, cancinoma, prostate carcinoma, carcinoma, neuroblastoma, central nervous system tumour, neuroblastem or melanoma (all claimed).
                                                                                                                The antibody,
                                                         The present sequence is that of the light chain variable region of IMC-ICII, a mouse-human chimeric antibody that has vascular endothelial growth factor (VECF) antagonist activity. The antibody or a fragment of it, can be used as an anti-angiogenic molecule, together with a chemotherapeutic acid, for the treatment of an angiogenic dependent condition in a mammal, especially a human. The invention relates generally to a method of treating or controlling an angiogenic dependent condition by administering an anti-angiogenic molecule and a chemotherapeutic agent, to produce a regression or arrest of the condition while minimising or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Antigen binding protein, single chain variable fragment version #2
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/label - VL
/note = "Light chain variable domain. Specifically
claimed in claim 61"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note= "Heavy chain variable domain. Specifically claimed in claim 61"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            100.0%; Score 48; DB 22; Length 125; 100.0%; Pred. No. 0.086; O; Mismatches 0; Indels .(
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAU74420 standard; Protein; 238 AA.
                   Disclosure; Fig 1; 42pp; English.
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/label- VH
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best Local Similarity
Matches 9; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   125 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  107 QQRSSYPFT 115
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Synthetic.
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Region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence
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RESULT 14

NO CONTRACTOR OF THE FET THE F

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Gaps

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The invention describes an antigen-binding protein (I) comprising a complex of two polypeptides (P1) and two second polypeptides (P2) which are stably associated in an immunoglobulin like complex. Pl has an antigen-binding site located to the N terminus of immunoglobulin (Ig) antigen-binding site located to the N terminus of immunoglobulin (Ig) cost can constant domain (CL domain), and P2 has an antigen-binding cost is located to the N terminus of the CH1 domain. (I) is useful for: neutralising the activation of a vascular endothelial growth factor (VEGF) receptor; reducing tumour growth; inhibiting angiogenesis.

CC reducing endothelial cell proliferation; inhibiting vEGF induced migration of human leukaemia cells; blocking interaction of a protein and its ligand; promoting interactions between immune cells and target cells; and in vivo and in vitro for investigative, diagnostic or treatment completentially all of the antigen-binding proteins production so that substantially all of the antigen-binding proteins production so that the desired configuration. (I) is bivalent and bispecific, homogeneous of an in tetrameric form. The heavy chain constant domains which constitute the Fc region (e.g., CH2 and CH3 for an Ig6 molecule) of a natural configuration equipment for processing in vitro to obtain the complete product. This is the amino acid sequence of a single chain variable fragment configuration containing a variable light and variable warnable in the method of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New bispecific immunoglobulin-like antigen-binding protein for reducing tunnour growth and for inhibiting anglogenesis, comprises a complex of two polypeptides and two second polypeptides  . \\
                                                                                                      /label= VL
/note= "Light chain variable domain. Specifically
claimed in claim 57"
                    /note= "15 amino acid linker joins the VH and VL
                                          regions of the single chain variable
fragment protein. Encoded by AAS20285"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 63; Page 62; 64pp; English.
/label= Linker
                                                                                                                                                                                                                                                                            24-MAY-2001; 2001WO-US16924.
                                                                                                                                                                                                                                                                                                                      24-MAY-2000; 2000US-206749P.
                                                                                                                                                                                                                                                                                                                                                              (IMCL-) IMCLONE SYSTEMS INC
                                                                                  133..240
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                                                                                  Region
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Query Match

Query Match

100.0%; Score 48; DB 23; Length 240;

Best Local Similarity 100.0%; Pred. No. 0.16;

Matches 9; Conservative 0; Mismatches 0; Indels (
QY 1 QQRSSYPFT 9

Db 220 QQRSSYPFT 228

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Gaps

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Search completed: December 23, 2002, 07:25:06 Job time : 4.8314 secs

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GenCore version 5.1.3
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 protein search, using sw model OM protein

December 23, 2002, 07:16:08 ; Search time 62.8081 Seconds (without alignments) 248.221 Million cell updates/sec Run on:

US-09-865-198-22 631 1 QVKLQQSGAELVGSGASVKL......AYYGDYEGYWGQGTTVTVSS 117 Perfect score:

Scoring table:

Sednence:

BLOSUM62 Gapop 10.0 , Gapext 0.5

908470 seqs, 133250620 residues

Searched:

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Maximum Match 100% Listing first 45 summaries Post-processing: Minimum Match 08

Database :

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Description	Humanised antibody	VEGF antaqonist an	Antigen-binding pr	VEGF antagonist an	Antigen-binding pr	Variable heavy cha	Antigen-binding pr	Antigen-binding pr	Chimeric p1C11 hea	Human p53 protein
COLUMNICO	ID	: ~	AAB82709	AAU74417	AAB82701	AAU74420	AAY97235	AAU74412	AAU74419	AAE13145	AAW28491
	DB	22	22	23	22	23	21	23	23	22	18
	Length	117	117	117	136	238	117	117	240	136	535
	% Query re Match Length DB]	100.0	100.0	100.0	100.0	100.0	98.9	98.9	98.9	98.1	88.5
	Score	631	631	631	631	631	624	624	624	619	558.5
	Result No.		7	3	4	S	9	7	ω	σ	10

Human p53 protein Murine anti-p53 mo Single chain antib Anti-p53 monoclona Lead binding MAb 1 MFE-23 antibody.	Scrv-rearranged ca Anti-carcinoembryo Single chain antib Single chain antib H22-anti-CEA antib Bispecific single Bispecific single Anti-carcinoembryo	RSV19 VH. Mus mus RSV19 heavy chain Murine COL1 VH cha Murine COL1 CLCB a Anti-CEA antibody Chimeric anti-CEA Fusion protein pIC 806.077 heavy chai	RSV19 heavy chain H3 region of MAb T TA1 antibody VH ch Modified H3 region Variable gamma hea Monoclonal antibod Mouse monoclonal a Mouse and human ch Monoclonal antibod Mouse and human ch
AAW28492 AAY70787 AAW60769 AAW9173 AAW01586 AAR75719	AAU80040 AAR60566 AAW60770 AAW11508 AAW73223 AAB85455 AAR60565	AAR24807 AAR42804 AAR39528 AAU76632 AAW41387 AAW82744 AAW82741	AAR4 2802 AAR1 4394 AAR1 4394 AAR1 4395 AAR1 1384 ABB05962 ABB05994 ABB05994 AAR7 9882 AAR7 9882
18 10 10 10 10 10 10 10 10 10 10 10 10 10	755 755 755 755 755 755 755 755 755 755	200 200 200 200 200 200 200 200 200	23 23 23 23 25 25 25 25 25 25 25 25 25 25 25 25 25
535 243 112 118 270 556	7 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7	1116 1116 1124 120 255 281 642	258 258 258 258 258 260 278 287 130
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558 558 558 553 533 517 517 517 517		00000000000000000000000000000000000000	489 487.5 487.5 487.5 487.5 487.5 487.5
11 113 114 116	18 20 22 23 24 25	22 22 23 23 23 24 25 26 27 27 27 27 27 27 27 27 27 27 27 27 27	1

ALIGNMENTS

AAE13143 ID AAE13143 standard; Protein; 117 AA. RESULT 1

AAE13143;

28-JAN-2002 (first entry)

Humanised antibody heavy chain fragment.

Vascular endothelial growth factor receptor; VEGFR; antagonist; tumour; cytostatic; heavy chain; myelocytic leukaemia; lymphocytic; erythrocytic; monocytic; multiple myeloma; lymphoid cell; Hodgkin's disease; mouse;

Chimeric - Homo sapiens. Chimeric - Mus sp. human; chimeric.

WO200174296-A2

11-OCT-2001.

30-MAR-2001; 2001WO-US10504 31-MAR-2000; 2000US-0540770

(IMCL-) IMCLONE SYSTEMS INC. (CORR) CORNELL RES FOUND INC.

Witte L, Rafii S;

WPI; 2001-662942/76. N-PSDB; AAD21669.

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                                                                                                         The invention relates to a method for inhibiting the growth of non-solid tumour cells that are stimulated by a ligand of vascular endothelial growth factor receptor (VEGER) in mammals particularly humans. The method involves treating the mammals with humanised VEGER monoclonal antibodies (antagonists). Humanised monoclonal antibody comprises humanised mouse variable region joined to human constant region, where the humanised mouse variable region contains mouse complementarity determining region (CDR) grafied into human variable region. The method is useful for treating leukaemias such as acute or chronic myelocytic leukaemia, acute or chronic lymphocytic leukaemia, erythrocytic or monocytic leukaemia, multiple myelomas and lymphoid cells, particularly those related to non-Hodgkin's and Hodgkin's disease. The present sequence is humanised annibody heavy chain frgament used in the exemplification of the
               non-solid tumor cells useful to treat bone marrow
                             tumors such as leukemias or multiple myeloma comprises treatment with
an antagonist of a vascular endothelial growth factor receptor -
                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     IMC-LCIM: chimeric antibody; mouse; human; antagonist; VEGF; vascular endothelial growth factor; angiogenesis; antiangiogenic; antitumour; neoplasm; collagen-vascular disease; autoimmune disease; tumour; breast carcinoma; lung carcinoma; prostate carcinoma; colon carcinoma; neuroblastoma;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AGKATMTADSSSNTAYLQLSSLTSEDTAVYYCNAYYGDYEGYWGQGTTVTVSS 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
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                                                                                                                                                                                                                                                                                                                                                                                                       Length 117;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        glioblastoma multiforme; melanoma; therapy; heavy chain.
                                                                                                                                                                                                                                                                                                                                                                                                     100.0%; Score 631; DB 22; 100.0%; Pred. No. 1.3e-47;
                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAB82709 standard; Protein; 117 AA.
                                                                               Claim 8; Pàge 15; 68pp; English.
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/label- CDR-H2
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/label- CDR-H3
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/label= CDR-H1
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                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
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Chimeric - Homo sapiens.
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               Inhibiting growth of
                                                                                                                                                                                                                                                                                                                                                                                                           Matches 117 Comment
                                                                                                                                                                                                                                                                                                                                                                   117 AA;
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29-JAN-2001; 2001WO-US02839

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The present sequence is that of the heavy chain variable region of IMC-ICI1, a mouse-human chimeric antibody that has vascular endothelial growth factor (VEGF) antagonist activity. The antibody, or a fragment of it, can be used as an anti-anglogenic molecule, together with a chemotherapeutic acid, for the treatment of an anglogenic dependent condition in a mammal, especially a human.

The invention relates generally to a method of treating or controlling an anglogenic dependent condition by administering an anti-anglogenic molecule and a chemotherapeutic agent, to produce a regression or arrest of the condition while minimising or preventing significant toxicity of the chemotherapeutic agent.

The anti-anglogenic molecule inhibits or blocks the action of a vascular endothelium survival factor such as VEGF or its receptor, and is especially IMC-ICI1. Conditions that can be treated include a neoplasm, a collageneral disease, an aneoplasm, a collageneral disease or an autoimmune disease,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 QVKLQQSGAELVGSGASVKLSCTTSGFNIKDFYMHWVKQRPEQGLEWIGWIDPENGDSDY 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      especially a solid tumour, including breast carcinoma, lung carcinoma, prostate carcinoma, colon carcinoma, prostate carcinoma, colon carcinoma, prostate carcinoma, central nervous system tumour, neuroblastoma, qlioblastoma multiforme or melanoma (all claimed).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                61 APKFQGKATMTADSSSNTAYLQLSSLTSEDTAVYYCNAYYGDYEGYWGQGTTVTVSS 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61 APKFQGKATMTADSSSNTAYLQLSSLTSEDTAVYYCNAYYGDYEGYWGQGTTVTVSS 117
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                                                                                                                                                                                                                                                    Treating or controlling an angiogenic dependent condition (e.g. neoplasm, collagen-vascular or autoimmune disease) in mammal by administering a combination of an antiangiogenic molecule and a chemotherapeutic agent
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100.0%; Pred. No. 1.3e-47;
tive 0; Mismatches 0;
                                                                               (SUNN-) SUNNYBROOK HEALTH SCI CENT. (IMCL-) IMCLONE SYSTEMS INC.
                                                                                                                                                                                                                                                                                                                                                             Disclosure; Page 38; 42pp; English.
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                 28-JAN-2000; 2000US-0178791.
31-MAR-2000; 2000US-0539692.
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Best Local Similarity 100.0
Matches 117; Conservative
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                                                                                                                                                                                                            N-PSDB; AAH26405.
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glioblastoma multiforme; melanoma; therapy; heavy chain.
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                                                                                                                                                                                                                                                                                                           The invention describes an antigen-binding protein (I) comprising a complex of two polypeptides (P1) and two second polypeptides (P2) which care stably associated in an immunoglobulin like complex. Pl has an antigen-binding site located to the N terminus of immunoglobulin (Ig) antigen-binding site located to the N terminus of immunoglobulin (Ig) (Stel located to the N terminus of the CH1 domain. (I) is useful for: contralising the activation of a vascular endothelial growth factor (VEGF) receptor; reducing tumour growth; inhibiting angiogenesis; constrain of human leukaemia cells; blocking interaction of a protein and its ligand; promoting interactions; inhibiting VEGF induced migration of human leukaemia cells; blocking interaction of a protein and its ligand; promoting interactions between immune cells and target cells; and in vivo and in vitro for investigative, diagnostic or treatment continuing proteins production so that the desired configuration. (I) is bivalent and bispecific, homogeneous or in the desired configuration. (I) is bivalent and bispecific, homogeneous or in the desired configuration. (I) is bivalent and bispecific, homogeneous can in tetrament form. The heavy chain constant domains which constitute the region (e.g., CH2 and CH3 for an IgG molecule) of a natural continuing and which provide other antibody functions can be present. There is no requirement for processing in vitro to obtain the complete product. This sequence represents a heavy chain variable domain (VH) incorporated into the mathem of the invention of a plant variable domain in one polypeptide chain, described in the mathematic form of the contraction of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
                                                                                                                                                                                                               New bispecific immunoglobulin-like antigen-binding protein for reducing tumour growth and for inhibiting angiogenesis, comprises a complex of two polypeptides and two second polypeptides .
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 QVKLQQSGAELVGSGASVKLSCTTSGFNIKDFYMHWVKQRPEQGLEWIGWIDPENGDSDY 60
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Pred. No. 1.3e-47;
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100.0%; Pred. No. 1...
0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           the method of the invention.
                               24-MAY-2001; 2001WO-US16924.
                                                                24-MAY-2000; 2000US-206749P.
                                                                                                 (IMCL-) IMCLONE SYSTEMS INC
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Best Local Similarity 100.
Matches 117; Conservative
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                                                                                                                                                                                    N-PSDB; AAS20288.
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29-NOV-2001
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The present sequence is that of the heavy chain variable region of IMC-ICI1, a mouse-human chimeric antibody that has vascular endothelial growth factor (VEGF) antagonist activity. The antibody, or a fragment of it, can be used as an anti-anglogenic molecule, copether with a chemotherapeutic acid, for the treatment of an angiogenic dependent condition in a mammal, especially a human. The invention relates generally to a method of treating or controlling an anglogenic dependent condition by administering an anti-anglogenic molecule and a chemotherapeutic agent, to produce a regression or arrest of the condition while minimising or preventing significant toxicity of the chemotherapeutic agent.

The anti-anglogenic molecule inhibits or blocks the action of a vascular endothelium survival factor such as VEGF or its receptor, and is especially IMC-ICII. Conditions that can be treated include
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/label= CDR-H3
/note= "complementarity determining region 3"
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                                                                                                                                                                                                                                                                      note= "complementarity determining region 1"
                                                                                                                                                                                                                                                                                                                                                     'note= "complementarity determining region 2"
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100.0%; Pred. No. 1.5e-47;
ive 0; Mismatches 0;
                                                                                                                                                               0..136
|abel= Mature_protein
                                                                                                                                   label= Signal_peptide
                                                                                 Location/Qualifiers
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/label= CDR-H2
                                                                                                                                                                                                                                             'label - CDR-H1
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- Mus sp.
- Homo sapiens
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N-PSDB; AAH26413.
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Best Local &
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                                                                                                                                                                                                                                                                           Antigen-binding protein; single chain variable fragment; svFv; antigen; cytostatig; anglogenesis inhibitor; tumour; leukaemia; antibody; vascular endothelial growth factor receptor; VEGF; cell proliferation inhibitor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New bispecific immunoglobulin-like antigen-binding protein for reducing tumour growth and for inhibiting anglogenesis, comprises a complex of two polypeptides and two second polypeptides
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /label= Linker
/note= "15 amino acid linker joins the VH and VL
regions of the single chain variable fragment
protein. Encoded by AAS20285"
                                     Antigen-binding protein, single chain variable fragment version #2
                  61 APKFQGKATMTADSSSNTAYLQLSSLTSEDTAVYYCNAYYGDYEGYWGQGTTVTVSS 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /label - VL
/note= "light chain variable domain. Specifically
claimed in claim 61"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Heavy chain variable domain. Specifically claimed in claim 61"
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                                                                                                                                           AAU74420 standard; Protein; 238 AA
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                                                                                                                                                                                                                                                                                                                                                                              Mus sp.
Synthetic.
                                                                                                                                                                              AAU74420;
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                                                                                                        RESULT
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                      and in tetrameric form. The heavy chain constant domains which constitute the Fc region (e.g., CH2 and CH3 for an IgG molecule) of a natural antibody and which provide other antibody functions can be present. There is no requirement for processing in vitro to obtain the complete product. This is the amino acid sequence of a single chain variable fragment (scFv), an engineered protein containing a variable light and variable heavy domain on one polypeptide, described in the method of the
In the desired configuration. (I) is bivalent and bispecific, homogeneous
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Novel immunoglobulin molecules binding kinase insert domain-containing receptor with the same affinity as vascular endothelial growth factor, used to reduce tumour growth
                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New immunoglobulin molecules are described that bind kinase insert domain-containing receptor (KDR) with a comparable affinity to human vascular endothelial growth factor (VEGF). The antibodies neutralise KDR activation. The immunoglobulin may be a multivalent single chain antibody, a monovalent single chain antibody, a diabody, a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 QVKLQQSGAELVGSGASVKLSCTTSGFNIKDFYMHWVKQRPEQGLEWIGWIDPENGDSDY 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Central nervous system neoplasms; AIDS associated Karpos1's sarcoma;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Immunoglobulin; antibody; complementary determing region; CDR; VEGF; vascular endothelial growth factor; KDR; Kinase insert domain containing receptor; multivalent; monovalent; humanised antibody; chimeric antibody; tumour; diabody; triabody; glioblastoma multiforme; hemangioblastoma; AIDS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 QVKLQQSGAELVGSGASVKLSCTTSGFNIKDFYMHWVKQRPEQGLEWIGWIDPENGDSDY
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                                                                                                                                                                                                                                                                                                                                                                                  Length 238;
                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Variable heavy chain fragment of anti-SI(KDR) antibody.
                                                                                                                                                                                                                                                                                                                                                                               Score 631; DB 23;
Pred. No. 2.8e-47;
0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       acquired immune deficiency syndrome; AIDS; human.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAY97235 standard; Protein; 117
                                                                                                                                                                                                                                                                                                                                                                                  100.0%;
100.0%;
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99US-0240736.
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                                                                                                                                                                                                                                                                                                                                                                                                                   Best Local Similarity 100.
Matches 117; Conservative
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N-PSDB; AAA53767.
                                                                                                                                                                                                                                                                                                                       238 AA;
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Synthetic.
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                                                                                                                                                                                                                                                     nvention.
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                                                                                                                                                                                                                                                                                                                       Sequence
                                                                                                                                                                                                                                                                                                                                                                                     Query Match
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AAU74419 standard; Protein; 240 AA.
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                                                                                                                                                                                                                     98.9%;
99.1%;
                                                                                                                                                                    the method of the invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /label- VH
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                                                                                                                                                                                                                                                Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        133..240
                                                                                                                                                                                                                                   Similarity
                                                                                                                                                                                             117 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WO200190192-A2.
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                                                                                                                                                                                                                                                Matches 116;
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Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                           AAU74419;
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Region
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New bispecific immunoglobulin-like antigen-binding protein for reducing tumour growth and for inhibiting angiogenesis, comprises a complex of two polypeptides and two second polypeptides
                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                       QVKLQQSGAELVGSGASVKLSCTTSGFNIKDFYMHWVKQRPEQGLEWIGWIDPENGDSDY 60
                                                                                                                                                                                                                                              1 QVKLQQSGAELVGSGASVKLSCTTSGFNIKDFYMHWVKQRPEQGLEWIGWIDPENGDSGY 60
                          as
                                                                                                                                                                                                                                                                       61 APKFQGKATMTADSSSNTAYLQLSSLTSEDTAVYYCNAYYGDYEGYWGQGTTVTVSS 117
                                                                                                                                                                                                                                                                                     The immunoglobulin molecules bind specifically to an extracellular domain of the KDR receptor with the same affinity a VEGF. Overexpression of VEGF has been implicated in a number of human tumour cell lines including glioblastoma multiforme, hemangioblastoma, central nervous system neoplasms and AIDS associated Karposi's sarcoma. The antibodies therefore have applications in treating these conditions. This sequence encodes preferred heavy chain complementary determining region of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Antigen-binding protein; antibody heavy chain variable domain; cytostatic, anglogenesis inhibitor; tumour; leukaemia; antibody; vascular endothelial growth factor receptor; VEGF; cell proliferation inhibitor.
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                                                                                                                                                                  Score 624; DB 21; Length 117;
Pred. No. 5.3e-47;
0; Mismatches 1; Indels
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                                                                                                                                                                                             1; Indels
triabody, a humanised antibody or a chimerised antibody.
                                                                                                                                                                                                                                                                                                                                                               AAU74412 standard; peptide; 117 AA
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                                                                                                                                                                    98.98;
99.18;
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                                                                                                                                                                  Query Match 98.9
Best Local Similarity 99.1
Matches 116; Conservative
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                                                                                                                                          117 AA;
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                       its ligand; promoting interactions between immune cells and target cells, and in vivo and in vitro for investigative, diagnostic or treatment methods: The design of (1) provides for efficient production so that substantially all of the antigon-binding proteins produced are assembled in the desired configuration. (1) is bivalent and bispecific, homogeneous and in tetrameric form. The heavy chain constant domains which constitute the Fc region (e.g., CH2 and CH3 for an IgG molecule) of a natural antibody and which provide other antibody functions can be present. There is no requirement for processing in vitro to obtain the complete product. This sequence represents a heavy chain variable domain (VH) incorporated into Fv, an engineered protein containing a heavy chain variable domain and a light chain variable domain in one polypeptide chain, described in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Antigen-binding protein; single chain variable fragment; scFv; antigen; exfostatic; angiogenesis inhibitor; tumour; leukaemia; antibody; vascular endothelial growth factor receptor; VEGF; cell proliferation inhibitor.
migration of human leukaemia cells; blocking interaction of a protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Antigen-binding protein, single chain variable fragment version #1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       61 APKFOGKATMTADSSSNTAYLQLSSLTSEDTAVYYCNAYYGDYEGYWGQGTTVTVSS 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APKFOGKATMTADSSSNTAYLQLSSLTSEDTAVYYCNAYYGDYEGYWGGGTVTVSS 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 QVKLQQSGAELVGSGASVKLSCTTSGFNIKDFYMHWVKQRPEQGLEWIGWIDPENGDSDY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /label- VL
/label- VL
/note= "Light chain variable domain. Specifically
claimed in claim 57"
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regions of the single chain variable
fragment protein. Encoded by AAS20285"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 117;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 624; DB 23;
Pred. No. 5.3e-47;
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RESULT 10
AAW28491
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                                                                                                                               The invention describes an antigen-binding protein (I) comprising a complex of two polypeptides (P1) and two second polypeptides (P2) which are stably associated in an immunoglobulin like complex. Pl has an antigen-binding site located to the N terminus of immunoglobulin (Ig) (Ight chain constant domain (CL domain), and P2 has an antigen-binding site located to the N terminus of the CH1 domain. (I) is useful for: neutralising the activation of a vascular endothelial growth factor (VEEF) receptor; reducing tumour growth; inhibiting angiogenesis.

CC (VEEF) receptor; reducing tumour growth; inhibiting wEGF induced migration of human leukaemia cells; blocking interaction of a protein and its light, promoting interactions between immune calls and target cells; and in vivo and in vitro for investigative, diagnostic or treatment methods. The design of (I) provides for efficient production so that substantially all of the antigen-binding proteins production so that substantially all of the antigen-binding proteins produced are assembled in the desired configuration. (I) is bivalent and bispecific, homogeneous and in tetrament for provide other antibody functions can be present. There is no regularement for processing in vitro to obtain the complete product. This is the amino acid sequence of a single chain variable fragment (sefv), an engineered protein containing a variable light and variable heavy chain on one polypeptide, described in the method of the
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Vascular endothelial growth factor receptor; VEGFR; antagonist; tumour; cytostatic; heavy chain; myelocytic leukaemia; lymphocytic; erythrocytic; multiple myeloma; lymphoid cell; Hodgkin's disease; chimeric; human, picll vector.
                                                    New bispecific immunoglobulin-like antigen-binding protein for reducing
                                                                 tumour growth and for inhibiting angiogenesis, comprises a complex of two polypeptides and two second polypeptides
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 QVÄLQQSGAELVGSGASVKLSCTTSGFNIKDFYMHWVKQRPEQGLEWIGWIDPENGDSDY 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 QVKLQQSGAELVGSGASVKLSCTTSGFNIKDFYMHWVKQRPEQGLEWIGWIDPENGDSGY 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "Mature chimeric plC11 heavy chain fragment"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 98.9%; Score 624; DB 23; Length 240; 99.1%; Pred. No. 1.1e-46; ive 0; Mismatches 1; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /label= Leader_peptide
20..136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Chimergic plC11 heavy chain fragment.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAE13145 standard; Protein; 136 AA.
                                                                                                          Claim 63; Page 62; 64pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         28-JAN-2002 (first entry)
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Matches 116, Conservative
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Chimeric - Unidentified.
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                          WPI; 2002-106189/14.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              240 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 Invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence
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zhu z;
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The invention relates to a method for inhibiting the growth of non-solid tumour cells that are stimulated by a ligand of vascular endothelial growth factor receptor (VEGER) in mammals particularly humans. The method involves treating the mammals with humanised VEGER monoclonal antibodies (antagonists). Humanised monoclonal antibody comprises humanised mouse variable region joined to human constant region, where the humanised mouse variable region contains mouse complementarly determining region (CDR) grafted into human variable region. The method is useful for treating leukaemias acute or chronic myelocytic leukaemia, acute or chronic lymphocytic leukaemia, erythrocytic or monocytic leukaemia, multiple myelomas and lymphoid cells, particularly those related to non-Hodgkin's and Hodgkin's disease. The present sequence is chimeric plc11 heavy chain fragment which is used for the construction of chimeric plc11 igg expression vector. Chimeric plc11 heavy chain contains cloned to the contains contains contains the constant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                              /note- "Residue 'O' is present at this location in the sequence shown in fig-11 of the specification" 119\dots125 /label- CDR_H3
                                                                                                                                        /note= "Residue '0' is present at this location in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Inhibiting growth of non-solid tumor cells useful to treat bone marrow tumors such as leukemias or multiple myeloma comprises treatment with an antagonist of a vascular endothelial growth factor receptor -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              20 QVKLQQSGAELVGSGASVKLSCTTSGFNIKDFYMHWVKGRPEQGLEWIGWIDPENGDSDY 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                61 APKFQGKATMTADSSSNTAYLQLSSLTSEDTAVYYCNAYYGDYEGYWGQGTTVTVSS 117
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                                                                                                                                                                              sequence shown in fig-11 of the specification
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAW28491 standard; Protein; 535 AA.
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                                  69..85
/label= CDR_H2
/label- CDR_H1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (IMCL-) IMCLONE SYSTEMS INC. (CORR ) CORNELL RES FOUND INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            31-MAR-2000; 2000US-0540770.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    30-MAR-2001; 2001WO-US10504.
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Best Local Similarity 98.39
Matches 115; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 2001-662942/76.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Witte L, Rafii S;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 136 AA;
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                                                                                                          Misc-difference
                                                                                                                                                                                                            Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                    WO200174296-A2
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                                     Region
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Leucine zipper domain; LZD; oligomerisation domain; mutant; mutein; substitution; replacement; transactivation; viral protein VPI6; HSV; anti-oncogene; hyperproliferation; cancer; restenosis; ScFv; tumour suppression; apoptosis; single chain antibody variable domain.
                                                                                                                                    Location/Qualifiers
361
Human p53 protein variant S-325H.
                                                                                         Chimeric - Homo sapiens.
Chimeric - Herpes simplex virus.
                                                                                                                                                                                                                                                                                                                                                                          WPI; 1997-132633/12.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       535 AA;
                                                                                                                                                          Misc-difference
                                                                                                                                                                                                                                                                   17-JUL-1996;
                                                                                                                                                                                                                                                                                            19-JUL-1995;
                                                                                                                                                                                                               WO9704092-A1
                                                                                                                                                                                                                                          06-FEB-1997.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   oligomers)
                                                                                                                                                                                                                                                                                                                                                 Bracco L,
                                                                                                                   Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence
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Matches 10
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AAY70787
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   coligomerisation domain deleted and replaced by a leucine zipper coligomerisation domain deleted and replaced by a leucine zipper domain. The mutants preferably also have at least part of the p53 transactivation domain (amino acids 1-74) deleted and replaced by the transactivation domain (TD) from herpes simplex virus viral protein vp16 (amino acids 411-490) or by a protein domain able to bind selectively to a transactivation, especially a single-chain and acids variable domain (ScPv). The present sequence is that of a specifically claimed p53 variant designated S-325 and comprising a ScPv domain, amino acids 75-325 of human wild-type p53 and a secretive and more stable tumour suppressors and apoptosis-inducing agence than wild-type p53 and are active where the wild-type protein case is not, i.e. they are not inactivated by dominant negative or oncogenic mutants, nor by other cellular proteins (because the leucine zipper commain prevents formation of inactive mixed oligomers).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ij
                                    Leucine zipper domain; LZD; oligomerisation domain; mutant; mutein; substitution; replacement; transactivation; viral protein VP16; HSV; anti-oncogene; hyperproliferation; cancer; restenosis; ScFv; tumour suppression; apoptosis; single chain antibody variable domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New p53 variants e.g. with oligomerisation domain replaced by leucine zipper - useful for treating hyper-proliferative disorders, esp. cancer and restenosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       63 APKFQGKATMTADTSSNTAYLQLSSLASEDTAVYYCN-FYGDALDYWGQGTTVTVSS 118
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           Human p53 protein variant S-325 encoded by pEC176,
                                                                                                                                                                                                                                                                                                                                                                                                                Claim 36; Pages 88-90; 133pp; French.
                                                                                                    Chimeric - Homo sapiens.
Chimeric - Herpes simplex virus.
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                                                                                                                                                                                                                                                                  (RHON ) RHONE POULENC RORER SA.
                                                                                                                                                                                                              96WO-FR01111.
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                                                                                                                                                                                                                                                                                                                  WPI; 1997-132633/12.
N-PSDB; AAT86221.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      535 AA;
                                                                                                                                                         WO9704092-A1
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                                                                                                                                 Synthetic.
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coligomerisation domain deleted and replaced by a leucine zipper domain. The mutants preferably also have at least part of the p53 transactivation domain (amino acids 1-74) deleted and replaced by transactivation domain (amino acids 1-74) from herpes simplex virus viral protein VP16 (amino acids 411-490) or by a protein domain able to bind selectively to a transactivator, especially a single-chain can ibody variable domain (ScFv). The present sequence is that of a specifically claimed p53 variant designated S-35H and comprising a ScFv domain, amino acids 75-325 of human wild-type p53 (but with a replaced by His) and a leucine zipper domain at the C-terminal. The p53 variants are more active and more stable tumour suppressors and apoptosis-inducing agents than wild-type p53 and are active where the wild-type protein is not, i.e. they are not inactivated by dominant negative or oncogenic mutants, nor by other cellular proteins (because
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New p53 variants e.g. with oligomerisation domain replaced by leucine zipper – useful for treating hyper-proliferative disorders,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        61 APKFQGKATMTADSSSNTAYLQLSSLTSEDTAVYYCNAYYGDYEGYWGQGTTVTVSS 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           63 APKFQGKATMTADTSSNTAYLQLSSLASEDTAVYYCN-FYGDALDYWGQGTTVTVSS 118
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/note= "Arg residue at position 182 of wild-type p53 has been mutated to His"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claimed variants of protein p53 have at least part of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 36; Page -; 133pp; French.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (RHON ) RHONE POULENC RORER SA.
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                                                                                                                                                                                                                                                                                                                                                                                              95FR-0008729
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1;

31-JUL-2000

Mus sp.

Region

Key

Region

Region

AAY70787:

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The present sequence represents a single chain antibody (ScFv) designated 421. The antibody binds to an epitope present in the C-terminal region of the p53 protein that includes oligomerisation and regulatory domains, specifically between positions 320 and 393. ScFv 421 is directed against p53 mutants, particularly H273, W248 and G281 mutants. When the ScFv is introduced into cells containing a mutant p53 protein, p53 dependent trans-activating activity is restored. ScFv 421 is specific for p53-mutants that have lost tunnour-suppressing activity and are present in tumnour cells. It is particularly used to treat hyper-proliferation be used in vitro for studying mechanisms of activity of p53 or its mutant and to purify or detect p53.
                                                                                                                                                                                        Single chain antibody; ScFv 421; mouse; p53 protein; oligomerisation; regulatory domain; p53 mutant; H273; W248; G281; p53-dependent trans-activating activity; restoration; tumour-suppressing activity; tumour cell; reatment; hyper-proliferation; cancer; re-stenosis; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 QVKLQQSGAELVGSGASVKLSCTTSGFNIKDFYMHWVKQRPEQGLEWIGWIDPENGDSDY 60
                                                                                                                                                  Single chain antibody (ScFv) 421 that binds to mutant p53 proteins.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Restoring p53-dependent trans-activating activity to cell containi mutant p53 - by delivering single-chain antibody specific for the mutant, particularly for treatment of tumours
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pred. No. 1.5e-40;
6; Mismatches 6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           87.7%; Score 553.5;
88.9%; Pred. No. 1.5
                   AAW60769 standard; Protein; 243 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       97WO-FR01921.
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                                                                                                          (first entry)
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Matches 104; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Debussche L, Bracco L;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 1998-272140/24.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 243 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  N-PSDB; AAV36236.
                                                                                                                                                                                                                                                                                                                                                                     WO9818825-A1
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                                                                                                        08-SEP-1998
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                                                                AAW60769;
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AAW60769
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                                                                                                                                                                                          dermatological; immunosuppressive; antiinflammatory; autoimmune response; SLE; systemic lupus erythematosus; diagnosis; treatment; autoantigen; heavy chain variable region; VH; complementarity determining region; CDR.
                                                                                                                          Murine ant	ilde{M}_{f H}-p53 monoclonal antibody PAb-421 heavy chain variable region.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The patent discloses a method for the treatment of systemic lupus erythematosus (SLE) by down-regulating the autoimmune response to the C-terminal DNA-binding domain of p53 protein by an active compound. The present sequence is a heavy chain variable region of monoclonal antibody PAb-421 which is specific to the C-terminal DNA-binding domain of murine p53 protein. PAb-421 antibody and peptides based on complementatity determining regions of light and heavy chain variable regions of the antibody, are examples of active compounds useful in the diagnosis, prevention and treatment of SLE in humans.
                                                                                                                                                                      Murine; p59 protein; monoclonal antibody; PAb-421; DNA-binding domain;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Treatment of systemic lupus erythematosus by down-regulating the ustucinmine response to the C-terminal DNA-binding domain of the p53 proteinthy an active compound comprising of antibodies to p53 or fragments of p53 -
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                                                                                                                                                                                                                                                                                                                                                                                                                               /label= CDR
/note= "Complementarity determining region"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note= "Complementarity determining region"
                                                                                                                                                                                                                                                                                                                                                                                         "Complementarity determining region"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 554.5; DB 21; DB 21; Pred. No. 5.8e-41;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Herkel J;
                                                                                                                                                                                                                                                                                                                           Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Erez-Alon N,
AAY70787 standard; Protein; 116 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 78; Fig 9; 87pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (YEDA ) NEDA RES & DEV CO LTD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   87.9%;
88.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       99..105
/label- CDR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                99WO-US24443.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          98US-0104816.
                                                                                                                                                                                                                                                                                                                                                                   /label- CDR
                                                                                    (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                              'note=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Rotter V,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 2000-339512/29
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WO200023082-A1.
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19-OCT-1999; 19-0CT-1998;

Cohen IR,

27-APR-2000

cell containing

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A.
                                        AAW89173 standard; peptide; 112
                                                               25-MAR-1999 (first entry)
                                         UXXXI
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Gaps

1;

DB 19; Length 243; Indels 9

Query Match Best Local S Matches 104

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RESULT 13

Sequence

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The present sequence represents the heavy chain variable region for monoclonal antibody (MAb) 14G11, which immunoreacts with a lead cation. The sequence was derived from RNA isolated from mouse hybridona cells. The protein can be used for binding heavy metals, such as lead cations. It can be used for detecting, removing, adding or neutralising the heavy metals in biological and inanimate systems. It can be used in e.g. aqueous liquid systems, in biological or environmental systems or in such compositions as perfames, cosmetics, pharmaceuticals, health care products, skin treatment products, pesticides, herbicides, solvents used in the production of semi-conductor and integrated circuit components and production materials for electronic components. The products can provide for applications involving minute amounts of specific heavy metals.
                                                                                                                        Monoclonal antibody; Fd fragment; lead cation; perfume; cosmetic; pharmaceutical; health care; skin treatment; pesticide; herbicide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DNA encoding heavy metal binding polypeptide sequences - used for detecting, removing, adding or neutralising heavy metals, such as
                                                            Lead binding MAb 14G11 heavy chain variable region.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 12; Page 75; 125pp; English.
22-AUG-1997 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (BION-) BIONEBRASKA INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 1997-043140/04.
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                                                                                                                                                                                                                                                          Mus musculus
                                                                                                                                                                                                 heavy metal.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        anti-tumour imvencing describes one use of an immunose of the control of the cont
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The present invention describes the use of an immunogen (A) to induce
                                                                                   Anti-p53; monoclonal antibody 240; immunogen; anti-tumour; immunity; immune response; tumour associated antigen; metastatic cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Use of a monoclonal antibody to a tumour-associated antigen - to induce anti-tumour immunity or elicit an increased immune response
                          Anti-p53 monoclonal antibody 421 variable heavy chain sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 20; Length 112;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ruiz PJ;
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88.5%; Pred. No. 2.1e-39;
iive 6; Mismatches 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Erez-Alon N, Herkel J, Rotter V,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Example 3; Fig 3; 47pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (YEDA ) YEDA RES & DEV CO LTD.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            97IL-0121041.
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                                                                                                                                                                                                                                                                                 W09856416-A1
                                                                                                                                                                                                                                                                                                                                                                                                                09-JUN-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Wolkowicz R;
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Synthetic.
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NAMES OF STREET OF STREET

Wylie DE;

Murray PJ,

96WO-US09258 95US-0541373 95US-0462798

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                                                                   Gaps
                                                                                                     1 QVKLQQSGAELVGSGASVKLSCTTSGFNIKDFYMHWVKQRPEQGLEWIGWIDPENGDSDY 60
                                                                                                                       1 EVOLQOSGABLVRSGASVKLSCTASGFNIKDYYMHWVKQRPEQGLEWIGWIDPENGDTEY 60
                                                                                                                                                                                         61 APKFQGKATMTADSSSNTAYLQLSSLTSEDTAVYYCNAY-YGDYEGYWGQGTTVTVSS 117
                                                                   ÷
                                 DB 18; Length 118;
                                Score 536.5; DB 18; Length
Pred. No. 2.2e-39;
7; Mismatches 9; Indels
                                 85.0%;
                                                                Matches 101; Conservative
                                                   Sest Local Similarity
118 AA;
   Sequence
                                 Query Match
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Gaps

1;

6; Indels

Best_Local Similarity 88.5 Matches 100; Conservative

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4 LQQSGAELVGSGASVKLSCTTSGFNIKDFYMHWVKQRPEQGLEWIGWIDPENGDSDYAPK 63

FQGKATMTADSSSNTAYLQLSSLTSEDTAVYYCNAYYGDYEGYWGQGTTVTVS 116

64 19 AAW01586 standard; Protein; 118 AA

RESULT 15 AAW01586 AAW01586;

ex x x

Search completed: December 23, 2002, 07:25:10 Job time : 63.8081 secs

• .

Mouse ganglioside KM-796 and KM-750 Anti-GM2 light cha Antibody chain use

Anti-p53 common mu Anti-p53 common mu Amino acid sequenc Murine VL kappa gr Partial amino acid

AAG63987 AAR21294

AAW73223 AAB85455

AAW11508

AAU81278 AAU80040

AAU97935 AAW03182

AAW82744

Chimeric anti-CEA Murine VL kappa gr Anti-CEA antibody

AAR21290

Anti-EGFR antibody

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(without alignments)
248.221 Million cell updates/sec
                                  December 23, 2002, 07:16:08; Search time 56.9031 Seconds
                                                    US-09-865-198-23
549
1 DIELTQSPAIMSASPGEKVT......CQQRSSXPFTFGSGTKLEIK 106
     GenCore version 5.1.3
Copyright (c) 1993 - 2002 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries
                         protein search, using sw model
                                                                        BLOSUM62
Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 2000000000
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Sequence:
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RESULT 1 **AAE13144**

A. Selbs24/geneseq/geneseqp-embl/AA1980.DAT:*

SIDS2/gcgdata/geneseq/geneseqp-embl/AA1981.DAT:*

SIDS2/gcgdata/geneseqp-embl/AA1981.DAT:*

SIDS2/gcgdata/geneseqp-embl/AA1991.DAT:*

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SIDS2/gcgdata/geneseqgp-embl/AA1992.DAT:*

ALIGNMENTS

Guy's laati-stre
Anti-Tac light cha
Protein SEQ ID NO:
Murine anti-Tac an
Murine anti-Tac an
Protein encoded by
Anti-TAC SFV prote
Anti-TAC SFV prote
Anti-Tac(FV)-PE40
Anti-Tac(FV)-PE40
Anti-Tac(FV)-PE40
Anti-Tac(FV)-PE40
Mouse monoclonal a

AAB69651 AAP93150 AAB12563

A_Geneseq_101002:*

Database

AAB69641

AAB36826 AAW37132 AAW95462 AAY87477

Bispecific single Bispecific single Fusion protein pIC Fusion protein (80 Murine trkC antibo scFv rearranged ca ScFv-rearranged ca

MFE-23 antibody. Single chain anti-H22-anti-CEA antib

(IMCL-) IMCLONE SYSTEMS INC. (CORR) CORNELL RES FOUND INC.

Humanised antibody Antigen-binding pr Variable light cha VEGF antagonist an Antigen-binding pr Chimeric pIC11 lig VEGF antagonist an Antigen-binding pr Antigen-binding pr SNV-eny leader/hum

AAU7418 AAY97236 AAB82710 AAU7413 AAB13146 AAB82702 AAB82702 AAU74420 AAU74419

106 106 108 108 108 125 125 238 240

100.0 100.0 100.0 100.0 100.0 100.0 100.0

4207800

Description

AAE13144

DB

Query Match Length

Score

Result Š Witte L, Rafii S;

WPI; 2001-662942/76. N-PSDB; AAD21670.

Vascular endothelial growth factor receptor; VEGFR; antagonist; tumour; cytostatic; light chain; myelocytic leukaemia; lymphocytic; erythrocytic; monocytic; multiple myeloma; lymphoid cell; Hodgkin's disease; mouse; Humanised antibody light chain fragment. AAE13144 standard; Protein; 106 AA. 30-MAR-2001; 2001WO-US10504 31-MAR-2000; 2000US-0540770 28-JAN-2002 (first entry) Chimeric - Homo sapiens. Chimeric - Mus sp. human; chimeric. WO200174296-A2 11-0CT-2001. AAE13144;

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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                                                                                                               The invention relates to a method for inhibiting the growth of non-solid tumour cells that are stimulated by a ligand of vascular endothelial growth factor receptor (VEGFR) in mammals particularly humans. The method involves greating the mammals with humanised VEGFR monoclonal antibodies (antagonists). Humanised monoclonal antibody comprises humanised mouse variable fegion joined to human constant region, where the humanised mouse variable region contains mouse complementarily determining region (CDR) grafted into human variable region. The method is useful for treating jeukaemias such as acute or chronic myelocytic leukaemia, acute or chronic lymphocytic leukaemia, erythrocytic or monocytic leukaemia, multiple jelomas and lymphoid cells, particularly those related to non-Rodgkin's and Hodgkin's alsease. The present sequence is humanised antibody light chain fragment used in the exemplification of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New bispecific immunoglobulin-like antigen-binding protein for reducing tumour growth and for inhibiting anglogenesis, comprises a complex of two polypeptides and two second polypeptides
              Inhibiting growth of non-solid tumor cells useful to treat bone marrow
                                  tumors such as leukemias or multiple myeloma comprises treatment with
an antagonist of a vascular endothelial growth factor receptor –
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 DIELIOSPAIMSASPGEKVTITCSASSSVSYMHWFQQKPGTSPKLWIYSTSNLASGVPAR 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Antigem, binding protein; antibody light chain variable domain; cytostatic; anglogenesis inhibitor; tumour; leukaemia; antibody; vascular endothelial growth factor receptor; VEGF; cell proliferation inhibitor.
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                                                                                                                                                                                                                                                                                                                                                                                                                         Length 106;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FSGSGSGTSYSLTISRMEAEDAATYYCQQRSSYPFTFGSGTKLEIK 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               61 FSGSGGTSYSLTISRMEAEDAATYXCQQRSSYPFTFGSGTKLEIK 106
                                                                                                                                                                                                                                                                                                                                                                                                                     Score 549; DB 22;
Pred. No. 5.7e-32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                        0
                                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAU74419 standard; peptide; 106 AA.
                                                                                  Claim 8; Rage 16; 68pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                     100.0%;
100.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (IMCL.) IMCLONE SYSTEMS INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                        Best Local Similarity 100. Matches 106, Conservative
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                                                                                                                                                                                                                                                                                                                                                                                    Sequence 106 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WO200190192-A2.
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                                                                                                                                                                                                                                                                                                                                                     invention
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arte standy associated in an immunogious in the complex. Fi mas an antigen-binding site located to the N terminus of immunoglobulin (Ig) light chain constant domain (CL domain), and P2 has an antigen-binding site located to the N terminus of the CH1 domain. (I) is useful for: neutralising the activation of a vascular endothelial growth factor (VEGF) receptor; reducing tumour growth; inhibiting vegenesis; creducing endothelial coll proliferation; inhibiting veger induced migration of human leukaemia cells; blocking interaction of a protein and its ligand; promoting interactions between immune cells and target cells; and in vivo and in vitor for investigative, diagnostic or treatment methods. The design of (I) provides for efficient production so that substantially all of the antigen-binding proteins produced are assembled in tetrameric form. The heavy chain constant domains which constitute the Fc region (e.g., CH2 and CH3 for an IgG molecule) of a natural continuement for provide other antibody functions can be present. There is no requirement for processing in vitro to obtain the complete product. This sequence represents a light chain variable domain (VH) incorporated incorporated function of the invention.

The method of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
                                                                                                                                The invention describes an antigen-binding protein (I) comprising a complex of two polypeptides (P1) and two second polypeptides (P2) which are stably associated in an immunoglobulin like complex. P1 has an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
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Claim 61; Page 61; 64pp; English.
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                                                       Novel immunoglobulin molecules binding kinase insert domain-containing receptor with the same affinity as vascular endothelial growth factor,
                                                                                                                                     Again in containing receptor (KDR) with a comparable affinity to human vascular endothelial growth factor (VEGF). The antibodies neutralise KDR activation. The immunoglobulin may be a multivatent single chain antibody, a monovatent single chain antibody, a diabody, a triabody, a humanised antibody or a chimerised antibody, a diabody, a triabody a humanised antibody or a chimerised antibody. The immunoglobulin molecules bind specifically to an extracellular domain of the KDR receptor with the same affinity as VEGF. Overexpression of VEGF has been implicated in a number of human tumour cell lines including giloblastoma multiforme, associated Karposi's sarcoma. The antibodies therefore have
                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  IMC-1C11; chimeric antibody; mouse; human; antagonist; VEGF; vascular endothelial growth factor; angiogenesis; antiangiogenic; antitumour; neoplasm; collagen-vascular disease; autoimmune disease; tumour; breast carcinoma; lung carcinoma; prostate carcinoma; colon carcinoma; ovarian carcinoma; neuroblastoma; glioblastoma multiforme; melanoma; therapy; light chain.
                                                                                                                      New immunoglobulin molecules are described that bind kinase insert
                                                                                                                                                                                                                                                                                                                                                                                           1 DIELTQSPAIMSASPGEKVTITCSASSSVSYMHWFQQKPGTSPKLWIYSTSNLASGVPAR 60
                                                                                                                                                                                                                                                                                                                                                                                                         applications in treating these conditions. This sequence encodes a preferred heavy chain complementary determining region of the
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              VEGF antagonist antibody IMC-1C11 light chain variable region.
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                                                                                                                                                                                                                                                                                                                                              Length 108;
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100.0%; Pred. No. 5.8e-32;
ive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Location/Qualifiers
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                                                                                                                                                                                                                                                                                                 .mmunoglobulins of the invention.
                                                                                                       Claim 4; Page 51; 55pp; English.
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/label= CDR-L1
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                                                                               used to reduce tumour growth
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                                                                                                                                                                                                                                                                                                                                                                     Matches 106; Conservative
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Chimeric - Homo sapiens.
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                      WPI; 2000-505966/45.
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                                  N-PSDB; AAA53768
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The present sequence is that of the light chain variable region of IMC-1C11, a mouse-human chimeric antibody that has vascular endothelial growth factor (VECF) antagonist activity. The antibody, or a fragment of it, can be used as an anti-angiogenic molecule, together with a chemotherapeutic acid, for the treatment of an angiogenic dependent condition in a mammal, especially a human. The invention relates generally to a method of treating or controlling an angiogenic dependent condition by administering an anti-angiogenic molecule and a chemotherapeutic agent, to produce a regression or arrest of the condition while minimising or preventing significant toxicity of the chemotherapeutic agent.

The anti-angiogenic molecule inhibits or blocks the action of a vascular endothelium survival factor such as VEGF or its receptor, and is especially IMC-1C11. Conditions that can be treated include a neoplasm, a collagen-vascular disease or an autoimmune disease, especially a solid tumour, including breast carcinoma, lung services and action of a specially a solid tumour, including breast carcinoma.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Treating or controlling an angiogenic dependent condition (e.g. neoplasm, collagen-vascular or autoimmune disease) in mammal by administering a combination of an antiangiogenic molecule and a
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Disclosure; Page 38-39; 42pp; English.
                                                                                                                                                                                              (SUNN-) SUNNYBROOK HEALTH SCI CENT.
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                                                                          28-JAN-2000; 2000US-0178791.
31-MAR-2000; 2000US-0539692.
29-JAN-2001; 2001WO-US02839.
                                                                                                                                                                                                                                    (IMCL-) IMCLONE SYSTEMS INC.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          chemotherapeutic agent
                                                                                                                                                                                                                                                                                                                                                                                         WPI; 2001-514531/56.
N-PSDB; AAH26406.
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endothelial growth factor receptor; VEGFR; antagonist; tumour;

/note= "Mature chimeric plCll light chain fragment"

43..52 /label= CDR_L1 68..74 /label= CDR_L2

107..115 /label= CDR_L3

1..19
/label= Leader_peptide Location/Qualifiers

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cytostatic; light chain; myelocytic leukaemia; lymphocytic; erythrocytic; monocytic; multiple myeloma; lymphoid cell; Hodgkin's disease; chimeric;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Inhibiting growth of non-solid tumor cells useful to treat bone marrow tumors such as leukemias or multiple myeloma comprises treatment with an antagonist of a vascular endothelial growth factor receptor -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Example 3; Fig 11; 68pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (IMCL-) IMCLONE SYSTEMS INC. (CORR ) CORNELL RES FOUND INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         30-MAR-2001; 2001WO-US10504.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           31-MAR-2000; 2000US-0540770.
                                                                                                 Chimeric - Homo sapiens
Chimeric - Unidentified
                                                      human; plC11 vector.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 2001-662942/76.
N-PSDB; AAD21683.
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                                                                                                                                                                               Peptide
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The invention describes an antigen-binding protein (I) comprising a complex of two polypeptides (P1) and two second polypeptides (P2) which are stably associated in an immunoglobulin like complex. Pl has an antigen-binding site located to the N terminus of immunoglobulin (Ig) in the fail constant domain (CL domain), and P2 has an antigen-binding site located to the N terminus of the CH1 domain. (I) is useful for: neutraliging the activation of a vascular endothelial growth factor (VECF) receptor; reducing tumour growth; inhibiting vEGF induced migration of human leutance cells; blocking interaction of a protein and its lighton promoting interactions between immune cells and target cells; and in vivo and in vitro for investigative, diagnostic or treatment comethods. The design of (I) provides for efficient production so that substantially all of the antigen-binding proteins produced are assembled in the desired configuration. (I) is bivalent and bispecific, homogeneous and in tetrament form. The heavy chain constant domains which constitute the region (e.g., CR2 and CR3 for an IgG molecules) of a natural cantibody and which provide other antibody functions can be present. There is no requirement for processing in vitro to obtain the complete product. This sequence represents a light chain variable domain (VH) incorporated into the method of the invention.
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                                                                                                                                                                                                                                                                                                                                                                 New bispečific immunoglobulin-like antigen-binding protein for reducing tumour gröwth and for inhibiting angiogenesis, comprises a complex of two polypěptides and two second polypeptides
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 DİELIQSPAIMSASPGEKVTITCSASSSVSYMHWFQQKPGTSPKLMIYSTSNLASGVPAR 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 57; Page 57; 64pp; English.
                                                                                                                                         24-MAY-2001; 2001WO-US16924
                                                                                                                                                                                 24-MAY-2000; 2000US-206749P.
                                                                                                                                                                                                                         (IMCL-) IMCLONE SYSTEMS INC.
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Matches 106; Conservative
                                                                                                                                                                                                                                                                                                        WPI; 2002-106189/14.
N-PSDB; AAS20284.
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                                                         WO200190192-A2.
                                                                                                 29-NOV-2001.
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                     Mus sp.
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The invention relates to a method for inhibiting the growth of non-solid tumour cells that are stimulated by a ligand of vaccular endothelial growth factor receptor (VESFR) in mammals particularly humans. The method involves treating the mammals with humanised VESFR monoclonal antibodies (antagonists). Humanised monoclonal antibody comprises humanised mouse variable region joined to human constant region, where the humanised mouse variable region contains mouse complementarity determining region (CDR) grafted into human variable region. The method is useful for treating leukaemias such as acute or chronic myelocytic leukaemia, acute or chronic lymphocytic leukaemia, erythrocytic or monocytic leukaemia, multiphe myelomas and lymphoid cells, particularly those related to non-Hodgkin's and Hodgkin's disease. The present sequence is chimeric picil light chain fragment which is used for the construction of chimeric picil light chain (VL) and human kappa light chain contains cloned ö 1 DIELTQSPAIMSASPGEKVTITCSASSSVSYMHWFQQKPGTSPKLWIYSTSNLASGVPAR 60 20 DIELTQSPAIMSASPGEKVTITCSASSSVSYMHWFQQKPGTSPKLWIYSTSNLASGVPAR 79 ; Length 125; Indels 100.0%; Score 549; DB 22; 100.0%; Pred. No. 6.6e-32; ive 0; Mismatches 0; Best Local Similarity 100. Matches 106; Conservative 125 AA; Sequence Query Match g ò ò

> 61 FSGSGSGTSYSLTISRMEAEDAATYYCQQRSSYPFTFGSGTKLEIK 106

61

οy g

δ g Chimeric plC11 light chain fragment

28-JAN-2002 (first entry)

XEXEXEX

AAE13146;

AAE13146 standard; Protein; 125 AA.

AAE13146 RESULT

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The present sequence is that of the light chain variable region of IMC-1C11, a mouse-human chimeric antibody that has vascular endothelial growth factor (VEGF) antagonist activity. The antibody, or a fragment of it, can be used as an anti-angiogenic molecule, together with a chemotherapeutic acid, for the treatment of an angiogenic dependent condition in a mammal, especially a human. The invention relates generally to a method of treating or controlling an angiogenic dependent condition by administering an anti-angiogenic molecule and a chemotherapeutic agent, to produce a crarest of the condition while minimising or preventing significant toxicity of the chemotherapeutic agent.

The anti-angiogenic molecule inhibits or blocks the action of a vascular endothelium survival factor such as VEGF or its receptor,
                                                                                                                                                       IMC-1C11; chimeric antibody; mouse; human; antagonist; VEGF; vascular endothelial growth factor; angiogenesis; antianglogenic; antitumour; neoplasm; collagen-vascular disease; autoimmune disease; tumour: breast carcinoma; lung carcinoma; prostate carcinoma; colon carcinoma; ovarian carcinoma; neuroblastoma; glioblastoma multiforme; melanoma; therapy; light chain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Treating or controlling an angiogenic dependent condition (e.g. neoplasm, collagen-vascular or autoimmune disease) in mammal by administering a combination of an antiangiogenic molecule and a
                                                                                                                            VEGF antagonist antibody IMC-1C11 light chain variable region.
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                                                                                                                                                                                                                                                                                                                                                                                                                                        'note= "complementarity determining region 1"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    107..115
/label= CDR-L3
/note= "complementarity determining region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note= "complementarity determining region 107..115
                                                                                                                                                                                                                                                                                                                                                        'label= Signal_peptide
                                                                                                                                                                                                                                                                                                                                                                                         /label= Mature_protein
                                                                                                                                                                                                                                                                                                                        Location/Qualifiers
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                              AAB82702 standard; Protein; 125 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                       /label= CDR-L1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /label= CDR-L2
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                                                                                           (first entry)
                                                                                                                                                                                                                                                                         Chimeric - Mus sp.
Chimeric - Homo sapiens.
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                                                                                           15-OCT-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Kerbel R;
                                                             AAB82702;
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RESULT 7
                AAB82702
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                                                                                                                                                                                                                                                                                                                                                                                                                                        Antigen-binding protein; single chain variable fragment; svFv; antigen; cytostatic; andiogenesis inhibitor; tumour; leukaemia; antibody; vascular endothelial growth factor receptor; VEGF; cell proliferation inhibitor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note= "15 amino acid linker joins the VH and VL regions of the single chain variable fragment protein. Encoded by AAS20285"
                                                                                                                                                   Gaps
                                                                                                                                                                               9
                                                                                                                                                                                           and is especially IMC-1C11. Conditions that can be treated include a neoplasm, a collagen-vascular disease or an autoimmune disease, especially a solid tumour, including breast carcinoma, lung carcinoma, prostate carcinoma, cancinoma, problastoma, central nervous system tumour, neuroblastoma carcinoma, meuroblastoma multiforme or melanoma (all claimed).
                                                                                                                                                                                                                                                                                                                                                                                                                 Antigen-binding protein, single chain variable fragment version #2.
                                                                                                                                                                               1 DIELTQSPAIMSASPGEKVTITCSASSSVSYMHWFQQKPGTSPKLWIYSTSNLASGVPAR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note= "Heavy chain variable domain. Specifically claimed in claim 61"
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                                                                                                                       Length 125;
                                                                                                                                                   Indels
                                                                                                                                                                                                                                   FSGSGSGTSYSLTISRMEAEDAATYYCQQRSSYPFTFGSGTKLEIK 106
                                                                                                                                                                                                                                                100.0%; Score 549; DB 22;
100.0%; Pred. No. 6.6e-32;
tive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     location/Qualifiers
                                                                                                                                                                                                                                                                                                                                 AAU74420 standard; Protein; 238 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 24-MAY-2001; 2001WO-US16924.
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'label= VH
                                                                                                                                                                                                                                                                                                                                                                                    26-MAR-2002 (first entry)
                                                                                                                                                   Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 2002-106189/14.
                                                                                                                                       Best Local Similarity
Matches 106; Conserv
                                                                                                125 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WO200190192-A2
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Synthetic.
                                                                                                                                                                                                                                                                                                                                                            AAU74420;
                                                                                                Sequence
                                                                                                                          Query Match
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Region
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The invention describes an antigen-binding process (12) comprising a complex of two polypeptides (P1) and two second polypeptides (P2) which are stably associated in an immunoglobulin like complex. Pl has an antigen-binding site located to the N terminus of immunoglobulin (Ig) is useful for: Ight chain constant domain (CL domain), and P2 has an antigen-binding cle site located to the N terminus of the CH1 domain. (I) is useful for: CC will be activation of a vascular endothelial growth factor (VEGF) receptor; reducing tumour growth; inhibiting anglogenesis; reducing endothelial cell proliferation; inhibiting vEGF induced in sugration of human leukaemia cells; blocking interaction of a protein and its ligand, promoting interactions between immune cells and target cells; and in vivo for investigative, diagnostic or treatment its ligand, promoting interactions between immune cells and target cells; and in vivo and in vitro for investigative, diagnostic or treatment substantially all of the antigen-binding produced are assembled in the design of (I) provides for efficient production so that substantially all of the antigen-binding proteins produced are assembled in the design of (I) provide other antibody functions can be present. There the Fc region (e.g., CH2 and CH3 for an IgG molecule) of a natural antibody and which provide other antibody functions can be present. There is the amino acid sequence of a single chain variable fragment (sefv), an engineered protein containing a variable light and variable heavy domain one polypeptide, described in the method of the
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Antigen, binding protein; single chain variable fragment; scFv; antigen; cytostéptic, angigenesis inhibitor; tumour; leukaemia; antibody; vasculár endothelial growth factor receptor; VEGF; cell přoliferation inhibitor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 DIELTQSPAIMSASPGEKVTITCSASSSVSYMHWFQQKPGTSPKLWIYSTSNLASGVPAR 60
                                     The invention describes an antigen-binding protein (I) comprising a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Antigen-binding protein, single chain variable fragment version #1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note= "Heavy chain variable domain. Specifically claimed in claim 57"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        100.0%; Score 549; DB 23; Length 238;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   61 FSGSGSSTSYSLTISRMEAEDAATYYCQQRSSYPFTFGSGTKLEIK 106
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pred. No. 1.2e-31;
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Page 62-63; 64pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             100.08;
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/label= VH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /label- VL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches 10g; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     .132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         133..240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 238 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               26-MAR-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mus sp.
Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAU74419
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 9
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The invention describes an antigen-binding protein (I) comprising a complex of two polypeptides (P1) and two second polypeptides (P2) which are stably associated in an immunoglobulin like complex. Pl has an antigen-binding site located to the N terminus of immunoglobulin (Ig) (Ight chain constant domain (CL domain), and P2 has an antigen-binding site located to the N terminus of the CH1 domain. (I) is useful for: neutralising the activation of a vascular endothelial growth factor (VEGF) receptor; reducing tumour growth; inhibiting angiogenesis, reducing endothelial cell proliferation; inhibiting VEGF induced (Is Igand; promoting interactions between immune cells and target cells; and in vivo and in viro for investigative, diagnostic or treatment can in vivo and in viro for investigative, diagnostic or treatment constantially all of the antigen-binding proteins production so that substantially all of the antigen-binding proteins production so that csubstantially all of the antigen-binding proteins production so that the desired configuration. (I) is bivalent and bispecific, homogeneous of in the desired configuration. (I) is bivalent and bispecific, nonstitute the FC region (e.g., CH2 and CH3 for an IgG molecule) of a natural contained which provide other antibody functions can be present. There is no requirement for processing in vitro to obtain variable fragment configuration containing a variable light and variable heavy chain on ne polypeptide, described in the method of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New bispecific immunoglobulin-like antigen-binding protein for reducing tumour growth and for inhibiting angiogenesis, comprises a complex of two polypeptides and two second polypeptides .
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      celi-targéting vector; antiviral; cytostatic; immunostimulant; AIDS; gene therapy; immunization; diagnosis; T cell-associated disease; SCID;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 DIELTQSPAIMSASPGEKVTITCSASSSVSYMHWFQQKPGTSPKLWIYSTSNLASGVPAR 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 240;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              61 FSGSGSGTSYSLTISRMEAEDAATYYCQQRSSYPFTFGSGTKLEIK 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    100.0%; Score 549; DB 23;
100.0%; Pred. No. 1.2e-31;
1ve 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SNV-env leader/human 7B2-scFv fusion construct.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAB70842 standard; Protein; 330 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 63; Page 62; 64pp; English.
                                                                                                                                                                                                                                           24-MAY-2000; 2000US-206749P
                                                                                                                                                                  24-MAY-2001; 2001WO-US16924
                                                                                                                                                                                                                                                                                                                                (IMCL-) IMCLONE SYSTEMS INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  25-JUN-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 100.0
Matches 106; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 2002-106189/14.
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WO200190192-A2.
                                                                                 29-NOV-2001
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Anti-EGFR antibody light chain variable region (Clone L2 8C).
           02-JUL-1996 (first entry)
                                                                                                                                                          Region
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                                                                                                                                                                                  DNA sequence (1) encoding a single-chain variable antibody fragment (scrv). The products of the invention have antiviral, cytostatic and immunostimulant activity and can be used in gene therapy, immunization and diagnosis particularly of real-associated diseases, specifically acquired immune deficiency syndrome (AIDS), severe combined immune deficiency syndrome (AIDS), severe combined immune of the CDA receptor, with high selectivity, 4-5 fold selectivity over human B cells, and 1000 fold selectivity, ver other human cells. A vector fragment, fully defined in the specification. It was used to transform but costeograrcoma cells susceptible to spleen necrosis virus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (SNV) cells, C0166 (human T lymphocyte) cells, and HeLa (human cervical carcinoma) cells. After 48 hours, the cells were stained with X-gal to determine transformation. The viral titer (infectious units/ml) was over 1 million for D17, 1 million for C0166 but less than 100 for HeLa, showing the high selectivity for human T cells. This sequence represents the SNV-env leader/human 7B2-scFv fusion construct used in the construction of novel cell targeting vectors described in the invention.
acquired immune deficiency syndrome; severe combined immune deficiency;
                                                                                                                                                                                                                                                                                                                                                                          This invention describes a novel cell-targeting vector (A) containing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                      Cell-targeting vector selective for T lymphocytes, useful in gene therapy of e.g. acquired immune deficiency syndrome, encodes a single-chain variable antibody fragment -
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    100.0%; Score 549; DB 22;
100.0%; Pred. No. 1.6e-31;
Live 0; Mismatches 0;
                                                                                                                                                                                                                         BUND ) BUNDESREPUBLIK DEUT PAUL-EHRLICH-INST
                                                              Location/Qualifiers
1.45
/label= SNV-env_leader
46..330
/label= 7B2-scFv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAR79884 standard; Protein; 108 AA
          cell lymphoma; fusion construct
                              Chimeric - Homo sapiens.
Chimeric - Spleen necrosis virus.
                                                                                                                                                                                                                                                                                                                                                 Claim 1; Fig 3; 18pp; German.
                                                                                                                                                                                                                                                 Engelstaedter M;
                                                                                                                                                                              99DE-1046142
                                                                                                                                                                                                    99DE-1046142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 100.0
Matches 106; Conservative
                                                                                                                                                                                                                                                                      WPI; 2001-246140/26.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      330 AA;
                                                                                                                                                                                                                                                                                 N-PSDB; AAF61511
                                                                                                                                  DE19946142-A1.
                                                                                                                                                                                                   27-SEP-1999;
                                                                                                                                                                                                                                                 Cichutek K,
                                                                                                                                                         29-MAR-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAR79884
                                                                           Protein
                                                                                                  Protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         241
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셤
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Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 DIELTQSPAIMSASPGEKVTITCSASSSVSYMHWFQQKPGTSPKLWIYSTSNLASGVPAR 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DIELTQSPAIMSASPGEKVTITCSASSSVSYMHWFQQKPGTSPKLWIYSTSNLASGVPAR 60
Single chain antibody, antibody, epidermal growth factor receptor; EGFR; tumour; cancer; glioma; melanoma; carcinoma; diagnosis; assessment; phage antibody library.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Anti-EGFR antibodies and single chain FV antibody fragments -obtained from phage-antibody libraries, useful for diagnosis and therapy of tumours
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Guessow D;
Rosell E;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 534; DB 16;
Pred. No. 6.6e-31;
                                                                                                                                                                                                                                                                                                                                                                                                                          97..108
/label= Framework region 4.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ansell KH, Bendig MM, Blasco F, cough AC, Mitjans F, Piulats J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mismatches
                                                                                                                                                                               'label= Framework region
                                                                                                                                                                                                                                                                      region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Disclosure; Figure 1A; 93pp; English.
                                                                                                                                   Location/Qualifiers
                                                                                                                                                                                                                                           34..48
/label= Framework r.
49..55
/label= CDR2.
                                                                                                                                                                                                                                                                                                                                                            Framework
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             using the phage antibody library.
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ش
                                                                                                                                                                                                                                                                                                                                                                                88..96
/label= CDR3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     97.3%;
96.2%;
                                                                                                                                                                                                   24..33
/label= CDR1
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94EP-0104160.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    95WO-EP00978
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                                                                                                                                                                                                                                                                                                                                       56..87
/label=
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Adan J, Ansell KH
Kettleborough AC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         108 AA;
                                                                                            Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              02-DEC-1994;
17-MAR-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             W09525167-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    16-MAR-1995;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence
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specific binding pairs; replicable genetic display package.
                                         Synthetic.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This sequence is the light chain variable region of the antibody of the invehicutor. The antibody is an anti-CEA (carcinoembryonic antigen) antibody (806.077 Ab). Host cells or transgenic organisms transformed with DNA encoding the antibody, are used to make the antibody or conjugate. The conjugate is used in a medicament suitable for intravenous administration. The conjugate can be used for cancer therapy, selectively killing tumour cells. The antibody can be used for in vivo or in vitro
                                                                                                                                                                                                Anti-CEA antibody; carcinoembryonic antigen; 806.077 Ab; cancer therapy; cancer diagnosis; complementarity determining region; light chain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        23 DĮĘLIOSPAIMSASPGEKVTITCSASSSVTYMHWFQQKPGTSPKLMIYSTSNLASGVPAR 82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 DIELTQSPAIMSASPGEKVTITCSASSSVSYMHWFQQKPGTSPKLWIYSTSNLASGVPAR 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Fd; bacteriophage; gene III; filamentous; phagemid; capsid; coat; pilus; 93p; binding; adsorption; gene VIII; diverse repertoire;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               noembryonic antigen antibody 806.077 Ab - used for and therapy of cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 235;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Murine VL kappa group VI chain "e", specific for phOx.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 534; DB 18;
Pred. No. 1.3e-30;
                                                                                                                                                          Chimeric anti-CEA antibody 806.077 light chain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         9; Page 100-101; 208pp; English.
                                       AAW41392 standard; Protein; 235 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAR21290 standard; Protein; 108 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Emery SC;
                                                                                                                                                                                                                                                                                                                                                                                                      97WO-GB01165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 96GB-0009405
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                                                                                                                       (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          21-MAY-1992 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity 96.2
Matches 102; Conservative
                                                                                                                                                                                                                                                            Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Edge MD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 1997-558987/51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       diagnosts of cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (ZENE ) ZENECA LID.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              235 AA;
                                                                                                                                                                                                                                                            Chimeric - Homo sa
Chimeric - Mus sp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAV17288
                                                                                                                                                                                                                                                                                                                       409742329 A1
                                                                                                                                                                                                                                                                                                                                                                                                    9-APR-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                            14-FEB-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 04 - MAY - 1996;
                                                                                                                  02-JUN-1998
                                                                                                                                                                                                                                                                                                                                                             13-NOV-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Anti-carci
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Copley CG,
                                                                               AAW41392
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Seguence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAR21290;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sxample
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           N-PSDB;
  RESULT 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAW41392
                                                                               NAME OF THE PROOF 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           용
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The VK sequence is one of seven (AAR21286-92) found to be expressed from a single chain FV library from an immunised mouse. The library reproduces a diverse reperfoire of antibody fragments specific for 2-phenyl-5-oxazolone (phox). It was prepd. using cDNA generated albumin. The VH and VL Kappa sequences were separately amplified by PCR (see AAQ23474-84) and ligated into fdCAT2 (see AAQ23463) for expression on the phage surface as fusions with gene III. The resulting line library of clones was diverse. Twenty three hapten binding clones were sequenced revealing eight different VH genes (A-H) (see AAR21264-71) in a variety of palrings with the seven different VK genes (a-g). Of the twenty three clones sequenced, four were of type "e", and were "ox-like" genes. (See Berek et al, Nature 316 412-418, 1985). They contain the DXGXX motif in CDR3, the central Colones were Vk-d combinations. The Kd of VH-B/VK-b for phox-GABA was 10 uM, one of the highest values found. This suggests that
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ex-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Hoogenboom HRJ, Griffiths AD;
Clackson TP, Chiswell DJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DIELTQSPAIMSASPGEKVTITCSASSSVSYMHWFQQKPGTSPKLWIYSTSNLASGVPAR 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          was 10 uM, one of the highest values found. This suggests that phage bearing scFv fragments having weak affinities can be selected with antigen, probably due to the avidity of the multiple antibody
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Producing members of specific binding pairs - by expression in recombinant host cells with a secreting replicable genetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 108;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         61 FSGSGSGTSYSLTISRMEAEDAATYYCQQRSSYPFTFGSGTKLEIK 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAR21260-307, 309-311; AAR22450, 565-581.
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Best Local Similarity 97.2%; Pred. No. 9.2e-31;
Matches 103; Conservative 1; Mismatches 2;
                                                                                                                                                                                                 D-X-G-X-X motif
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pope AR, Johnson KS,
Holliger KP, Marks JD,
Location/Qualifiers
24..33
/label- CDR1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Example 21; F1g 24; 209pp; English.
                                                                                                                                          88..96
/label= CDR3
/note=" D-X-G
                                                                                                                                                                                                                                                                                                                                                                                                                           91GB-0010549.
90GB-0015198.
90GB-0022845.
90GB-0024503.
                                                                                        49..55
/label= CDR2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (CAMB-) CAMBRIDGE ANTIBODY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (MEDI-) MED RES COUNCIL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Winter GP, Bonnert TP;
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10-JUL-1990;
19-OCT-1990;
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                                Binding-site
                                                                                  Binding-site
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Jackson RH,
                                                                                                                                               Binding-site
                                                                                                                                                                                                                                                                                                                                                                      10-JUL-1991;
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06-MAR-1991;
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Conservative
                                                                                                                                                          Hanai N, Nakamura K,
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                                                                                                                                                                                                                                                                                                                                         Similarity
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                                                   WO200123431-A1.
                                                                                                                  30-SEP-1999;
                                                                        05-APR-2001
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Matches 102:
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                                                                                                                                             Anti-CEA antibody; carcinoembryonic antigen; 806.077 Ab; cancer therapy; cancer diagnosis; complementarity determining region; light chain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 DIELTQSPAIMSASPGEKVTITCSASSSVTYMHWFQQKPGTSPKLWIYSTSNLASGVPAR 60
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                                                                                                                                                                                                                                                                                                                                                                      Anti-carcinoembryonic antigen antibody 806.077 Ab - used for diagnosis and therapy of cancer
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FSGSGSGTSYSLTISRMEAEDAATYYCQQRSSYPFTFGSGTKLEIK 106
                                                                                                                          Anti-CEA antibody 806.077 light chain variable region.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mouse ganglioside GM2 antibody-related protein #2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 532; DB 18;
Pred. No. 9.2e-31;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              4; Mismatches
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                                                            AAW41388 standard; Protein; 108 AA
                                                                                                                                                                                                                                                                                                                                                                                                    Claim 3; Page 196; 208pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAB83159 standard; protein; 107
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95.38;
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96GB-0009405.
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                                                                                                      (first entry)
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                                                                                                                                                                                                                                                                                                                                       WPI; 1997-558987/51.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 diagnosis of cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                              (ZENE ) ZENECA LTD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     108 AA;
                                                                                                                                                                                                                                                                                                                                                   N-PSDB; AAV17270
                                                                                                                                                                                                 W09742329-A1
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Matches 101;
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                                                                                                                                                                              Synthetic
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                                                                                 AAW41388;
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AAB83159
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Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The present invention relates to derivatives of an antibody against gandlisside GM2. The antibody may be a monoclonal antibody or its fragments. The antibody is combined with a radioactive isotope, protein or small drug in the treatment and diagnosis of cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2 IVLTQSPAIMSASPGEKVTITCSASSSVSYMHWFQQKPGTSPKLMIYSTSNLASGVPARF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Monoclonal antibodies against ganglioside GM2 combined with drugs, radioisotopes or proteins for treatment and diagnosis of cancer
Mouse; ganglioside; GM2; antibody; cytostatic; cytotoxic; cancer.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                96.4%; Score 529; DB 22; 97.1%; Pred. No. 1.5e-30; Live 1; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Search completed: December 23, 2002, 07:25:10 Job time : 56.9031 secs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 29; Page 69-70; 80pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                        Niwa R;
                                                                                                                                                                                                                                                                                                                                                                     (KYOW ) KYOWA HAKKO KOGYO KK.
                                                                                                                                                                                                                                                                                                               99JP-0278292.
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Sequence 21, Appl
Sequence 23, Appl
Sequence 22, Appl
Sequence 29, Appl
Sequence 2, Appli
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Sequence 7, Appli
Sequence 1, Appli
Sequence 3, Appli
Sequence 3, Appli
Sequence 6, Appli
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/cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep:*
/cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep:*
/cgn2_6/ptodata/2/pubpaa/USO6_NEW_PUB.pep:*
/cgn2_6/ptodata/2/pubpaa/USO7_NEW_PUB.pep:*
/cgn2_6/ptodata/2/pubpaa/USO7_PUBCOMB.pep:*
/cgn2_6/ptodata/2/pubpaa/USO7_PUBCOMB.pep:*
/cgn2_6/ptodata/2/pubpaa/USO9_NEW_PUB.pep:*
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/cgn2_6/ptodata/2/pubpaa/USO0_PUBCOMB.pep:*
GenCore version 5.1.3
Copyright (c) 1993 - 2002 Compugen Ltd
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US-09-865-198-21
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US-09-976-787-2
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Maximum Match 100%
Listing first 45 summaries
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Gapop 10.0 , Gapext 0.5
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Sequence 7, Apr
Sequence 9, Apr
Sequence 10, Apr
Sequence 11, Apr
Sequence 28, A
Sequence 27, A
Sequence 21, A
Sequence 31, A
Sequence 51, A
Sequence 75, Al
Sequence 75, Al
Sequence 85, Al
Sequence 89, Ar
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        Sequence Sequence
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100.0%; Pred. No. 1.1e-09;
ive 0; Mismatches 0;
US-09-974-052-11

US-09-974-052-12

US-09-974-051-1

US-09-974-051-4

US-09-974-051-4

US-09-974-051-5

US-09-974-051-7

US-09-974-051-7

US-09-974-051-10

US-09-974-051-11

US-09-974-051-11

US-09-974-051-11

US-09-974-051-12

US-09-974-051-11

US-09-974-051-11

US-09-974-051-11

US-09-974-051-11

US-09-910-059-31

US-09-910-059-31

US-09-910-059-35

US-09-910-059-75

US-09-910-059-91
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        Query Match
Best Local Similarity
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        SEQ ID NO 22
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Sequence 21, Application US/09865198
Patent NO. US20020103345A1
GENERAL INFORMATION:
APPLICANT: Zhu, Zhenping
TITLE OF INVENTION: Bispecific Immunoglobulin-Like Antigen Binding Proteins and Me
FILE REFERENCE: 11245/47102
CURRENT APPLICATION NUMBER: US/09/865,198

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US-09-974-052-7 US-09-974-052-8 US-09-974-052-9 US-09-974-052-10

Sequence 4, Al Sequence 5, Al Sequence 6, Al Sequence 7, Al Sequence 9, Al Sequence 9, Al

RESULT 2 US-09-865-198-21

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GENERAL INFORMATION:
APPLICANT: Zhu, Zhenping
TITLE OF INVENTION: Bispecific Immunoglobulin-Like Antigen Binding Proteins and Me
TITLE OF INVENTION: Production
FILE REFERENCE: 11245/47102
CURRENT APPLICATION NUMBER: US/09/865,198
CURRENT FILING DATE: 2001-05-24
PRIOR FILING DATE: 2000-05-24
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Sequence 29, Application US/09976787

Sequence 29, Application US/09976787

GENERAL INFORMATION:

APPLICANT: Zhu, Zhenping

APPLICANT: Witte, Larry

TITLE OF INVENTION: Antibodies Specific to KDR and Uses Thereof

FILE REFERENCE: 11245/46505

CURRENT APPLICATION NUMBER: US/09/976,787

CURRENT FILING DATE: 2001-10-12

PRIOR PPLICATION NUMBER: US 60/117,726

PRIOR PPLICATION NUMBER: US 60/117,726

PRIOR FILING DATE: 1999-01-29
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Query Match 100.0%; Score 101; DB 10;
Best Local Similarity 100.0%; Pred. No. 8.3e-09;
Matches 17; Conservative 0; Mismatches 0;
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100.0%; Score 101; DB 10;
Best Local Similarity 100.0%; Pred. No. 1.7e-08;
Matches 17; Conservative 0; Mismatches 0;
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Best Local Similarity 100.0%; Pred. No. 1.7e-08;
Matches 17; Conservative 0; Mismatches 0;
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SOFTWARE: WordPerfect 8.0 for Windows
SEQ ID NO 29
LENGTH: 238
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SOFTWARE: WordPerfect 8.0 for Windows
SEQ ID NO 28
LENGTH: 238
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US-09-865-198-28
; Sequence 28, Application US/09865198
; Patent No. US20020103345A1
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US-09-976-787-29
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US-09-976-787-2
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APPLICANT: Zhu, Zhenping
TITLE OFINVENTION: Baspecific Immunoglobulin-Like Antigen Binding Proteins and Methor TITLE OFINVENTION: Baspecific Immunoglobulin-Like Antigen Binding Proteins and Methor TITLE OFINVENTION: Production
FILE REFERENCE: 11245/47102
CURRENT APPLICATION NUMBER: US/09/865,198
CURRENT FILING DATE: 2001-05-24
PRIOR FIGURE OF SEQ ID NOS: 34
SOFTWARE; WordPerfect 8.0 for Windows
SEQ ID NO 22
LENGTHE: 177
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Patent No. U$20020064528A1

GENERAL INFORMATION:
APPLICANT: Zhu, Zhenping
APPLICANT: Zhu, Zhenping
APPLICANT: Zhu, Zhenping
TITLE OF INVENTION: Antibodies Specific to KDR and Uses Thereof
ITILE NOT INVENTION: ANTIBODIS: US/09/976,787

CURRENT APPLICATION NUMBER: US/09/976,787

CURRENT APPLICATION NUMBER: US 09/493,539

PRIOR APLICATION NUMBER: US 09/493,539

PRIOR FILING DATE: 1000-01-28

PRIOR FILING DATE: 1000-01-28

NUMBER OF SEQ ID NOS: 40

SEQ ID NOS: 40

SEQ ID NOS: 40

LENGTH: U$7

THE: PRIOR FILING
ORGANISM: WordPerfect 8.0 for Windows

SEQ ID NO 23

LENGTH: U$7

THE: PRIOR FILING
ORGANISM: WordPerfect 8.0 for Windows

SEQ ID NO 23

LENGTH: U$7

ORGANISM: WordPerfect 8.0 for Windows

SEQ ID NO 23

LENGTH: U$7

ORGANISM: WordPerfect 8.0 for Windows

SEQ ID NO 23

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ORGANISM: WordPerfect 8.0 for Windows

SEQ ID NO 23

LENGTH: U$7

ORGANISM: WordPerfect 8.0 for Windows

SEQ ID NO 23

CONTRANTED THE PRIOR 
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CURRENT FILING DATE: 2001-05-24
PRIOR APPLICATION NUMBER: US 60/206,749
PRIOR FILING DATE: 2000-05-24
NUMBER OF SEG ID NOS: 34
SOFTWARE: WordPerfect 8.0 for Windows
SEG ID NO 21
LENGTH: 17
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; Sequence 22, Application US/09865198
; Patent Noj US20020103345A1
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Best Local Similarity
Matches 17; Conserva
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; ORGANISM: MOUSE
US-09-865-198-21
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APPLICANT: Zhu, Zhenping
TITLE OF INVENTION: Bispecific Immunoglobulin-Like Antigen Binding Proteins and Me
TITLE OF INVENTION: Production
FILE REPERBUCE: 11245,47102
CURRENT APPLICATION NUMBER: US/09/865,198
CURRENT FILING DATE: 2001-05-24
PRIOR APPLICATION NUMBER: US 60/206,749
PRIOR PILING DATE: 2000-05-24
NUMBER OF SEQ ID NOS: 34
SOFTWARE: WordPerfect 8.0 for Windows
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US-09-974-052-1

US-09-974-052-1

Sequence 1. Application US/09974052

Patent No. US20020165387A1

GENERAL INFORMATION:

APPLICANT: Anderson, W.H. Kerr

APPLICANT: Tempest, Philip R.

APPLICANT: Carr, Frank J.

APPLICANT: Harris, William J.

APPLICANT: Harris, William J.

APPLICANT: Armour, Kathryn

TITLE OF INVENTION: High Affinity Humanized Anti-CEA Monoclonal Antibodies

FILE REPERBENCE:

CURRENT APPLICATION NUMBER: US/09/974,052

CURRENT FILING DATE: 2001-10-09

PRIOR FILING DATE: 1998-02-18

PRIOR FILING DATE: 1998-02-18

PRIOR PLICATION NUMBER: US 60/025,403

PRIOR PLICATION NUMBER: US 60/025,694

PRIOR PLING DATE: 1996-10-31

NUMBER OF SEQ ID NOS: 50

SOFTWARE: Microsoft Word 97 SR-2

SEQ ID NO 1

LENGTH: 124
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Pred. No. 9.7e-08;
0; Mismatches 1; Indels
                                                                                                                                                                                                                 Length 117;
                                                                                                                                                                                                                                                        1; Indels
                                                                                                                                                                                                             Score 94; DB 10;
Pred. No. 9.7e-08;
0; Mismatches 1.
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    PRIOR APPLICATION NUMBER: US 60/117,726
PRIOR FILING DATE: 1999-01-29
NUMBER OF SEQ ID NOS: 40
SOFTWARE: WordPerfect 8.0 for Windows
SEQ ID NO 7
                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 7, Application US/09865198 Patent No. US20020103345Al GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              93.18;
94.18;
                                                                                                                                                                                                               Query Match 93.1%;
Best Local Similarity 94.1%;
Matches 16; Conservative
                                                                                                                                                                                                                                                                                                                         50 WIDPENGDSGYAPKFQG 66
                                                                                                                                                                                                                                                                                                 1 WIDPENGDSDYAPKFQG 17
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Best Local Similarity 94.1
Matches 16; Conservative
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                                                                                                                                                     ; ORGANISM: Mus musculus US-09-976-787-7
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                                                                                                            117
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                                                                                                         LENGTH: 11
TYPE: PRT
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APPLICANT: Zhu, Zhenping
APPLICANT: Zhu, Zhenping
TITLE OF INVENTION: Bispecific Immunoglobulin-Like Antigen Binding Proteins and Methor TITLE OF INVENTION: Production
FILE REFERENCE: 11245/47102
CURRENT APPLICATION NUMBER: US/09/865,198
CURRENT APPLICATION NUMBER: US 60/206,749
PRIOR PILING DATE: 2001-05-24
NUMBER OF SEQ ID NOS: 34
SOFTWARE: WordPerfect 8.0 for Windows
SEQ ID NO 2
LENGTH: 17
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                                                            APPLICANT: 2hu, Zhenping
APPLICANT: Witte, Larry
TITLE COF INVENTION: Antibodies Specific to KDR and Uses Thereof
TITLE REFERENCE: 11245/46505
CURRENT APPLICATION NUMBER: US/09/976,787
CURRENT FILING DATE: 2001-110-12
PRIOR APPLICATION NUMBER: US 09/493,539
PRIOR FILING DATE: 2000-01-28
PRIOR FILING DATE: 1999-01-29
NUMBER OF SEQ ID NOS: 40
SEQ ID NO 2
LENGTH: 17
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Patent No. US20020064528A1

GENERAL INFORMATION:

APPLICANT: Witte, Larry

APPLICANT: Witte, Larry

TITLE OF INVENTION: Antibodies Specific to KDR and Uses Thereof

FILE REFERENCE: 11245/46505

CURRENT FILING DATE: 2001-10-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          93.1%; Score 94; DB 10; Length 17; 94.1%; Pred. No. 1.3e-08; Live 0; Mismatches 1; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1; Indels
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Pred. No. 1.3e-08;
0; Mismatches 1;
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US-09-865-198-2
; Sequence 2, Application US/09865198
; Patent No. US20020103345A1
Sequence 2, Application US/09976787 Patent No. US20020064528A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                           93.18;
94.18;
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                                                                                                                                                                                                                                                                                                                                                         TYPE: PRT
CORGANISM: Mus musculus
US-09-976-787-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Best Local Similarity
Matches 16; Conserv
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Matches 16; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; TYPE: PRT
; ORGANISM: Mouse
US-09-865-198-2
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50 WIDPENGDIEYAPKFQG 66
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Best Local Similarity
Matches 15; Conserv
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Sequence 3, Application US/09974052

Sequence 3, Application US/09974052

GENERAL INFORMATION:

APPLICANT: Anderson, W.H. Kerr

APPLICANT: Armour, Wally R.

APPLICANT: Harris, William J.

PRIOR REFERENCE: 2001-10-09

PRIOR PRILING DATE: 2001-10-30

PRIOR PRILING DATE: 1998-02-18

PRIOR FILING DATE: 1998-10-13

NUMBER OF SEQ ID NOS: 50

SOFTWARE: Microsoft Word 97 SR-2

SEQ ID NO 3

LENGTH: DATE: DAT
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1 Sequence 4, Application US/09974052

5 Sequence 4, Application US/09974052

5 Patent No: US20201055387A1

5 Patent No: US20201055387A1

5 APPLICANT: Tempest, Philip R.

6 APPLICANT: Tempest, Philip R.

7 APPLICANT: Armour, Kathryn

7 TITLE REFERENCE:

7 TITLE REFERENCE:

7 CURRENT APPLICATION NUMBER: US/09/974,052

7 CURRENT FILING DATE: 2001-10-09
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FEATURE:
NAME/KEY; Humanized COL-1 VH, HuVH
LOCATION: 1.124
OTHER INFORMATION: Humanized heavy chain variable region containing human OTHER INFORMATION: NEWM VH FRs, murine COL-1 VH CDRs, and Phe-27, Asn-28, OTHER INFORMATION: Ile-29, Lys-30, Asn-97, and Thr-98
                                                                                                                                                                                                                                                                                                                     Gaps
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Pred. No. 1e-07;
2; Mismatches 0; Indels
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                                                                                                                                                                                                                                        93.1%;
88.2%;
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Best Local, Similarity 88.2
Matches 15; Conservative
                                                                 FEATURE:
NAMB/KEY:
LOCATION: 11 124
US-09-974-052-1
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TYPE: PRT . ORGANISM: Mựs musculus
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Best Local Similarity
Matches 15; Conserv
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LOCATION: 1..124
COTHER INFORMATION: Humanized heavy chain variable region containing human OTHER INFORMATION: NEWM VH FRS, murine COL-1 VH CDRS, and Ala-24, Phe-27, Asn-28, COTHER INFORMATION: Ile-29, Lys-30, Asn-97, and Thr-98
US-09-974-052-4
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LOCATION: 1..124
COTHER INFORMATION: Humanized heavy chain variable region containing human
OTHER INFORMATION: NEWM VH FRS, murine COL-1 VH CDRS, and Ala-24, Phe-27, Asn-28,
COTHER INFORMATION: Ile-29, Lys-30, Thr-78, Asn-97, and Thr-98
US-09-974-052-5
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APPLICANT: Tempest, Philip R.
APPLICANT: Tempest, Philip R.
APPLICANT: Carr, Frank J.
APPLICANT: Harris, William J.
APPLICANT: Armour, Kathryn
TITLE OF INVENTION: High Affinity Humanized Anti-CEA Monoclonal Antibodies
FILE REFERENCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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Pred. No. 1e-07;
2; Mismatches 0; Indels
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CURRENT FILING DATE: 2001-10-09
PRIOR APPLICATION NUMBER: US 09/025,403
PRIOR FILING DATE: 1998-02-18
PRIOR FILING DATE: 1997-10-30
PRIOR FILING DATE: 1997-10-30
PRIOR APPLICATION NUMBER: US 60/029,694
PRIOR FILING DATE: 1996-10-31
NUMBER OF SEQ ID NOS: 50
PRIOR APPLICATION NUMBER: US 09/025,403
PRIOR FILING DATE: 1998-02-18
PRIOR APPLICATION NUMBER: PCT US97/19642
PRIOR PILING DATE: 1997-10-30
PRIOR FILING DATE: 1996-10-31
PRIOR FILING DATE: 1996-10-31
NUMBER OF SEQ ID NOS: 50
SOFTWARE: Microsoft Word 97 SR-2
LENGTH: 124
                                                                                                                                                                                                                                                                                                                                                                                   NAME/KEY: Humanized COL-1 VH, HuVHA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 5, Application US/09974052 Patent No. US20020165387A1
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SEQ ID NO 5
LENGTH: 124
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88.28;
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Best Local Similarity 88.2
Matches 15; Conservative
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Gaps

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TYPE: PRT
OKCANISM: Artificial Sequence
FEATURE:
NAME/KEY: Humanized COL-1 VH, HuVHAA
LOCATION: 1..124
COTHER INFORMATION: Humanized heavy chain variable region containing human
OTHER INFORMATION: WERS, muxine COL-1 VH CDRs, and Ala-24, Phe-27, Asn-28,
COTHER INFORMATION: IE-29, Lys-30, Ala-79, Asn-97, and Thr-98
Sequence 6, Application US/09974052

Sequence 6, Application US/09974052

Patent No. US20020165387A1

SERBRAL INFORMATION:

APPLICANT: Anderson, W.H. Kerr

APPLICANT: Tempest, Philip R.

APPLICANT: Haris, William J.

APPLICANT: Harris, William J.

APPLICANT: Howering Nathryn

TITLE OF INVENTION: High Affinity Humanized Anti-CEA Monoclonal Antibodies

CURRENT APPLICATION NUMBER: US/09/974,052

CURRENT FILING DATE: 1996-02-18

PRIOR FILING DATE: 1999-02-18

PRIOR APPLICATION NUMBER: US 60/029,694

PRIOR APPLICATION NUMBER: US 60/029,694

PRIOR FILING DATE: 1996-10-31

NUMBER OF SEQ ID NOS: 50

SOFTWARE: Microsoft Word 97 SR-2

SEQ ID NO 6

LENGTH: 124
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Pred. No. 1e-07;
2; Mismatches 0; Indels
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88.2%;
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Best Local Similarity 88.2's
Matches 15; Conservative
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December 23, 2002, 07:16:08; Search time 57.9767 Seconds Run on:

(without alignments) 248.221 Million cell updates/sec

US-09-865-198-8 558 1 DIELTQSPAIMSASPGEKVT.....QRSSYPFTFGSGTKLEIKRA 108 Title: Perfect score:

Scoring table:

Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5

908470 seqs, 133250620 residues

Searched:

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Listing first 45 summaries Post-processing: Minimum Match 0% Maximum Match 100%

Database :

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SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1999.DAT:*
SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1999.DAT:*
SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1999.DAT:*
SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1000.DAT:*
SIDS2/gcgdata/geneseq/geneseqp-emb1/AA2001.DAT:*
SIDS2/gcgdata/geneseq/geneseqp-emb1/AA2001.DAT:* | SIDS2/gcgdata/geneseq/geneseqp-embl/AA1980.DAT:*
| SIDS2/gcgdata/geneseq/geneseqp-embl/AA1981.DAT:*
| SIDS2/gcgdata/geneseq/geneseqp-embl/AA1981.DAT:*
| SIDS2/gcgdata/geneseq/geneseqp-embl/AA1983.DAT:*
| SIDS2/gcgdata/geneseq/geneseqp-embl/AA1984.DAT:*
| SIDS2/gcgdata/geneseq/geneseqp-embl/AA1984.DAT:*
| SIDS2/gcgdata/geneseq/geneseqp-embl/AA1986.DAT:*
| SIDS2/gcgdata/geneseq/geneseqp-embl/AA1986.DAT:*
| SIDS2/gcgdata/geneseq/geneseqp-embl/AA1988.DAT:*
| SIDS2/gcgdata/geneseq/geneseqp-embl/AA1988.DAT:*
| SIDS2/gcgdata/geneseq/geneseqp-embl/AA1988.DAT:* A_Geneseq_101002: 110... 1122... 113... 114... 116... 119... 122... 123... 123...

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

			Description	Variable light cha	VEGF antagonist an	Antigen-binding pr	Antigen-binding pr	SNV-env leader/hum	Humanised antibody	Antigen-binding pr	Chimeric plC11 lig	VEGF antagonist an	Antigen-binding pr
COLUMNICO			ID	AAY97236	AAB82710	AAU74413	AAU74419	AAB70842	AAE13144	AAU74418	AAE13146	AAB82702	AAU74420
			DB	21	22	23	23	22	22	23	22	22	23
			Match Length DB ID		•			330	. ,	•			•
	æ	Query	Match	100.0	100.0	100.0	100.0	100.0	98.4	98.4	98.4	98.4	98.4
			Score	558	558	558	558	558	549	549	549	549	549
		Result	No.		7	9	4	S	9	7	80	6	10

EGFR antibod e VL kappa g CEA antibody ric anti-CEA p53 common m p53 common m p53 common m p63 common m p63 common m p63 common m p63 common m p63 common m p63 common m	when the control of t	ScFv-rearranged ca Guy's 13 anti-Stre Anti-Tac light stre Anti-Tac light NO: Murine anti-Tac an Murine anti-Tac an Murine anti-Tac an Murine anti-Tac an Protein encoded by Anti-Tac SFv prote Anti-Tac(Fv)-PE40 Anti-Tac(Fv)-PE40 Anti-Tac(Fv)-PE40 Anti-Tac(Fv)-PE40
23 2 2 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3	AAR21294 AAR75129 AAW11508 AAW1323 AAB85455 AAB85455 AAB8734096 AAW82744 AAW82745 AAW81278	3744
118 118 122 122 123 125 126 127	53 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5	22 113 123 221 221 220 221 221 221
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11111111111111111111111111111111111111	22 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2	

ALIGNMENTS

AAY97236 standard; Protein; 108 AA. RESULT 1 AAY97236

AAY97236;

(first entry) 19-DEC-2000 Variable light chain fragment of anti-SI(KDR) antibody.

central nervous system neoplasms; AIDS associated Karposi's sarcoma; acquired immune deficiency syndrome; AIDS; human. Immunoglobulin; antibody; complementary determing region; CDR; VEGF; vascular endothelial growth factor; KDR; tinase insert domain containing receptor; multivalent; monovalent; humanised antibody; chimeric antibody; tumour; diabody; triabody; glioblastoma multiforme; hemangioblastoma; AIDS;

sapiens

Synthetic.

WO200044777-A1.

03-AUG-2000.

28-JAN-2000; 2000WO-US02180.

99US-0117726. 99US-0240736. 29-JAN-1999; 29-JAN-1999;

(IMCL-) IMCLONE SYSTEMS INC.

Witte L; Zhu Z,

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                                                                      Novel immunoglobulin molecules binding kinase insert domain-containing receptor with the same affinity as vascular endothelial growth factor,
                                                                                                                                                                               New immunoglobulin molecules are described that bind kinase insert domain-containing receptor (KDR) with a comparable affinity to human vascular endothelial growth factor (VEGF). The antibodies neutralise KDR activation. The immunoglobulin may be a multivalent single chain antibody, a monovalent single chain antibody, a diabody, a triabody, a humanised antibody or a chimerised antibody, a finencial lamunoglobulin molecules bind specifically to an extracellular domain of the KDR receptor with the same affinity as VEGF. Overexpression of VEGF has been implicated in a number of human tumogur cell lines including glioblastoma multiforme.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 DIELTQSPAIMSASPGEKVTITCSASSSVSYMHWFQQKPGTSPKLWIYSTSNLASGVPAR 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 DIEUTQSPAIMSASPGEKVTITCSASSSVSYMHWFQQKPGTSPKLMIYSTSNLASGVPAR 60
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                                                                                                                                                                                                                                                                                                                                                                 hemangiobistoma, central nervous system neoplasms and AIDS associated Karposi's sarcoma. The antibodies therefore have applications in treating these conditions. This sequence encodes a preferred heavy chain complementary determining region of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   VEGF antagonist antibody IMC-1C11 light chain variable region.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note= "complementarity determining region 1"
49..55
/label= CDR-L2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              100.0%; Score 558; DB 21; Length 108; 100.0%; Pred. No. 1.9e-32;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAB82710 standard; Protein; 108 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                            immunoglobulins of the invention.
                                                                                                                                              Claim 4; Pāge 51; 55pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                88..96
/label= CDR-L3
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/label= CDR-L1
                                                                                                          used to reduce tumour growth
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Chimeric - Homo sapiens.
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               WPI; 2000-505966/45.
N-PSDB; AAA53768.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence ?
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The present sequence is that of the light chain variable region of IMC-1C11, a mouse-human chimeric antibody that has vascular endothelial growth factor (VEGF) antagonist activity. The antibody, or a fragment of it, can be used as an anti-angiogente molecule, together with a chemotherapeutic acid, for the treatment of an angiogenic dependent condition in a mammal, especially a human. The invention relates generally to a method of treating or controlling an angiogenic dependent condition by administering an anti-angiogenic molecule and a chemotherapeutic agent, to produce a regression or arrest of the condition while minimising or preventing significant toxicity of the chemotherapeutic agent. The anti-angiogenic molecule inhibits or blocks the action of a vascular endothelium survival factor such as VEGF or its receptor, and is especially IMC-1C11. Conditions that can be treated include a neoplasm, a collagen vascular disease or an autoimmune disease, carcinoma, prostate carcinoma, colon carcinoma, lung carcinoma, prostate carcinoma, covarian carcinoma, neuroblastoma multiforme or melanoma (all claimed).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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                                                                                                                                                                                                                                                                                                           Treating or controlling an angiogenic dependent condition (e.g. neoplasm, collagen-vascular or autoimmune disease) in mammal by administering a combination of an antiangiogenic molecule and a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
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100.0%; Pred. No. 1.9e-32;
tive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                          Disclosure; Page 38-39; 42pp; English.
                                                                                                                                                       SUNN-) SUNNYBROOK HEALTH SCI CENT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAU74413 standard; peptide; 108
                                                      29-JAN-2001; 2001WO-US02839.
                                                                                             28-JAN-2000; 2000US-0178791
                                                                                                                 31-MAR-2000; 2000US-0539692
                                                                                                                                                                          (IMCL-) IMCLONE SYSTEMS INC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches 108; Conservative
                                                                                                                                                                                                                                                                                                                                                                    chemotherapeutic agent
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
                                                                                                                                                                                                                                                     WPI; 2001-514531/56.
N-PSDB; AAH26406.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 108 AA;
                  02-AUG-2001
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Mon Dec 23 08:53:56 2002
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The invention describes an antigen-binding protein (I) comprising a complex of two polypeptides (P1) and two second polypeptides (P2) which can estably associated in an immunoglobulin like complex. Pl has an antigen-binding site located to the N terminus of immunoglobulin (Ig) indicated to the N terminus of immunoglobulin (Ig) catical coated to the N terminus of the CH1 domain. (I) is useful for:

CC site located to the N terminus of the CH1 domain. (I) is useful for:

CC site located to the N terminus of the CH1 domain. (I) is useful for:

CC site located to the N terminus of the CH1 domain. (I) is useful for:

CC reducing endothelial call proliferation; inhibiting angiogenesis;

CC reducing endothelial cell proliferation; inhibiting vEGF induced

CM ingration of human leukaemia cells; blocking interaction of a protein and can size in the design of (1) provides for efficient production so that

CC and in vivo and in vitro for investigative, diagnostic or treatment combinated are assembled in the desired configuration. (I) is bivalent and bispecific, homogeneous cond in tetrameric form. The heavy chain constant domains which constitute the Fc region (e.g., CH2 and CH3 for an IgG molecule) of a natural continue containing a heavy chain variable domain. (VH) incorporated into Fv, an engineered protein containing a heavy chain variable domain containing the marked the complex processor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ó
                                                                                                                                                                                                                                                                                                                          New bispecific immunoglobulin-like antigen-binding protein for reducing tumour growth and for inhibiting angiogenesis, comprises a complex of two polypeptides and two second polypeptides
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Antigen-binding protein; single chain variable fragment; scFv; antigen;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 DIELTQSPAIMSASPGEKVTITCSASSSVSYMHWFQQKPGTSPKLWIYSTSNLASGVPAR 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Antigen-binding protein, single chain variable fragment version #1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           100.0%; Score 558; DB 23; Length 108; 100.0%; Pred. No. 1.9e-32; 1ve 0; Mismatches 0; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      61 FSGSGSGTSYSLTISRMEAEDAATYYCQQRSSYPFTFGSGTKLEIKRA 108
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                                                                                                                                                                                                                                                                                                                                                                                                      Claim 57; Page 57; 64pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   the method of the invention.
                                                                                                                                                 24-MAY-2000; 2000US-206749P.
                                                                                                                                                                                         (IMCL-) IMCLONE SYSTEMS INC.
                                                                                                               24-MAY-2001; 2001WO-US16924
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                                     WO200190192-A2.
                                                                           29-NOV-2001
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The invention describes an antigen-binding protein (I) comprising a complex of two polypeptides (P1) and two second polypeptides (P2) which are stably associated in an immunoglobulin like complex. Pl has an antigen-binding site located to the N terminus of immunoglobulin (Ig) light chain constant domain (CL domain), and P2 has an antigen-binding site located to the N terminus of the CH1 domain. (I) is useful for: clare to the N terminus of the CH1 domain. (I) is useful for: neutralising the activation of a vacular endothelial growth factor (VEGF) receptor: reducing tumour growth; inhibiting vEGF induced migration of human leukaemia cells; blocking interaction of a protein and its ligand; promoting interactions between immune cells and target cells; and in vivo and in vitro for investigative, diagnostic or treatment methods. The design of (I) provides for efficient production so that substantially all of the antigen-binding proteins produced are assembled in the desired configuration. (I) is bivalent and bispecific, homogeneous and in tetrameric form. The heavy chain constant domains which constitute the FC region (e.g., CH2 and CH3 for an IgG molecule) of a natural continuous and which provide other antibody functions can be present. There is no requirement for processing in vitro to obtain the campiete product.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New bispecific immunoglobulin-like antigen-binding protein for reducing tumour growth and for inhibiting angiogenesis, comprises a complex of two polypeptides and two second polypeptides  \  \, .
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ), an engineered protein containing a variable light and variable domain on one polypeptide, described in the method of the \,
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                                                                                                                                                                                                                                                                                                                  133..240
/label= VL
/note= "Light chain variable domain. Specifically
claimed in claim 57"
                                                                                                                                                                                            /note= "Heavy chain variable domain. Specifically claimed in claim 57"
                                                                                                                                                                                                                                                                 /note= "15 amino acid linker joins the VH and VL regions of the single chain variable fragment protein. Encoded by AAS20285"
cytostatic; angiogenesis inhibitor; tumour; leukaemia; antibody; vascular endothelial growth factor receptor; VEGF; cell proliferation inhibitor.
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                                                                                                                                    Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 63; Page 62; 64pp; English.
                                                                                                                                                                                                                                                   /label= Linker
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  24-MAY-2000; 2000US-206749P.
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                                                                                    Mus sp.
Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sednence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Local
                                                                                                                                        Key
Region
                                                                                                                                                                                                                                  Region
                                                                                                                                                                                                                                                                                                                              Region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Zhu Z;
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1 DIELTQSPAIMSASPGEKVTITCSASSSVSYMHWFQQKPGTSPKLWIYSTSNLASGVPAR 60

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Length 330;

Score 558; DB 22; Pred. No. 5.2e-32;

100.0%; 100.0%;

Similarity

330 AA;

8 à a

No.

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Sequence
                                                             Query Match
Best Local 8
                                                                                                                                                                                                                                                                                                                           RESULT 6
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        X S
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                                                                                                                                                                                                                                                                                                                                                                                                          This invention describes a novel cell-targeting vector (A) containing a DNA sequence (I) encoding a single-chain variable antibody fragment (SCEV). The products of the invention have antiviral, cytostatic and immunostimulant activity and can be used in gene therapy, immunization and diagnosis particularly of T cell-associated diseases, specifically cand diagnosis particularly of T cell-associated diseases, specifically control of the CD4 receptor, with high selectivity, 4-5 fold selectivity over the CD4 receptor, with high selectivity, 4-5 fold selectivity over cheman-(B cells, and 1000 fold selectivity) over other human cells. A vector designated 7A5 encodes a 329 amino acid single-chain variable antibody fragment, fully defined in the specification. It was used to transform CC (SNV), cells (Muman T lymphocyte) cells, and Hela (Human cervical carcinoma) cells. After 48 hours, the cells were stained with X-gal to determine transformation. The viral titer (infectious units/ml) was over a million for D17, in million for CB166 but less than 100 for HeLa, showing the high selectivity for human T cells. This sequence represents the SNV-env leader/human 7B2-scrv fusion construct used in the invention.
                                                                                                                                                                                                                                                                                                                                                        T lymphocyte; antibody; single chain variable antibody; scFv; human; cell-targeting vector; antiviral; cytostatic; immunostimulant; AIDS; gene themapy; immunisation; diagnosis; T cell-associated disease; SCID; acquired manune deficiency syndrome; severe combined immune deficiency; T cell lymphoma; fusion construct.
Cell-targeting vector selective for T lymphocytes, useful in gene therapy of e.g. acquired immune deficiency syndrome, encodes a single-chain variable antibody fragment .
                                                         SNV-env leader/human 7B2-scFv fusion construct.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (BUND ) BUNDESREPUBLIK DEUT PAUL-EHRLICH-INST.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1..45
/label= SNV-env_leader
46..330
/label= 7B2-scFv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Location/Qualifiers
                                                                                                                                                                                                  AAB70842 §tandard; Protein; 330 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Spleen necrosis virus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 1; Fig 3; 18pp; German.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Cichutek K, Engelstaedter M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      99DE-1046142.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             99DE-1046142.
                                                                                                                                                                                                                                                                          25-JUN-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 2001-246140/26.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     N-PSDB; AAF61511.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DE19946142-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           27-SEP-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      27-SEP-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               29-MAR-2001.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Chimeric:-
Chimeric:-
                                                                                                                                                                                                                                         AAB70842;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Key
Protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Vascular endothelial growth factor receptor; VEGFR; antagonist; tumour; cytostatic; light chain; myelocytic leukaemia; lymphocytic; erythrocytic; monocytic; multiple myeloma; lymphoid cell; Hodgkin's disease; mouse; human; chimeric.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Inhibiting growth of non-solid tumor cells useful to treat bone marrow
                                                                                                           tumors such as leukemias or multiple myeloma comprises treatment with an antagonist of a vascular endothelial growth factor receptor -
Gaps
                                                                  1 DIELTQSPAIMSASPGEKVTITCSASSSVSYMHWFQQKPGTSPKLWIYSTSNLASGVPAR
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0
                                                                                                                                                                                                                   FSGSGSGTSYSLTISRMEAEDAATYYCQQRSSYPFTFGSGTKLEIKRA 108
                                                                                                                                                                                                                                                 241 FSGSGSGTSYSLTISRMEAEDAATYYCQORSSYPFTFGSGTKLEIKRA 288
Indels
ö
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Humanised antibody light chain fragment.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAE13144 standard; Protein; 106 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (IMCL-) IMCLONE SYSTEMS INC. (CORR ) CORNELL RES FOUND INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 30-MAR-2001; 2001WO-US10504.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        31-MAR-2000; 2000US-0540770.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               28-JAN-2002 (first entry)
   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Chimeric - Homo sapiens.
Chimeric - Mus sp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 2001-662942/76.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Witte L, Rafii S;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          106 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               N-PSDB; AAD21670.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WO200174296-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              11-OCT-2001.
Matches 108;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAE13144;
                                                                                                                                                                                                                   61
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the method of the invention.

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The invention describes an antigen-binding protein (I) comprising a complex of two polypeptides (P1) and two second polypeptides (P2) which are stably associated in an immunoglobulin like complex. Pl has an antigen-binding site located to the N terminus of immunoglobulin (Ig) (Ig) (Ight chain constant domain (CL domain), and P2 has an antigen-binding site located to the N terminus of the CH1 domain. (I) is useful for: Site located to the N terminus of the CH1 domain. (I) is useful for: neutralising the activation of a vascular endothelial growth factor (VEGF) receptor; reducing tumour growth; inhibiting angiogenesis, creducing endothelial coll proliferation; inhibiting vEGF induced migration of human leukaemia cells; blocking interaction of a protein and its ligand; promoting interactions between immune cells and target cells; creducing endothelial coll for investigative, diagnostic or treatment cand in vivo and in vitro for investigative, diagnostic or treatment cand in vitro for investigative, diagnostic or treatment cand in vitro for investigative, diagnostic or treatment constitute constitute constitute configuration. (I) is bivalent and bispecific, homogeneous and in tetrameric form. The heavy chain constant domains which constitute configuration (ECC) the configuration. (I) is bivalent and bispecific, and in tetrameric form. The heavy chain constant domains which constitute configuration or provessing in vitro to obtain the complete product. This sequence represents a light chain variable domain wariable domain and a light chain variable domain in one polypeptide chain, and a light chain variable domain in one polypeptide chain, and a light chain variable domain in one polypeptide chain, and in the complex constitute and a light chain variable domain in one polypeptide production.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New bispecific immunoglobulin-like antigen-binding protein for reducing tumour growth and for inhibiting angiogenesis, comprises a complex of two polypeptides and two second polypeptides
                                                     Gaps
                                                                                                1 DIELTQSPAIMSASPGEKVTITCSASSSVSYMHWFQQKPGTSPKLWIYSTSNLASGVPAR 60
                                                                                                                         1 DIELTQSPAIMSASPGEKVTITCSASSSVSYMHWFQQKPGTSPKLMIYSTSNLASGVPAR 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Antigen-binding protein; antibody light chain variable domain; cytostatic; angiogenesis inhibitor; tumour; leukaemia; antibody; vascular endothelial growth factor receptor; VEGF;
                                                     ö
  DB 22; Length 106;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Antigen-binding protein light chain variable domain (VH) #2.
                                                  Indels
                                                                                                                                                                                                                      61.FSGSGSGTSYSLTISRMEAEDAATYYCQQRSSYPFTFGSGTKLEIK 106
                                                                                                                                                                                             61 FSGSGSGTSYSLTISRMEAEDAATYYCQQRSSYPFTFGSGTKLEIK 106
                                                ;
                         8e-32;
Query Match 98.4%; Score 549; DE Best Local Similarity 100.0%; Pred. No. 8e-Matches 106; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                  AAU74418 standard; peptide; 106 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 61; Page 61; 64pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   cell proliferation inhibitor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               24-MAY-2001; 2001WO-US16924.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            24-MAY-2000; 2000US-206749P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mus sp.
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                                                                                                                                                                                                                                                                                                                                                Vascular endothelial growth factor receptor; VEGFR; antagonist; tumour; cytostatic; light chain; myelocytic leukaemia; lymphocytic; erythrocytic; monocytic; multiple myeloma; lymphoid cell; Hodgkin's disease; chimeric; human; plCll vector.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Inhibiting growth of non-solid tumor cells useful to treat bone marrow tumors such as leukemias or multiple myeloma comprises treatment with an antagonist of a vascular endothelial growth factor receptor -
                                                                           Gaps
                                                                                                                 1 DIELTQSPAIMSASPGEKVTITCSASSSVSYMHWFQQKPGTSPKLWIYSTSNLASGVPAR 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "Mature chimeric plC11 light chain fragment"
                                                                           ö
                                               Length 106;
                                                                         0; Indels
                                                                                                                                                       61 FSGSGSGTSYSLTISRMEAEDAATYYCQQRSSYPFTFGSGTKLEIK 106
                                                                                                                                                                    DB 23;
                                              98.4%; Score 549; DB 23, 100.0%; Pred. No. 8e-32; ive 0; Mismatches (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /label- Leader_peptide
                                                                                                                                                                                                                                                                                                                           Chimeric plC11 light chain fragment.
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Location/Qualifiers
                                                                                                                                                                                                                                                AAE13146 standard; Protein; 125 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               107..115
/label= CDR_L3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /label= CDR_L1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /label= CDR_L2
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                                                                                                                                                                                                                                                                                                   28-JAN-2002 (first entry)
                                                                           106; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                    Chimeric - Homo saplens.
Chimeric - Unidentified.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  20..125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note=
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                                                              Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Witte L, Rafii S;
                        106 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       N-PSDB; AAD21683
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                         Seguence
                                                                                                                                                                                                                                                                          AAE13146;
                                                 Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Protein
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                                                                           Matches
                                                                                                                                                                                61
                                                                                                                                                                                                                      RESULT 8
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(IMCL-) IMCLONE SYSTEMS INC.
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Synthetic.
                                          Kerbel R;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence
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Best Local
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Reqion
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                                                                                                                                                                                                                                                                                                                                                         ö
               variable region joined to human constant region, where the humanised mouse variable region contains mouse complementarity determining region (CDR) graffed into human variable region. The method is useful for treating leukaemias such as acute or chronic myelocytic leukaemia, acute or chronic myelocytic leukaemia, acute or chronic myelocytic leukaemia, multiple myelomas and lymphoid cells, particularly those related to mon-Hodgkin's and Hodgkin's Alsease. The present sequence is chimeric picli light chain fragment which is used for the construction of chimeric picli light chain contains choned variable light chain (VL) and human kappa light chain constant region
(antagonists). Humanised monoclonal antibody comprises humanised mouse
                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        IMC-1C1]; chimeric antibody; mouse; human; antagonist; VEGF; vascular endothelial growth factor; anglogenesis; antiangiogenic; antiumour; neoplasm; collagen-vascular disease; autoimmune disease; tumour; breast carcinoma; lung carcinoma; prostate carcinoma; colon carcinoma; colon carcinoma; neuroblastoma; glioblastoma; autiforme; melanoma; therapy; light chain.
                                                                                                                                                                                                                                                                                                                                                                                              DIELTOSPAIMSASPGEKVTITCSASSSVSYMHWFQQKPGTSPKLWIYSTSNLASGVPAR 60
                                                                                                                                                                                                                                                                                                                                                                                                                     VEGF antagonist antibody IMC-1C11 light chain variable region.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -
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                                                                                                                                                                                                                                                                                                                Length 125;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  43..52
/label- CDR-L1
/note- "complementarity determining region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "complementarity determining region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     61 FSGŞGSGTSYSLTISRMEAEDAATYYCQQRSSYPFTFGSGTKLEIK 106
                                                                                                                                                                                                                                                                                                            98.4%; Score 549; DB 22;
100.0%; Pred. No. 9.2e-32;
ive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /label= Signal_peptide
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/label= Mature_protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAB82702 standard; Protein; 125 AA
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/label= CDR-L2
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2000US-0539692.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (first entry)
                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             107..115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     - Mus sp.
- Homo sapiens.
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                                                                                                                                                                                                                                                                                                                             Best Local Similarity
Matches 106; Conserv
                                                                                                                                                                                                                                                                   Sequence | 125 AA;
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31-MAR-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          15-OCT-2001
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Chimeric
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAB82702;
                                                                                                                                                                                                                                                                                                                Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAB82702
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The present sequence is that of the light chain variable region of IMC-1C11, a mouse-human chimeric antibody that has vascular conditionalial growth factor (VEGF) antagonist activity. The antibody, or a fragment of it, can be used as a nati-antiogenic molecule, together with a chemotherapeutic acid, for the treatment of an antiogenic dependent condition in a mammal, especially a human. The invention relates generally to a method of treating or controlling an angiogenic dependent condition by administering an anti-angiogenic molecule and a chemotherapeutic agent, to produce a regression or arrest of the condition while minimising or preventing significant toxicity of the chemotherapeutic agent.

The anti-angiogenic molecule inhibits or blocks the action of a vascular endothelium survival factor such as VEGF or its receptor, and is especially IMC-1C11. Conditions that can be treated include a neoplasm, a collagen-vascular disease or an autoimmune disease, especially a soil tumour, including breast carcinoma, lung especially a soil tumour, including breast carcinoma.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      20 DIELTQSPAIMSASPGEKVTITCSASSSVSYMHWFQQKPGTSPKLMIYSTSNLASGVPAR 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Antigen-binding protein, single chain variable fragment version #2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       carcinoma, prostate carcinoma, colon carcinoma, prostate carcinoma, ovarian carcinoma, neuroblastoma, central nervous system tumour, neuroblastoma, glioblastoma multiforme or melanoma (all claimed).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /label= VH
/note= "Heavy chain variable domain. Specifically
claimed in claim 61"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Antigen-binding protein; single chain variable fragment; svFv; an expostatic, anglogenesis inhibitor; tumour; leukaemia; antibody; vascular endothelial growth factor receptor; VEGF; cell proliferation inhibitor.
                                                                                                                                                                 neoplasm, collagen-vascular or autoimmune disease) in mammal by administering a combination of an antiangiogenic molecule and a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 125;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               98.4%; Score 549; DB 22;
100.0%; Pred. No. 9.2e-32;
tive 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AA.
                                                                                                                                                                                                                                                                                                                                   Disclosure; Fig 1; 42pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches 106; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    118..132
                                                                                                                           Treating or controlling
                                                                                                                                                                                                                                                  chemotherapeutic agent
WPI; 2001-514531/56.
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                                              N-PSDB; AAH26414
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Anti-EGFR antibody light chain variable region (Clone L2 8C).
               02-JUL-1996 (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                The invention describes an antigen-binding protein (I) comprising a complex of two polypeptides (PI) and two second polypeptides (P2) which are stably associated in an immunoglobulin like complex. PI has an antigen-binding site located to the N terminus of immunoglobulin (Ig) is useful for: antigen-binding stee located to the N terminus of the CH1 domain. (I) is useful for: neutralising the activation of a vascular endothelial growth factor (VEGF) receptor; reducing tumour growth; inhibiting angiogenesis, reducing endothelial cell proliferation; inhibiting vEGF induced migration of human leukaemia cells; blocking interaction of a protein and its ligand; promoting interactions between immune cells and target cells; and in vivo and in vitro for investigative, diagnostic or treatment methods. The design of (I) provides for efficient production so that substantially all of the antigen-binding proteins production so that substantially all of the antigen-binding proteins production so that the desired configuration. (I) is bivalent and bispecific, homogeneous of in the desired configuration. (I) is bivalent and bispecific, antibody and which provide other antibody functions can be present. There the FC region (e.g., CH2 and CH3 for an IgG molecule) of a natural configuration containing a variable light and variable fragment (C Fh1s is the amino acid sequence of a single chain variable light and variable homes the complete processing in the method of the configuration.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                                                                                                                  New bispecific immunoglobulin-like antigen-binding protein for reducing tumour growth and for inhibiting angiogenesis, comprises a complex of two polypeptides and two second polypeptides
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          regions of the single chain variable fragment protein. Encoded by AAS20285"
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                                                                                /note= "Light chain variable domain. Specifically claimed in claim 61"
              /note= "15 amino acid linker joins the VH and VL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     98.4%; Score 549; DB 23; Length 238; 100.0%; Pred. No. 1.6e-31; Live 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FSGSGSGTSYSLTISRMEAEDAATYYCQQRSSYPFTFGSGTKLEIK 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                193 FSGSGSGTSYSLTISRMEAEDAATYYCQQRSSYPFTFGSGTKLEIK 238
                                                                                                                                                                                                                                                                                                                                                                            Claim 63; Page 62-63; 64pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAR79884 standard; Protein; 108 AA.
/label= Linker
                                                                                                                                                                                                          24-MAY-2000; 2000US-206749P.
                                                                                                                                                                                                                                    (IMCL-) IMCLONE SYSTEMS INC.
                                                                                                                                                                              24-MAY-2001; 2001WO-US16924
                                                                     /label- VL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Best Local Similarity 100.
Matches 106; Conservative
                                                      133..238
                                                                                                                                                                                                                                                                                         WPI; 2002-106189/14.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           238 AA;
                                                                                                                         WO200190192-A2
                                                                                                                                                    29-NOV-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence
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                                                      Region
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ID AAR7
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AC AAR7
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compostion for the therapy of e.g. melanomas, gliomas and carcinomas. The antibodies and fragments are derived from mice but are humanised so as to cause minimum reaction against them. They are produced
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Anti-epidermal growth factor receptor (EGFR) single chain antibodies and antibodies constructed from anti-EGFR antibody fragments can be used for diagnosis of tumours and assessment of tumour growth in vivo. They may also be used in a pharmaceutical
Single chain antibody; antibody; epidermal growth factor receptor; EGFR; tumour; cancer; glioma; melanoma; carcinoma; diagnosis; assessment; phage antibody library.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Anti-EGFR antibodies and single chain Fv antibody fragments -obtained from phage-antibody libraries, useful for diagnosis and
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Rosell E;
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Pred. No. 2.1e-31;
                                                                                                                                                                                                                                                                                                                                                                                   97..108
/label= Framework region 4.
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                                                                                                                                                              /label= Framework region 1.
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Piulats J,
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                                                                                                                                                                                                                         34..48
/label= Framework region
                                                                                                                                                                                                                                                                                                                             Framework region
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                                                                                                                       Socation/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        using the phage antibody library.
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Mitjans F, F
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'label= CDR1
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94EP-0104160.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               95WO-EP00978
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/label= I
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Best Local Similarity
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Kettleborough AC,
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                                                                                   Mus musculus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             16-MAR-1995;
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from a single chain Fv library from an immunised mouse. The libra-
from a single chain Fv library from an immunised mouse. The libra-
ry produces a diverse repertoire of antibody fragments specific for
2-phenyl-5-oxazolone (phox). It was prepd. using cDNA generated
from man from mice immunised with phox coupled to chicked serum
albumin. The VH and VL kappa sequences were separately amplified
by PCR (see AAQ2344-84) and ligated into fdCaT2 (see AAQ23463) for ex-
pression on the phage surface as fusions with gene III. The result-
ing library of clones was diverse. Twenty three hapten binding
clones were sequenced revealing eight different VH genes (A+H) (see
AAR21264-71) in a variety of pairings with the seven different VK
genes (a-9). Of the twenty three clones sequenced, four were of
typer (a-7) in a variety of pairings with the seven different VK
genes (a-9). They contain the DXGXX motif in CDR3, the central
cly of which is needed to reade a cavity for phox. Most of the
clones were VK-d combinations. The Kd of VH-BVK b for phox-GABA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Hoogenboom HRJ, Griffiths AD;
Clackson TP, Chiswell DJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           clones were Vk-d combinations. The Kd of VH-B/Vk-b for phox-GABA was \frac{1}{10}0 uM, one of the highest values found. This suggests that phage bearing scFv fragments having weak affinities can be selected with antigen, probably due to the avidity of the multiple antibody
                                                                                                                                                            Fd; bacteřlophage; gene III; filamentous; phagemid; capsid; coaplus; g3p; binding; adsorption; gene VIII; diverse repertoire; specific plading pairs; replicable genetic display package.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Producing members of specific binding pairs - by expression in recombinant host cells with a secreting replicable genetic
                                                                                                                                Murine VL kappa group VI chain "e", specific for phOx.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAR21260-307, 309-311; AAR22450, 565-581.
                                                                                                                                                                                                                                                                                                             49..55
/label= CDR2
88..96
/label= CDR3
/note=" D-x-G-x-x motif "
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pope AR, Johnson KS,
olliger KP, Marks JD,
                                                                                                                                                                                                                                                               Location/Qualifiers
                                standard; Protein; 108 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Example 21; Fig 24; 209pp; English.
                                                                                                                                                                                                                                                                                  24..33
/label= CDR1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               90GB-0015198.
90GB-0022845.
90GB-0024503.
91GB-0004744.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CAMBRIDGE ANTIBODY.
                                                                                                 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RES COUNCIL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Jackson RH, Holliger KI
Winter GP, Bonnert TP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 1992-056862/07
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              display package.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            McCafferty J,
                                                                                                                                                                                                                                                                                  Binding-site
                                                                                                                                                                                                                                                                                                             Binding-site
                                                                                                                                                                                                                                                                                                                                                Binding-ŝite
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               10-JUL-1991;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1991;
                                                                                                                                                                                                                                                                                                                                                                                                                 W09201047-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                23-JAN-1992.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               .5-MAY-1991;
                                                                                                21-MAY-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Œ
                                                                                                                                                                                                                               Synthetic
                                AAR21290
                                                               AAR21290;
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19 - OCT - 1
12 - NOV - 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (MEDI-)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               06-MAR-
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RESULT 12
                 AAR21290
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This sequence is the light chain variable region of the antibody of the invention. The antibody is an anti-CEA (carcinoembryonic antigen) antibody (806.077 Ab). Host cells or transgenic organisms transformed with DNA encoding the antibody, are used to make the antibody or conjugate. The conjugate is used in a medicament suitable for intravenous administration. The conjugate can be used for cancer therapy, selectively killing tumour cells. The antibody can be used for in vivo or in vitro
                                                                                                                                                                                                                                                                                                                                                     Anti-CEA antibody; carcinoembryonic antigen; 806.077 Ab; cancer therapy; cancer diagnosis; complementarity determining region; light chain.
                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                         1 DIELTQSPAIMSASPGEKVTITCSASSSVNYMHWFQQKPGTSPKLWIYSTSNLASGVPTR 60
                                                                                         DIELTQSPAIMSASPGEKVTITCSASSSVSYMHWFQQKPGTSPKLWIYSTSNLASGVPAR 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 DIELTQSPAIMSASPGEKVTITCSASSSVSYMHWFQQKPGTSPKLWIYSTSNLASGVPAR 60
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                                      Length 108;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 541; DB 18; Length 108;
                                                                                                                                                            61 FSGSGSGTSYSLTISRMEAEDAATYYCQQRSSYPFTFGSGTKLEIKRA 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        61 FSGSGSGTSYSLFISRMEAEDAATYYCQQRSSYPFTFGSGTKLEIKRA 108
                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                          Anti-CEA antibody 806.077 light chain variable region.
                                    Score 541; DB 13;
Pred. No. 3e-31;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3e-31;
                                                              1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pred. No. 3e-3
1; Mismatches
                                                                                                                                                                                                                                          AAW41388 standard; Protein; 108 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 3; Page 196; 208pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        diagnosis and therapy of cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Emery SC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          4,
                                    97.0%;
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96GB-0009405.
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                                                                                                                                                                                                                                                                                                 02-JUN-1998 (first entry)
                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches 103; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Edge MD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 1997-558987/51.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          diagnosis of cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (ZENĖ ) ZENECA LTD.
                                                 Similarity
           108 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    108 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       14-FEB-1997;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    04-MAY-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                  13-NOV-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Copley CG,
                                                               Matches 105;
                                                                                                                                                                                                                                                                                                                                                                                               Synthetic.
                                                                                                                                                                                                                                                                      AAW41388;
           Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence
                                    Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
                                                    Local
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                                                                                                                                                                                                                   RESULT 13
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Novel single chain antibody molecule specifically recognizing common mutant epitope in mutant p53 but not in wild-type p53, and polynucleotides encoding antibodies, useful for preparing medicament
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               epitope peptide. Gene segments encoding the antibody heavy and light chain variable regions were amplified by PCR from the spleen obtained. When the genes isolated from the antibody genes was obtained. When the genes isolated from the antibody genes was subjected to panning, scFv DNA, expressed as phage antibodies and subjected to panning, scFv MEI was isolated, which possessed a significant affinity (0.1 uM) towards mutant p53. MEI was successfully expressed as a soluble antibody, separate from the phage fusion. MEI, DNA encoding if (see AAH26790-91) and a vector comprising the DNA, are used in claimed methods for treating a patient suffering from a disease related to mutation of the p53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The present sequence is that of a single chain antibody (scFv), designated MEI, which specifically recognises the common mutant epitope (see AAB82900) in mutant p53 protein but not in wild-type p53. To obtain the scFv, mice were immunized with the mutant p53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                /label= CDR3
/note= "light chain complementarity determining
                                                                                                                                                                                                                                             /note= "heavy chain complementarity determining
                                                                                                                                                                                                                                                                                                                                                                                                      /label= CDR2
/note= "light chain complementarity determining
                                                                                                                                                                                   /note= "heavy chain complementarity determining
                                                                                                                                                                                                                                                                                                     /note= "heavy chain complementarity determining
                                                                                                                                                                                                                                                                                                                                                            /note= "light chain complementarity determining
           Single chain antibody; ME1; mouse; p53; common mutant epitope;
tumour suppressor protein; therapy; cancer.
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                                                                                  Socation/Qualifiers
                                                                                                                'label= Heavy_chain
                                                                                                                                         'label= Light_chain
                                                                                                                                                                                                    region 1"
                                                                                                                                                                                                                                                            region 2"
                                                                                                                                                                                                                                                                                                                     region 3"
                                                                                                                                                                                                                                                                                                                                                                              region 1"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Govorko
                                                                                                                                                                                                                                                                                       CDR3
                                                                                                                                                          27..35
/label= CDR1
                                                                                                                                                                                                                                /label= CDR2
                                                                                                                                                                                                                                                                                                                                                /label= CDR1
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                                                                                                                                                                                                                                                                                                                                 .164
                                                                                                                                                                                                                                                                                                                                                                                          .186
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                                                                                                                                                                                                                                                                        99..105
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 2001-590047/66.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     for treating cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                N-PSDB; AAH26790
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WO200168801-A2.
                                                        Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      20-SEP-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      'n
                                                                                                                               Protein
                                                                                     Key
Region
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            This sequence is the light chain variable region of the antibody of the invention. The antibody is an anti-CEA (carcinoembryonic antigen) antibody (806.077 Ab). Host cells or transgenic organisms transformed with DNA encoding the antibody, are used to make the antibody or conjugate. The conjugate is used in a medicament suitable for intravenous administration. The conjugate can be used for cancer therapy, selectively killing tumour cells. The antibody can be used for in vivo or in vitro
                                                                                                                                                                                   Anti-CEA antibody; carcinoembryonic antigen; 806.077 Ab; cancer therapy; cancer diagnosis; complementarity determining region; light chain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 DIELTQSPAIMSASPGEKVTITCSASSSVSYMHWFQQKPGTSPKLWIYSTSNLASGVPAR 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                23 DIELTQSPAIMSASPGEKVTITCSASSSVTYMHWFQQKPGTSPKLWIYSTSNLASGVPAR 82
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0
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Pred. No. 8.2e-31;
3; Mismatches 1; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Anti-carcinoembryonic antigen antibody 806.077 Ab - used for
61 FSGSGSGTSYSLTISRMEAEDAATYYCQQRSTYPLTFGAGTKLELKRA 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Anti-p53 common mutant antigen single chain antibody ME1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FSGSGSGTSYSLTISRMEAEDAATYYCQQRSSYPFTFGSGTKLEIKR 107
                                                                                                                                                     Chimeric anti-CEA antibody 806.077 light chain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Example 8; Page 100-101; 208pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAB82897 standard; Protein; 256 AA
                                                                   AAW41392 standard; Protein; 235
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        diagnosis and therapy of cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                    Emery SC;
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96.38;
                                                                                                                                                                                                                                                                                                                                97WO-GB01165.
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                                                                                                                                                                                                                             Chimeric - Homo sapiens.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   diagnosis of cancer.
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                                                                                                                          02-JUN-1998
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                                                                                                                                                                                                                                                                                                                                                                                                                                    Copley CG,
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                                                                                                 AAW41392;
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                                         RESULT 14
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BX EX SX
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gene, especially cancer. scfv MEI serves as a powerful auxiliary agent capable of specifically enhancing the specificity and effectiveness of the two major existing anti-cancer gene therapies. Expression of the serv MEI molecules as an intrabody fused to the Expression of the serv MEI molecules as an intrabody fused to the degradation cascade may be capable of significantly reducing the level of mutant p53 in the cell, thereby broadening the range of possible tumour targets for the original therapy. The substitution of the original antibody by the scfv MEI specific to the mutant form of p53 may restrict the therapeutic effect to cancer cells only, allowing a systemic application of this therapy. MEI continuity and mad mas high permeability in the cells, and thus is a suitable probe for immunodiagnostic clinical detection of mutant is b53 in tissues using conventional immunohistochemistry techniques.
                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               QSPAIMSASPGEKVTITCSASSSVSYMHWFQQKPGTSPKLWIYSTSNLASGVPAR 60
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                                                                                                                                                                                                                                                                                                                                                                       96.1%; Score 536; DB 22; Length 256; 95.4%; Pred. No. 1.4e-30; Live 3; Mismatches 2; Indels (
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                                                                                                                                                                                                                                                                                                                                 256 AA;
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GenCore version 5.1.3 Copyright (c) 1993 - 2002 Compugen Ltd.
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                                                                          OM protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 200000000
                                                                                                                                                                                              Title:
Perfect score:
Sequence:
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A Genesea 101002:* Database

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Description	Variable heavy cha Antigen-binding pr Antigen-binding pr Humanised antibody VEGF antegonist an Antigen-binding pr VEGF antegonist an Antigen-binding pr Chimeric plc11 hea Human p53 protein
SUMMARIES	AXY97235 AAU7419 AAE13143 AAE13143 AAE82709 AAU74417 AAE82701 AAE82701 AAE13145 AAE13145
DB	22 22 22 22 22 18
% Query Match Length DB	117 117 117 117 117 117 1136 238 136
% Query Match	100.0 100.0 100.0 98.9 98.9 98.9 98.9
Score	631 631 624 624 624 624 624 612 612
Result No.	10084001

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AAW28492 AAX70787 AAW89173 AAW89173 AAW89173 AAW8917319 AAR75719 AAR75719 AAR75719 AAR75719 AAR75719 AAW1323 AAR860565 AAW1323 AAR60565 AAR60565 AAR60565 AAR60565 AAR60565 AAR60565 AAR61334 AAR61334 AAR1334 AAR1334 AAR1334 AAR1334 AAR1334 AAR1335 AAR1336 AAR14394 AAR14395 AA	AABU/96/
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ALIGNMENTS

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                                                                     Novel immunoglobulin molecules binding kinase insert domain-containing receptor with the same affinity as vascular endothelial growth factor, used to reduce tumour growth
                                                                                                                                                                            New immunoglobulin molecules are described that bind kinase insert domain-containing receptor (KDR) with a comparable affinity to human vascular endothelial growth factor (VEGF). The antibodies neutralise KDR activation The immunoglobulin may be a multivalent single chain antibody, a monovalent single chain antibody, a diabody, a triabody, a monovalent single chain antibody, a diabody, a triabody, a humanised antibody or a chimerised antibody, a diabody, a triabody, a humanised antibody or a chimerised antibody. The immunoglobulin molecules bind specifically to an extracellular domain of the KDR receptor with the same affinity as VEGF. Overexpression of VEGF has been implicated in a number of human tumour cell lines including glioblastoma multiforme, hemangioblastoma, central nervous system neoplasms and AIDS associated Karposi's sarcoma. The antibodies therefore have
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LQQSGAELVGSGASVKLSCTTSGFNIKDFYMHWVKQRPEQGLEWIGWIDPENGDSGY 60
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                                                                                                                                                                                                                                                                                                                                                                                                         ions in treating these conditions. This sequence encodes heavy chain complementary determining region of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Antigen-binding protein; antibody heavy chain variable domain; cytostéatus, anglogenesis inhibitor; tumour; leukaemia; antibody; vascular endothelial growth factor receptor; VEGF; cell groliferation inhibitor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             tch, 100.0%; Score 631; DB 21; Length 117; al Similarity 100.0%; Pred. No. 7.1e-47; 117; Conservative 0; Mismatches 0; Indels 0:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Antigen-binding protein heavy chain variable domain (VH) #1.
                                                                                                                                              Claim 4; Page 50-51; 55pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ANU74418 standard; peptide; 117 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     26-MAR 2002 (first entry)
               WPI; 2000-505966/45.
N-PSDB; AAA53767.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                            preferred
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The invention describes an antigen-binding protein (I) comprising a complex of two polypeptides (P1) and two second polypeptides (P2) which are stably associated in an immunoglobulin like complex. Pl has an antigen-binding site located to the N terminus of immunoglobulin (Ig) is useful for:

1 ight chain constant domain (CL domain), and P2 has an antigen-binding site located to the N terminus of the CHI domain. (I) is useful for:

1 centralising the activation of a vascular endothelial growth factor.

2 (VEGF) receptor: reducing tumour growth; inhibiting vEGF induced myration of human leukaemia cells; blocking interaction of a protein and instration of human leukaemia cells; blocking interaction of a protein and invivo and in vitro for investigative, diagnostic or treatment methods. The design of (I) provides for efficient production so that substantially all of the antigen-binding proteins produced are assembled in the desired configuration. (I) is bivalent and bispecific, homogeneous and in tetrameric form. The heavy chain constant domains which constitute the FC region (e.g., CH2 and CH3 for an IgG molecule) of a natural antibody and which provide other antibody functions can be present. There is no requirement for processing in vitro to obtain the complete product. This sequence represents a heavy chain variable domain (YH) incorporated the provider of the antiger than the domain the complete broader.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         into Fv, an engineered protein containing a heavy chain variable domain and a light chain variable domain in one polypeptide chain, described in the method of the invention.
New bispecific immunoglobulin-like antigen-binding protein for reducing tumour growth and for inhibiting angiogenesis, comprises a complex of two polypeptides and two second polypeptides
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Antigen-binding protein; single chain variable fragment; scFv; antigen; cytostatic, angiogenesis inhibitor; tumour; leukaemia; antibody; vascular endothelial growth factor receptor; VEGF; cell proliferation inhibitor.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note= "Heavy chain variable domain. Specifically claimed in claim 57"
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/note= "15 amino acid linker joins the VH and VL
regions of the single chain variable
fragment protein. Encoded by AAS20285"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAU74419 standard; Protein; 240 AA.
                                                                                         Claim 57; Page 57; 64pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /label= VH
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Matches 117;
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Synthetic.
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AAU74419
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Chimeric - Mus sp.
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                                                                                                                       WO200174296-A2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The invention describes an antigen-binding protein (I) comprising a complex of two polypeptides (P1) and two second polypeptides (P2) which are stably associated in an immunoglobulin like complex. Pl has an antigen-binding site located to the N terminus of immunoglobulin (Ig) light chain constant domain (CL domain), and P2 has an antigen-binding site located to the N terminus of the CH1 domain. (I) is useful for: neutralising the activation of a vascular endothelial growth factor (VEGF) receptor; reducing tumour growth; inhibiting angiogenesis; reducing endothelial cell proliferation; inhibiting vEGF induced migration of human leukaemia cells; blocking interaction of a protein and its ligand; promoting interactions between immune cells and target cells; and in vivo and in vitro for investigative, diagnostic or treatment methods. The design of (I) provides for efficient production so that substantially all of the antigen-binding proteins produced are assembled in the desired configuration. (I) is bivalent and bispecific, homogeneous and in tetrameric form. The heavy chain constant domains which constitute the Er region (e.g., CH2 and CH3 for an IgG molecule) of a natural antibody and which provide other antibody functions can be present. There have is the amino acid encounted the complete product.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ó
                                                                                                                                                                                                                                                      New bispecific immunoglobulin-like antigen-binding protein for reducing tumour growth and for inhibiting angiogenesis, comprises a complex of two polypeptides and two second polypeptides \cdot
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             variable
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               is the amino acid sequence of a single chain variable fragment
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   61 APKFQGKATMTADSSSNTAYLQLSSLTSEDTAVYYCNAYYGDYEGYWGQGTTVTVSS 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /label VL
/note= "Light chain variable domain. Specifically
claimed in claim 57"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (scFv), an engineered protein containing a variable light and venteavy domain on one polypeptide, described in the method of the
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          100.0%; Score 631; DB 23; Length 240; llarity 100.0%; Pred. No. 1.5e-46; Conservative 0; Mismatches 0; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Humanised antibody heavy chain fragment.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAE13143 standard; Protein; 117 AA.
                                                                                                                                                                                                                                                                                                             Claim 63; Page 62; 64pp; English.
                                                                                                                       24-MAY-2001; 2001WO-US16924.
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                                                                                                                                                                           (IMCL-) IMCLONE SYSTEMS INC
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Matches 117; Conserv
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                                                                 WO200190192-A2.
                                                                                            29-NOV-2001
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The invention relates to a method for inhibiting the growth of non-solid tumour cells that are stimulated by a ligand of vascular endothelial growth factor receptor (VEGFR) in mammals particularly humans. The method involves treating the mammals with humanised VEGFR monoclonal antibodies
Vascular endothelial growth factor receptor; VEGFR; antagonist; tumour; cytostatic; heavy chain; myelocytic leukaemia; lymphocytic; erythrocytic; multiple myeloma; lymphoid cell; Hodgkin's disease; mouse; human; chimeric.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (antagonists). Humanised monoclonal antibody comprises humanised mouse variable region joined to human constant region, where the humanised mouse variable region ontains mouse complementarity determining region (CDR) grafted into human variable region. The method is useful for treating leukaemias such as acute or chronic myelocytic leukaemia, acute or chronic lymphocytic leukaemia, erythrocytic or monocytic leukaemia, multiple myelomas and lymphoid cells, particularly those related to non-Hodgkin's and Hodgkin's disease. The present sequence is humanised antibody heavy chain frgament used in the exemplification of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Inhibiting growth of non-solid tumor cells useful to treat bone marrow tumors such as leukemias or multiple myeloma comprises treatment with an antagonist of a vascular endothelial growth factor receptor -
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61 APKFQGKATMTADSSSNTAYLQLSSLTSEDTAVYYCNAYYGDYEGYWGQGTTVTVSS 117
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vascular endothelial growth factor; angiogenesis; antiangiogenic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ;
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0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (IMCL-) IMCLONE SYSTEMS INC. (CORR ) CORNELL RES FOUND INC.
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Local Similarity 99.1
Les 116; Conservative
                                                                                                                                                                                                                             sapiens.
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61 APKFQGKATMTADSSSNTAYLQLSSLTSEDTAVYYCNAYYGDYEGYWGQGTTVTVSS 117

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collagen-vascular disease; autoimmune disease;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             preventing significant toxicity of the chemotherapeutic agent. The anti-angiogenic molecule inhibits or blocks the action of a vascular endothelium survival factor such as VEGF or its receptor, and is especially INC-1211. Conditions that can be treated include a neoplasm, a collagen vascular disease or an autoimmune disease, especially a solid tumour, including breast carcinoma, lung
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     carcinoma, prostate carcinoma, colon carcinoma, prostate carcinoma, ovarian carcinoma, neuroblastoma, central nervous system tumour, neuroblastoma, glioblastoma multiforme or melanoma (all claimed).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Treating or controlling an angiogenic dependent condition (e.g. neoplasm, collagen-vascular or autoimmune disease) in mammal by administering a combination of an antiangiogenic molecule and a
                  tumour; bréast carcinoma; lung carcinoma; prostate carcinoma; colon carcínoma; ovarian carcinoma; neuroblastoma; glioblastoma multiforme; melanoma; therapy; heavy chain.
                                                                                                                                                                                             "complementarity determining region 1"
                                                                                                                                                                                                                                              /note= "complementarity determining region 2"
                                                                                                                                                                                                                                                                                                    /note= "complementarity determining region 3"
                                                                                                                                          Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SUNNYBROOK HEALTH SCI CENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Disclosure; Page 38; 42pp; English.
                                                                                                                                                                                                               50..66
/label= CDR-H2
                                                                                                                                                                                                                                                            99..106
/label- CDR-H3
                                                                                                                                                              26..35
/label= CDR-H1
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                                                                                       - Mus sp.
- Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        chemothérapeutic agent
                                                                                                                                                                                               /note=
 neoplasm;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2001-514531/56.
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N-PSDB; #AAH26405.
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                                                                                       Chimeric
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The invention describes an antigen-binding protein (I) comprising a complex of two polypeptides (P1) and two second polypeptides (P2) which are stably associated in an immunoglobulin like complex. Pl has an antigen-binding site located to the N terminus of immunoglobulin (Ig) light chain constant domain (CL domain), and P2 has an antigen-binding site located to the N terminus of the CH1 domain. (I) is useful for: neutralising the activation of a vascular endothelial growth factor (VEGF) receptor: reducing tumour growth; inhibiting vegf induced migration of human leukaemia cells; blocking interaction of a protein and its ligand; promoting interactions between immune cells and target cells; and in vivo and in vitro for investigative, diagnostic or treatment methods. The design of (I) provides for efficient produced are assembled in the desired configuration. (I) is bivalent and bispecific, homogeneous and in tetrameric form. The heavy chain constant domains which constitute and in tetrameric form. The heavy chain constant domains which constitute antibody and which provide other antibody functions can be present. There is no requirement for processing in vitro to obtain the complete product. This sequence represents a heavy chain variable domain (VH) incorporated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   an engineered protein containing a heavy chain variable domain jht chain variable domain in one polypeptide chain, described in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New bispecific immunoglobulin-like antigen-binding protein for reducing tumour growth and for inhibiting angiogenesis, comprises a complex of two polypeptides and two second polypeptides.
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cytostatic; angiogenesis inhibitor; tumour; leukaemia; antibody; vascular endothelial growth factor receptor; VEGF; cell proliferation inhibitor.
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                                                                                                                                                                                                                                                         protein; antibody heavy chain variable domain;
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Pred. No. 2.8e-46;
); Mismatches 1;
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                                                                                                           AAU74417 standard; peptide; 117
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99.18;
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                                                                                                                                                                                                                                                       Antigen-binding
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Gaps

Length 117; 1; Indels 1 OVKLOQSGAELVGSGASVKLSCTTSGFNIKDFYMHWVKQRPEQGLEWIGWIDPENGDSGY 60

98.9%; Score 624; DB 22; 99.1%; Pred. No. 2.8e-46; ive 0; Mismatches 1;

Best Local Similarity 99.1 Matches 116; Conservative

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Local Similarity

Query Match

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RESULT 8
AAU74420
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The present sequence is that of the heavy chain variable region of IMC-1C11, a mouse-human chimeric antibody that has vascular endothelial growth factor (VBGF) antagonist activity. The antibody, orr a fragment of it, can be used as an anti-anglogenic molecule, together with a chemotherapeutic acid, for the treatment of an
                                                                                                                                                                              IMC-1c11; chimeric antibody; mouse; human; antagonist; VEGF; vascular endothelial growth factor; angiogenesis; antiangiogenic; antitumour; neoplasm; collagen-vascular disease; autoimmune disease; tumour; breast carcinoma; lung carcinoma; prostate carcinoma; colon carcinoma; ovarian carcinoma; neuroblastoma; glioblastoma multiforme; melanoma; therapy; heavy chain.
                                      APKFQGKATMTADSSSNTAYLQLSSLTSEDTAVYYCNAYYGDYEGYWGQGTTVTVSS 117
                                                61 APKFQGKATWTADSSSNTAYLQLSSLTSEDTAVYXCNAYYGDYEGYWGQGTTVTVSS 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Treating or controlling an angiogenic dependent condition (e.g. neoplasm, collagen-vascular or autoimmune disease) in mammal by administering a combination of an antiangiogenic molecule and a
                                                                                                                                                              VEGF antagonist antibody IMC-1C11 heavy chain variable region.
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                                                                                                                                                                                                                                                                                                /label= Signal_peptide
                                                                                                                                                                                                                                                                                                          20..136
/label= Mature_protein
                                                                                                                                                                                                                                                                              Location/Qualifiers
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                                                                                                       AAB82701 standard; Protein; 136 AA
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                                                                                                                                                                                                                                                                                                                              45..54
/label= CDR-H1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               28-JAN-2000; 2000US-0178791.
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                                                                                                                                             (first entry)
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                                                                                                                                                                                                                                                  - Mus sp.
- Homo sapiens.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  chemotherapeutic agent
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                                                                                                                        AAB82701;
                                                                                                                                                                                                                                                 Chimeric
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angiogenic dependent condition in a mammal, especially a human.

The invention relates generally to a method of treating or controlling an angiogenic dependent condition by administering an antiogenic molecule and a chemotherapeutic agent, to produce a carest of the condition while minimising or preventing significant toxicity of the chemotherapeutic agent.

The anti-angiogenic molecule inhibits or blocks the action of a vascular endothelium survival factor such as VEGF or its receptor, and is especially IMC-IC11. Conditions that can be treated include a neoplasm, a collagen-vascular disease or an autoimmune disease, especially a solid tumour, including breast carcinoma, lung carcinoma, prostate carcinoma, colon carcinoma, prostate carcinoma, covarian carcinoma, neuroblastoma multiforme or melanoma (all claimed).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Antigen-binding protein; single chain variable fragment; svFv; antigen; cytostatic; anglogenesis inhibitor; tumour; leukaemia; antibody; vascular endothelial growth factor receptor; VEGF; cell proliferation inhibitor.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                20 QVKLQQSGAELVGSGASVKLSCTTSGFNIKDFYMHWVKQRPEQGLEWIGWIDPENGDSDY 79
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 QVKLQQSGAELVGSGASVKLSCTTSGFNIKDFYMHWVKQRPEQGLEWIGWIDPENGDSGY 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                61 APKFQGKATMTADSSSNTAYLQLSSLTSEDTAVYYCNAYYGDYEGYWGQGTTVTVSS 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note= "Heavy chain variable domain. Specifically claimed in claim 61"
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/label= VL
/note= "Light chain variable domain. Specifically
claimed in claim 61"
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/note= "15 amino acid linker joins the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 624; DB 22;
Pred. No. 3.3e-46;
0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAU74420 standard; Protein; 238 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              98.98;
99.18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (IMCL-) IMCLONE SYSTEMS INC.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              24-MAY-2001; 2001WO-US16924
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches 116; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    . 238
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                                                                                                                                                                                                                                                                                                                                                                                                                                            136 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mus sp.
Synthetic.
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Region
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/label- CDR_H1

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              g
                                                                                                                                        The invention describes an antigen-binding protein (I) comprising a complex of two polypeptides (P1) and two second polypeptides (P2) which are stably associated in an immunoglobulin like complex. Pl has an antigen-binding site located to the N terminus of immunoglobulin (Ig) antigen-binding site located to the N terminus of immunoglobulin (Ig) is useful for:

CC light chain constant domain (CL domain), and P2 has an antigen-binding site located to the N terminus of the CH1 domain. (I) is useful for:

CC site located to the N terminus of the CH1 domain. (I) is useful for:

CC site located to the N terminus of the CH1 domain. (I) is useful for:

CC site located to the N terminus of the CH1 domain. (I) is useful for:

CC station for the name leavening two substantial and interaction of a protein and its ligadid; promoting interactions between immune cells and target cells; and in vivo and in vitro for investigative, diagnostic or treatment completent production so that methods from design of (I) provides for efficient production so that the desired configuration. (I) is bivalent and bispecific, homogeneous of in the desired configuration. (I) is bivalent and bispecific, homogeneous continued experiment for provide other antibody functions can be present. There is no regularement for provide other antibody functions can be present. There is no regularement for processing in vitro to obtain the complete product. This is the amino acid sequence of a single chain variable fragment (SPSY), the mediane protein containing a variable light and variable fragment for processing in the method of the survey.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Vasculiar endothelial growth factor receptor; VEGFR; antagonist; tumour; vertostatic; heavy chain; myelocytic leukaemia; lymphocytic; erythrocytic; monocytic; multiple myeloma; lymphoid cell; Hodgkin's disease; chimeric; human; plCl1 vector.
                                                      New bispecific immunoglobulin-like antigen-binding protein for reducing tumour growth and for inhibiting angiogenesis, comprises a complex of two polypeptides and two second polypeptides
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 QUKLQQSGAELVGSGASVKLSCTTSGFNIKDFYMHWVKQRPEQGLEWIGWIDPENGDSGY 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note= "Mature chimeric plCll heavy chain fragment"
45..54
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61 ABKFOGKATMTADSSSNTAYLQLSSLTSEDTAVYYCNAYYGDYEGYWGQGTTVTVSS 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61 APKFQGKATMTADSSSNTAYLQLSSLTSEDTAVYYCNAYYGDYEGYWGQGTTVTVSS 117
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0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       98.9%; Score 624; 'DB 23; Length 238; 99.1%; Pred. No. 5.9e-46; 1ive 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /label- Leader_peptide
20..136
                                                                                                                   Claim 63; Page 62-63; 64pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Chimeric p1C11 heavy chain fragment.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Location/Qualifiers
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hes 116; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Chimeric - Homo sapiens.
Chimeric - Unidentified.
                        WPI; 2002-106189/14.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           238 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAE13145;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Peptide
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Zhu Z;
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                p1C11 IgG expression vector. Chimeric p1C11 heavy chain contains cloned variable heavy chain (VH) and human IgG1 (gamma) heavy chain constant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Inhibiting growth of non-solid tumor cells useful to treat bone marrow tumors such as leukemias or multiple myeloma comprises treatment with an antagonist of a vascular endothelial growth factor receptor
                                                              /note= "Residue 'O' is present at this location in the
                                                                                                                                                           in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      61 APKFQGKATMTADSSSNTAYLQLSSLTSEDTAVYYCNAYYGDYEGYWGQGTTVTVSS 117
                                                                                                                                                        /note= "Residue 'O' is present at this location sequence shown in fig-11 of the specification" 119..125
/label= CDR_H3
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                                                                  sequence shown in fig-11 of the specification"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
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Pred. No. 3.5e-45;
0; Mismatches 3;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Example 3; Fig 11; 68pp; English.
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Tabel- CDR_H2
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97.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                    30-MAR-2001; 2001WO-US10504.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   31-MAR-2000; 2000US-0540770.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 2001-662942/76.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Witte L, Rafii S;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           N-PSDB; AAD21682
                                 Misc-difference
                                                                                                                                                                                                                                                                                                                      WO200174296-A2
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                                                                                                                                                                                                                                                                                                                                                                                     11-OCT-2001
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AAW28491
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The p53 variants are more active and more stable tumour suppressors and apoptosis-inducing agents than wild-type p53 and are active where the wild-type protein is not, i.e. they are not inactivated by dominant negative or oncogenic mutants, nor by other cellular proteins (because
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           oligomerisation domain deleted and replaced by a leucine zipper domain. The mutants preferably also have at least part of the p53 transactivation domain (amino acids 1-74) deleted and replaced by the transactivation domain (TD) from herpes simplex virus viral protein vpi6 (amino acids 411-40) or by a protein domain able to bind selectively to a transactivator, especially a single-chain antibody variable domain (ScFv). The present sequence is that of a specifically claimed p53 variant designated 8.325 and morphisms a ScFv domain, amino acids 75-325 of human wild-type p53 (but with a Arg182 replaced by His) and a leucine zipper domain at the C-terminal.
                                        Leucine zipper domain; LZD; oligomerisation domain; mutant; mutein; substitution; replacement; transactivation; viral protein VPIG; HSV; anti-oncogene; hyperproliferation; cancer; restenosis; SCFV; tumour suppression; apoptosis; single chain antibody variable domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New p53 variants e.g. with oligomerisation domain replaced by leucine zipper - useful for treating hyper-proliferative disorders,
                                                                                                                                                                                                                                                                                           /note= "Arg residue at position 182 of wild-type p53 has been mutated to His"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              the leucine zipper domain prevents formation of inactive mixed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claimed variants of protein p53 have at least part of the
                                                                                                                                                                                                                                              Location/Qualiflers
Human p53 protein variant S-325H.
                                                                                                                                                         Chimeric - Homo sapiens.
Chimeric - Herpes simplex virus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 36; Page -; 133pp; French.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (RHON ) RHONE POULENC RORER SA.
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ilarity 88.9%;
Conservative (
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                                                                                                                                                                                                                                                                                                                                                                WO9704092-A1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bracco L,
                                                                                                                                                                                                    Synthetic.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            claimed variants of protein p53 have at least part of the oligomerisation domain deleted and replaced by a leucine zipper domain. The mutants preferably also have at least part of the p53 transactivation domain (amino acids 1.74) deleted and replaced by the transactivation domain (TD) from herpes simplex virus viral proferant VPIG (amino acids 411-49) or by a protein domain able to bind selectively to a transactivator, especially a single-chain antibody variable domain (ScFv). The present sequence is that of a specifically claimed p53 variant designated S-325 and comprising a ScFv domain, amino acids 75-325 of human wild-type p53 and a leucine zipper domain at the C-terminal. The p53 variants are more active and more stable tumour suppressors and apoptosis-inducing agents than wild-type p53 and are active where the wild-type protein is not, i.e. they are not inactivated by dominant negative or oncogenic mutants, nor by other cellular proteins (because the leucine zipper comain prevents formation of inactive mixed oligomers).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ĥ
                                                               Leucine zipper domain; LZD; oligomerisation domain; mutant; mutein; substitution; replacement; transactivation; viral protein VP16; HSV; anti-oncogene; hyperproliferation; cancer; restenosis; ScFv; tumour suppression; apoptosis; single chain antibody variable domain.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New p53 variants e.g. with oligomerisation domain replaced by leucine zipper - useful for treating hyper-proliferative disorders, esp. cancer and restenosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          61 APKFQGKATMTADSSSNTAYLQLSSLTSEDTAVYYCNAYYGDYEGYWGQGTTVTVSS 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 554.5; DB 18; Length 535; Pred. No. 1.3e-39;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
                     Human p53 protein variant S-325 encoded by pEC176.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                6; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 36; Pages 88-90; 133pp; French
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAW28492 standard; Protein; 535
                                                                                                                                                                                                    - Herpes simplex virus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                       (RHON ) RHONE POULENC RORER SA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               87.9%;
                                                                                                                                                                                                                                                                                                                                                                96WO-FR01111.
                                                                                                                                                                                                                                                                                                                                                                                                        95FR-0008729
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches 104; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bracco L, Conseiller E;
                                                                                                                                                                              Chimeric - Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 1997-132633/12.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      535 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    N-PSDB; AAT86221
                                                                                                                                                                                                                                                                      WO9704092-A1
                                                                                                                                                                                                                                                                                                                                                           17-JUL-1996;
                                                                                                                                                                                                                                                                                                                                                                                                          19-JUL-1995;
                                                                                                                                                                                                                                                                                                                 06-FEB-1997
                                                                                                                                                                                                                           Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAW28492
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
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AAW28492
ID AAW28
XX
AC AAW28
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DT 25-NO
XX
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ä Gaps 1 QVKLQQSGAELVGSGASVKLSCTTSGFNIKDFYMHWVKQRPEQGLEWIGWIDPENGDSGY (Note: this sequence does not appear in the specification and has been produced by modifying the given sequence of variant V - 325). 1; Length 535; Indels DB 18; Score 554.5; DB 18; Pred. No. 1.3e-39; 6; Mismatches 6;

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AAW60769 standard; Protein; 243 AA.

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AAW60769
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                                                                                                                      Murine; psp protein; monoclonal antibody; PAD-421; DNA-binding domain; dermatological; immunosuppressive; antiinflammatory; autoimmune response; SLE; systemic lupus erythematosus; diagnosis; treatment; autoantigen; heavy chajn variable region; VH; complementarity determining region; CDR.
                                                                                           Murine ant pp3 monoclonal antibody PAb-421 heavy chain variable region.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The patent discloses a method for the treatment of systemic lupus erythematosus (SLE) by down-regulating the autoimmune response to the c-terminal DNA-binding domain of p53 protein by an active compound. The present sequence is a heavy chain variable region of monoclonal antibody PND-421 which is specific to the C-terminal DNA-binding domain of mutine p53 protein. PAD-421 antibody and peptides based on complementarity determining regions of light and heavy chain variable regions of the antibody, are examples of active compounds useful in the diagnomis, prevention and treatment of SLE in humans.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           OVKLOOSGAELVGSGASVKLSCTTSGFNIKDFYMHWVKQRPEQGLEWIGWIDPENGDSGY 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Treatment of systemic lupus erythematosus by down-regulating the utclimming response to the C-terminal DNA-binding domain of the p53 protein by an active compound comprising of antibodies to p53 or fragments of p53.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APKFOGKATMTADSSSNTAYLQLSSLTSEDTAVYYCNAYYGDYEGYWGQGTTVTVSS 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 21; Length 116;
                                                                                                                                                                                                                                                                                                    /label= CDR
/note= "Complementarity determining region"
99..105
/label= CDR
                                                                                                                                                                                                                                                                                  "Complementarity determining region"
                                                                                                                                                                                                                                                                                                                                                                          /note= "Complementarity determining region"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 550.5; DB 21; Length
Pred. No. 5.6e-40;
5; Mismatches 7; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Herkel J;
                                                                                                                                                                                                                                    Location/Qualifiers
AAY70787 standard; Protein; 116 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Erez-Alon N,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 78; Fig 9; 87pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (YEDA ) YEDA RES & DEV CO LTD
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88.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    99WO-US24443.
                                                                                                                                                                                                                                                      26..35
/label- cdr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 98US-0104816.
                                                               (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Rotter V,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 2000-339512/29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   116 AA;
                                                                                                                                                                                                                                                                                                                                                                                                       WO200023082-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  19-0CT-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 19-OCT-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                    27-APR-2000.
                                                              31-JUL-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Cohen IR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence
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                                                                                                                                                                                                       Mus sp
                                                                                                                                                                                                                                                  Region
                                                                                                                                                                                                                                                                                                                                              Region
                                                                                                                                                                                                                                                                                                  Region
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Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        61
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The present sequence represents a single chain antibody (ScFv) designated 421. The antibody binds to an epitope present in the C-terminal region of the p53 protein that includes oligomerisation and regulatory domains, specifically between positions 320 and 393. ScFv 421 is directed against p53 mutants, particularly H273, W248 and G281 mutants. When the ScFv is tirroduced into containing a mutant p53 protein, p53 dependent trans-activating activity is restored. ScFv 421 is specific for p53-mutants that have lost tumour-suppressing activity and are present in tumour cells. It is particularly used to treat hyper-proliferation associated with these mutants (e.g. cancer and re-stenosis) but may also be used in vitro for studying mechanisms of activity of p53 or its mutant and to purify or detect p53.
                                                                                                                                                          Single chain antibody; ScFv 421; mouse; p53 protein; oligomerisation; regulatory domain; p53 mutant; H273; W248; G281; p53-dependent trans-activating activity; restoration; treatment; tumour-suppressing activity; tumour cell; treatment; hyper-proliferation; cancer; re-stenosis; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           containing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 OVKLOOSGAELVGSGASVKLSCTTSGFNIKDFYMHWVKQRPEQGLEWIGWIDPENGDSGY 60
                                                                                                       Single chain antibody (ScFv) 421 that binds to mutant p53 proteins.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Restoring p53-dependent trans-activating activity to cell containi mutant p53 - by delivering single-chain antibody specific for the mutant, particularly for treatment of tumours
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 QVQLQQSGAELVRSGASVKLSCTASGFNIKDYYMHWVKQRPEQGLEMIGWIDPENGDTEY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 19; Length 243;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pred. No. 1.5e-39; 
; Mismatches 7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        87.1%; Score 549.5;
88.9%; Pred. No. 1.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ä.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAW89173 standard; peptide; 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              .;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 5; Page 31; 54pp; French
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (RHON ) RHONE-POULENC RORER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        96FR-0013176.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 97WO-FR01921
                                                      (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Similarity 88.9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bracco L;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 1998-272140/24.
N-PSDB; AAV36236.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    243 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Debussche L,
                                                      08-SEP-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    27-OCT-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        29-OCT-1996;
                                                                                                                                                                                                                                                                                                                                                                                       WO9818825-A1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 07-MAY-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Local Sim
Matches 104;
AAW60769;
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                                                                                                                                                                                                                                                                                                                                    Mus sp.
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RESULT 13

ò qq ò a cosmetic; herbicide;

Monoclonal antibody; Fd fragment; lead cation; perfume; pharmaceutical; health care; skin treatment; pesticide; Lead binding MAb 14G11 heavy chain variable region.

22-AUG-1997 (first entry)

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The present invention describes the use of an immunogen (A) to induce anti-tumnour immunity; to elicit an increased immune response to tumnour associated antigen (TAA) and/or to induce an immune response to mutant or wild-type forms of TAA in mammals. (A) is: (i) a monoclonal antibody (MAb) to TAA, or its fragment; (ii) a peptide based on a CDR (complementerity determining region) on the heavy or light chain of MAb (able to elicit antibodies to TAA); or (iii) a DNA that encodes the variable (V) region of MAb, in a gene delivery vehicle. The present sequence represents the variable heavy chain sequence from anti-p53 MAb (al. Also described is a method for generating sequence specific, anti-DNA antibodies (Ab) by immunising a mammal with a MAb directed to a commin containing a DNA-binding site of a DNA-binding protein. (A) is used to treat a wide variety of primary and metastatic cancers, condensing a man other language of primary and metastatic cancers, condensing and other parasites; to determine parentage; in forensic science; to isolate specific genes for DNA vaccination; in gene sequencing and cloning; also possibly for activation of selected thrappeutic genes in plants, animals and humans. (A) induce an effective anti-tumour response without causing harm to the patient. The method uses (A) to generate anti-TAA by exploiting the anti-idiotype network.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    4 LQQSGAELVGSGASVKLSCTTSGFNIKDFYMHWVKQRPEQGLEWIGWIDPENGDSGYAPK 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Anti-p53; monoclonal antibody 240; immunogen; anti-tumour; immunity; immune response; tumour associated antigen; metastatic cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Use of a monoclonal antibody to a tumour-associated antigen - to induce anti-tumour immunity or elicit an increased immune response
Anti-p53 monoclonal antibody 421 variable heavy chain sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            64 FQGKATMTADSSSNTAYLQLSSLTSEDTAVYYCNAYYGDYEGYWGQGTTVTVS 116
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Rotter V, Ruiz PJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Erez-Alon N, Herkel J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Example 3; Fig 3; 47pp; English.
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Matches 100; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           to the antigen
                                                                                                                                                                                                                                                                                        WO9856416-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                            09-JUN-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  09-JUN-1997;
                                                                                                                                                                                                                                                                                                                                                                      17-DEC-1998
                                                                                                                                                                               Mus sp.
Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Wolkowicz
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DNA encoding heavy metal binding polypeptide sequences – used for detecting, removing, adding or neutralising heavy metals, such as

Wylie DE;

Lopez O, Murray PJ, WPI; 1997-043140/04

N-PSDB; AAT58260

Lead cations

95US-0541373. 96WO-US09258

05-JUN-1996;

12-DEC-1996.

10-0CT-1995; 05-JUN-1995;

Mus musculus WO9639518-A1

neavy metal.

(BION-) BIONEBRASKA INC.

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                                                                                                                                                                                                                                                                                                                                                                                                                                                           The present sequence represents the heavy chain variable region for monoclonal antibody (MAD) 14G11, which immunoreacts with a lead cation. The sequence was derived from RNA isolated from mouse hybridoma cells. The protein can be used for binding heavy metals, such as lead cations. It can be used for detecting, removing, adding or neutralising the heavy metals in biological and inanimate systems. It can be used in e.g. aqueous liquid systems, in biological or environmental systems or in such compositions as perfumes, cosmetics, pharmaceuticals, health care products, skin treatment products, pesticides, herbicides, solvents used in the production of semi-conductor and integrated circuit components and production materials for electronic components. The products can provide for applications involving minute amounts of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      61 APKFQGKATMTADSSSNTAYLQLSSLTSEDTAVYYCNAY-YGDYEGYWGQGTTVTVSS 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                61 DPKFQGKATMTADISSNIAYLQLSSLISEDTAVYYCNPYGYDDAMDYWGQGTSVTVSS 118
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 532.5; DB 18; Length 118;
Pred. No. 2e-38;
6; Mismatches 10; Indels 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 12; Page 75; 125pp; English.
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85.6%;
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Matches 101; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          specific heavy metals.
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Search completed: December 23, 2002, 07:25:08 Job time : 64.8081 secs

AAW01586 standard; Protein; 118 AA

RESULT 15

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AAW01586
ID AAW0
XX
AC AAW0
XX

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Sequence 49, Appl Sequence 108, Ann
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                                                                        (without alignments)
163.250 Million cell updates/sec
                                                      December 33, 2002, 07:20:23 ; Search time 1.80233 Seconds
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/cgn2_6/ptodata/1/iaa/5B_COMB.pep:*
/cgn2_6/ptodata/1/iaa/6A_COMB.pep:*
/cgn2_6/ptodata/1/iaa/6B_COMB.pep:*
/cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
/cgn2_6/ptodata/1/iaa/pcTuS_COMB.pep:*
GenCore version 5.1.3
Copyright (c) 1993 - 2002 Compugen Ltd.
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US-09-280-028-4
US-08-344-000A-12
US-08-444-000A-12
US-08-434-000A-12
US-08-835-561-33
US-08-116-778E-2
US-08-438-562-2
US-09-393-385B-113
US-09-393-385B-113
US-09-393-385B-113
US-09-393-385B-113
US-08-438-562-37
US-08-190-199A-67
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US-08-836-561-49
                                                                                                                                                                                                Total number of hits satisfying chosen parameters:
                                                                                                                                                                              262574 segs, 29422922 residues
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Listing first 45 summaries.
                                        · protein search, using sw model
                                                                                                                                                          Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 200000000
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                                                                                                  US-09-865-198-4
48
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Match 1
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                                        OM protein
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                                                            Run on:
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Appli Appli Appli Appli Appli Appli Appli Appli Appli Sequence 8, Al Sequence 16, Al Sequence 1, Al Sequence 7, Al Sequence 165 Sequence 163 Sequence Seq Sequence Sequence Length 10; SOFTWARE: PatentIn Release #1.0, Version #1.25 CURRENT APPLICATION DATA: 100.0%; Score 48; DB 2; 1 100.0%; Pred. No. 0.0036; ive 0; Mismatches 0; US-08-477-728-19 US-08-477-728-19 US-08-477-728-16 US-08-477-728-16 US-08-474-040-1 US-08-474-040-16 US-08-474-040-16 US-08-487-200-1 US-08-487-200-1 US-08-487-200-1 US-08-487-200-1 US-08-487-200-1 US-08-487-200-16 US-08-487-200-16 US-08-488-1138-163 US-08-488-1138-165 US-08-488-1138-165 APPLICANT: SHITARA, KENYA
APPLICANT: HANAI, NOBUO
APPLICANT: HOWANA, YOSHIHISA
APPLICANT: HASEGAWA, MAMORU
TITLE OF INVENTION: HUMANIZED ANTIBODIES
NOMBER OF SEOGENCES: 49
CORRESPONDENCE ADDRESS:
ADDRESSEE: NIXON & VANDERHYE P.C. ALIGNMENTS APPLICATION NUMBER: US/08/116,778E FILING DATE: 07-SEP-93 CLASSIFICATION: 424 ATTORNEY/AGENT INFORMATION: NAME: WILSON, MARY J. E: NIXON & VANDERHYE P.C. 1100 NORTH GLEBE ROAD COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS 32,955 ER: 249-59 (9, Application US/08116778E APPLICANT: NAKAMURA, KAZUYASU STREET: 1100 NORTH GLEBE RC CITY: ARLINGTON STATE: VIGGINIA COUNTRY: U.S.A. ZIP: 22201-4714 COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk REFERENCE/DOCKET NUMBER: 24
TELECOMMUNICATION INFORMATION: KOIKE, MASAMICHI SHITARA, KENYA TELEFAX: (703)816-4100
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 10 amino acids TELEPHONE: (703)816-4000 TELEFAX: (703)816-4100 TOPOLOGY: linear MOLECULE TYPE: peptide 1006 1006 1006 1006 1006 1006 1006 REGISTRATION NUMBER: amino acid Query Match Best Local Similarity Matches 10; Conserv INFORMATION US-08-116-778E-9 APPLICANT: ; Patent No ; GENERAL US-08-116

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Gaps

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Indels

Conservative

SASSSVSYMH 10

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Sequence 1 Sequence 1 Sequence 1

US-07-634-278-7

Sequence Sequence

Sequence Sequence

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APPLICANT: FURUYA, Akiko
APPLICANT: FURUYA, Akiko
APPLICANT: NAKAMURA, Kazuyasu
APPLICANT: IIDA, Akihiro
APPLICANT: ANAZAWA, Hideharu
APPLICANT: ANAZAWA, Hideharu
APPLICANT: TAKATSU, Kiyoshi
TITLE OF INVENTION: Receptor Alpha Chain
NUMBER OF SEQUENCES: 106
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds LLP
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: NY
COUNTRY: USA
ZIP: 1006
COMPUTER READABLE FORM:
MEDIUM TYPE: Disketica
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 10;
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                                                                                   STREET: 1100 NOATH CLARK
COUNTR: ARLINGTON
STATE: VIGGINA
COUNTR: U.S.A.
ZIP: 22201-4714
COMBUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMBUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.25
CURRENT APPLICATION NUMBER: US/08/483,528B
FILING DATE: 07-JUN-95
CLASSIFICATION: 536
FILING DATE: (703)816-4000
TELECHMONICATION INFORMATION:
TELEPHONE: (703)816-4000
INFORMATION FOR SEQ ID NO: 97:
SEQUENCE CHARRACTERISTICS:
LENGTH: 10 amino acids
"VDF. AMINO ACIDS
"VDF. AMINO ACIDS
"WDF. AMINO ACIDS
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100.0%; Pred. No. 0.0036;
Live 0; Mismatches 0
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OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/836,561
FILING DATE: 09-MAY-1997
CLASSIFICATION: 424
                                              VANDERHYE P.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE: 09-MAY-1997
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 232384/95
FILING DATE: 11-SEP-1995
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME: Lawrence, III, Stanton T
REGISTRATION NUMBER: 25,736
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 49, Application US/08836561 Patent No. 6018032 GENERAL INFORMATION:
                                                  S: NIXON & VANDERHYE F
1100 NORTH GLEBE ROAD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 100.
Best Local Similarity 100.
Matches 10; Conservative
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CUNTRY, U.S.A.
ZIP: 2201-4714
COMPUTER FRAABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
COMPUTER: IBM PC COMPATIBLE
COMPUTER: IBM PC COMPATIBLE
COMPATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN BATE:
APPLICATION NUMBER: US/08/438,562
FLING-DATE: 10 MAY-95
CLASSIFICATION DATA:
APPLICATION NUMBER: 08/116,778
FILNG-DATE: 07-SEP-93
CLASSIFICATION: 424
ATONNEY/AGENT INFORMATION:
NAME: WILSON, MARY J.
REGISTERATION NUMBER: 32,955
REFERENCE/MONEY INFORMATION:
NAME: WILSON, MARY J.
REFERENCE/MONEY INFORMATION:
TELEPHONE: (70.3)816-4000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                100.0%; Score 48; DB 2; 100.0%; Pred. No. 0.0036;
                                                                                                                                                                                                                                                                                                                                       APPLICANT: RAKAWURA, KAZUYASU
APPLICANT: RAKAWURA, KAZUYASU
APPLICANT: KOTKE, MASAMICHI
APPLICANT: RITTANT, NOBUO
APPLICANT: HANAI, NOBUO
APPLICANT: HASEGAWA, MAMORU
APPLICANT: HASEGAWA, MAMORU
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APPLICANT: HASEGAWA, MAMORU
APPLICANT: HASEGAWE, MAMORU
APPLICANT: MASANI, MAMORU
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                                                                                                                                                                                                                        Sequence 9, Application US/08438562
Patent No. 587/4255
GENERAL INFORMATION:
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INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERRISTICS:
LENGTH: 10 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 100.

Best Local Similarity 100.
Matches :10; Conservative
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; MOLECURE TYPE: peptide
US-08-438-562-9
1 SASSSVSYMH 10
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US-08-483-528B-97
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Sequence 19, Application US/08308494A Patent No. 5959083
                                   Sequence 4, Application US/09280028 Patent No. 6241961
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                                                                                                                                                                                                                                                                                                                                                                                                ; ORGANISM: Mus musculus
US-09-280-028-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CITY: Washington STATE: D.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
Matches 10; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 SASSSVSYMH 10
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                 US-09-280-028-4
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                                                                                                                                                                                                                                                             Score 48; DB 3; Length 10;
Pred. No. 0.0036;
Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STATE: vince.

COUNTRY: U.S.A.

ZID: 22201-4714

COMPUTER: READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC COMPATIBLE
COPERATING SYSTEM: PC-DOS/Ms-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/393,385B
FTIING DATE: 27-JUN-96
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
APPLICANT: NAKAMURA, KAZUYASU
APPLICANT: STOTRE, MASAMICHI
APPLICANT: SHITARA, KENYA
APPLICANT: HANAI, NOBUO
APPLICANT: HASEGAWA, MAMORU
ITTLE OF INVENTION: HUMANIZED ANTIBODIES
NUMBER OF SEQUENCES: 113
CORRESPONDENCE ADDRESS:
ADDRESSEE: NIXON & VANDERHYE P.C.
STREET: 1100 NORTH GLEBE ROAD
7005-115-999
                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 5
US-09-393-385B-108
; Sequence 108, Application US/09393385B
; Patent No. 6423511
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE: 27-JUN-96
CLASSIFICATION:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703)816-4100
INFORMATION FOR SEQ ID NO: 108:
SEQUENCE CHARACTERISTICS:
LENGTH: 10 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
TOPOLOGY: linear
TOPOLOGY: linear
               TELECOMMUNICATION INFORMATION:
TELEPAX: 212-790-9090
TELEPAX: 212-86-9741
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 49:
SEQUENCE CHARACTERISTICS:
LENGTH: 10 amino acids
                                                                                                                                                                                                                                                                                                   0;
                                                                                                                                                                                                                                                             Query Match 100.0%;
Best Local Similarity 100.0%;
Matches 10; Conservative 0;
REFERENCE/DOCKET NUMBER:
                                                                                                                                                                    single
                                                                                                                                                                                                 , MOLECULE TYPE: peptide US-08-836-561-49
                                                                                                                                                  TYPE: amino acid
                                                                                                                                                                                       linear
                                                                                                                                                                                                                                                                                                                                                             1 SASSSVSYMH 10
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FACENT NO. 0.441901.

GENERAL INFORMATION:

APPLICANT: BENES, IVAN FRIEDRICH

APPLICANT: BENES, IVAN FRIEDRICH

APPLICANT: BOSSLET, KLAUS

TITLE OF INVENTION: RADIOIMMUNO CONJUGATES FOR USE IN HUMAN THERAPY AND

TITLE OF INVENTION: METHOD FOR THEIR PREPARATION

FILE REFERENCE: BENES

CURRENT APPLICATION NUMBER: US/09/280,028

CURRENT FILING DATE: 1999-03-15

EARLIER FILING DATE: 1999-03-15

EARLIER FILING DATE: 1998-03-27

NUMBER OF SEQ ID NOS: 16

SOFTWARE: Patentin Ver. 2.0

SEC ID NO 4

LENGTH: 97
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APPLICANT: Seeman, Gerhard
TITLE OF INVENTION: Tetravalent Bispecific Receptors, The
TITLE OF INVENTION: Preparation and Use Thereof
NUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     100.0%; Score 48; DB 4; Length 97; 100.0%; Pred. No. 0.038;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Indels
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COUNTRY D.C.

ZIP: 20005-3315

COMPUTER READBLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM FC Compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/308,494A

FLING DATE: 21-SEP-1994

CLASSIFICATION: 424

PRIOR APPLICATION NUMBER: US 07/891,739

FILING DATE: 01-JUN-1992

CLASSIFICATION DATA:

APPLICATION NUMBER: DE P4118120.4

FILING DATE: 03-JUN-1991

ATONNEY/AGENT INFORMATION:

NAME: KULIK, DATA:

NAME: KULIK, DATA:

NAME: NUMBER: 36,576
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADDRESSEE: Finnegan, Henderson, Farabow, Garrett
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REFERENCE/DOCKET NUMBER: 05552-1186-02000
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-408-4000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADDRESSEE: Dunner
STREET: 1300 I Street, N.W., Suite 700
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RESULT 9
US-09-312-157-12
US-09-312-157-12
Sequence 12, Application US/09312157
Fatent No. 6303341
GENERAL INFORMATION:
APPLICANT: ANDREW C. HIATT, JULIAN
H. R.-C. MA, THOMAS LEHNER
TITLE OF INVENTION: IMMUNOGLOBULINS CONTAINING PROTECTION
PROTEINS IN PLANTS AND THEIR USES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      100.0%; Score 48; DB 4; Length 105; 100.0%; Pred. No. 0.041;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DESCRIPTION: Guy's 13 Kappa SEQUENCE DESCRIPTION: SEQ ID NO: 12:
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OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: WORD Perfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/312,157
FILING DATE: 14-May-1999
CLASSIFICATION: CURNOWN>
PRIOR APPLICATION UNMBER: 08/43,000
FILING DATE: CUNKNOWN>
APPLICATION NUMBER: 08/43,000
FILING DATE: CUNKNOWN>
ATORNEY/AGENT INFORMATION:
NAME: Guise, Jeffrey W.
REGISTRATION NUMBER: 314,613
REFERENCE/DOCKET NUMBER: 312/127
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 552-8400
TELEPHONE: (619) 552-8400
TELEFRX: (679) 552-8400
TELEFRX: (679) 552-8400
TELEFRX: (679) 552-8159
                                                                                                                                                                                                                                                                                                                                                                                                                                                             COUNTRY: U.S.A.
ZIP: 90071
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
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                                                                                                                                                                                                                                                                                                                                             CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
Suite 4700
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Patent No. 6018032
GENERAL INFORMATION:
APPLICANT: KOIKE, Masamichi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE LISTING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LENGTH: 105 amino acids TYPE: amino acid
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NAKAMURA, Kazuyasu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 storage
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                                                                                                                                                                                                                                                                                                                                                                                                                            CITY: Los Angeles
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 100.

Best Local Similarity 100.

Matches 10; Conservative
                                             1 SASSSVSYMH 10
                                                                    24 SASSSVSYMH 33
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24 SASSSVSYMH 33
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APPLICANT:
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                                                                                                                                                                                                                        Length 100;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
ANDREW C. HIATT, JULIAN
APPLICANT: ANDREW C. HIATT, JULIAN
APPLICANT: K.-C. MA, THOMAS LEHNER
TITLE OF TRIVENTION: IMMUNOGLOBULINS CONTAINING PROTECTION
TITLE OF TRIVENTION: PROTEINS IN PLANTS AND THEIR USES
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
ADDRESSEE: LYON & LYON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 100.0%; Score 48; DB 3; Length 105; Best Local Similarity 100.0%; Pred. No. 0.041; Matches 10; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                  0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CLASSIFICATION: 435
PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/367,395
FILING DATE: 12/30/94
ATTORNEG GUISE, JEffrey W.
REGISTRATION NUMBER: 34,613
REFERENCE/DOCKET NUMBER: 34,613
REFERENCE/DOCKET NUMBER: 34,613
TELEPHONE: (619) 552-8400
                                                                                                                                                                                                                        Score 48; DB 2;
Pred. No. 0.039;
; Mismatches 0.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Guy's 13 Kappa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 READABLE FORM:
TYPE: 3.5" Diskette, 1.44 Mb
TYPE: storage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: Word Perfect 5.1
CURRENT PAPLICATION DATA:
APPLIGATION NUMBER: US/08/434,000A
                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 12 Application US/08434000A Patent No. 6046037
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633 West Fifth Street
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TELEGA. (01.)
TELEX: SEQUENCE LISTING
TELEX: SEQUENCE LISTING
SEQUENCE CHARACTERISTICS:
SEQUENCE CHARACTERISTICS:
LENGTH: 105 amino acids
TVPE: amino acids
TVPE: amino acids
Query Match % 100.0%;
Best Local Similarity 100.0%;
Matches 10% Conservative 0
                                                                             LENGTH: F00 amino acid
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY 1 linear
MOLECULE TYPE: peptide
US-08-308-494A-109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; TOPOLOGY: linear
; TOPOLOGY: DESCRIPTION:
US-08-434-000A-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Suite 4700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Los Angeles
California
                                                                                                                                                                                                                                                                                                   U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DATE:
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Gaps

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Gaps
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MAME/KEY: domain
LOCATION: 88..96
IDENTIFICATION METHOD: BY SIMILARITY
IDENTIFICATION METHOD: WITH KNOWN SEQUENCE OR TO AN ESTABLISHED
IDENTIFICATION METHOD: CONSENSUS
IDENTIFICATION METHOD: /product= "HYPERVARIABLE REGION 3"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     BY SIMILARITY WITH KNOWN SEQUENCE TO TO AN ESTABLISHED CONSENSUS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BY SIMILARITY WITH KNOWN SEQUENCE OR TO AN ESTABLISHED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        BY SIMILARITY WITH KNOWN SEQUENCE OR TO AN ESTABLISHED
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               IDENTIFICATION METHOD: CONSENSUS
OTHER INFORMATION: /product- "HYPERVARIABLE REGION 1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        IDENTIFICATION METHOD: CONSENSUS
OTHER INFORMATION: /product- "HYPERVARIABLE REGION 2"
                                                         MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
DERATIG SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/116,778E
FILING DATE: 07-SEP-93
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: WILSON, MARY J.
REGISTRATION NUMBER: 249-59
TELEPHONE: (703)816-4100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: HASEGAWA, MAMORU
TITLE OF INVENTION: HUMANIZED ANTIBODIES
NUMBER OF SEQUENCES: 49
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 12
US-08-438-562-2
; Sequence 2, Application US/08438562
; Patent No. 5874255
; GENERAL INFORMATION:
APPLICANT: NAKAMURA, KAZUYASU
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    HANAI, NOBUO
KUWANA, YOSHIHISA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: KOIKE, MASAMICHI
APPLICANT: SHITARA, KENYA
APPLICANT: HANAI, NOBUO
APPLICANT: KUWANA, YOSHIHISI
APPLICANT: HASEGAWA, MAMORU
                                                                                                                                                                                                                                                                                                                                                                                                                                          i: 129 amino acids
amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FEATURE:
NAME/KEY: sig_peptide
LOCATION: -22...1
IDENTIFICATION METHOD: I
IDENTIFICATION METHOD: I
IDENTIFICATION METHOD: I
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LOCATION: 49..55
IDENTIFICATION METHOD:
IDENTIFICATION METHOD:
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LOCATION: 24..33
IDENTIFICATION METHOD:
IDENTIFICATION METHOD:
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Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TOPOLOGY: linear
MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 SASSSVSYMH 10
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APPLICANT: IIDA, Akihiro
APPLICANT: ANAZANA, Hideharu
APPLICANT: HANAI, No. 6018032uo
APPLICANT: TAKATSI, No. 6018032uo
APPLICANT: TAKATSI, Kiyoshi
TITLE OF INVENTION: Antibody Against Human Interleukin-5
TITLE OF INVENTION: Receptor Alpha Chain
NUMBER OF SEQUENCES: 106
CORRESPONDENCE ADDRESS: ADDRESSE: Pennie & Edmonds LLP
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: NY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: NAKAWURA, KAZUYASU
APPLICANT: NAKAWURA, KAZUYASU
APPLICANT: SHITARA, KENYA
APPLICANT: HANAI, NOBUO
APPLICANT: HASEGAWA, MAMORU
TITLE OF INVENTION: HUMANIZED ANTIBODIES
CORRESPONDENCE ADDRESSE: A 74
ADDRESSEE: NIXON & VANDERYXE P.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME: LAWFERCE, III, Stanton T
REGISTRATION NUMBER: 25,736
REFERENCE/DOCKET NUMBER: 7005-115-999
TELECOMMUNICATION INFORMATION:
TELEFAX: 212-790-9090
TELEFAX: 212-869-944
TELER: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 33:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: US/08/836,561
FILING DATE: 09-MAY-1997
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: UP 232384/95
FILING DATE: 11-SEP-1995
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3: NIXON & VANDERHYE P.C. 1100 NORTH GLEBE ROAD
                                                                                                                                                                                                                                                                                                                                              ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ Version 2.0
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 2, Application US/08116778E Patent No. 5830470
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TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity 100
Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TOPOLOGY: linear MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                  USA
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                                                                                                                                                                                                                                                                                                                                  COUNTRY:
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IDENȚIFICATION METHOD: WITH KNOWN SEQUENCE OR TO AN ESTABLISHED
IDENȚIFICATION METHOD: CONSENSUS
IDENȚIFICATION METHOD: CONSENSUS
INFORMATION: /product= "HYPERVARIABLE REGION 3"
US-08-438-562-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         BY SIMILARITY WITH KNOWN SEQUENCE OR TO AN ESTABLISHED CONSENSUS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WITH KNOWN SEQUENCE TO TO AN ESTABLISHED
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             OTHER INFORMATION: /product= "HYPERVARIABLE REGION 1"
                                                                                COUNTRY TO U.S.A.

ZIP: 22201-4714
COMPUTER READABLE FORM:
MEDTION TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/NS-DOS
SOFTWARF: PATENTIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/438,562
FILING DATE: 10-MAY-95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     BY SIMILARITY
                                                                                                                                                                                                                                                                                                             CLASSIFICATION: 424

PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/116,778
FILING PARTE: 07-SEP-93
CLASSIFICATION: 424
ATONEV AGANT INFORMATION:
NAME: MILSON, MARY J.
REGISTRATION NUMBER: 32,955
REBERBING-PROCKET NUMBER: 249-76
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CONSENSUS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEFAX: (703)816-4100
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE, CHARACTERISTICS:
LENGTH: 129 amino acids
TYPE: (Amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME/KEY: domain
LOCATION: 88..96
IDENTIFICATION METHOD:
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IDENTIFICATION METHOD:
IDENTIFICATION METHOD:
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IDENTIFICATION METHOD:
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LOCATION: 49..55
IDENTIFICATION METHOD:
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IDENȚIFICATION METHOD:
OTHER INFORMATION: /pr
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Matches $ 10; Conservative
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LOCATION: -22..-1
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ADDRESSEE
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RESULT 13' US-08-483-528B-92 ; Sequence 92, Application US/08483528B

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME/KEY: domain
LOCATION: 88.96
IDENTIFICATION METHOD: BY SIMILARITY
IDENTIFICATION METHOD: WITH KNOWN SEQUENCE OR TO AN ES
IDENTIFICATION METHOD: CONSENSUS
IDENTIFICATION METHOD: CONSENSUS
IDENTIFICATION METHOD: CONSENSUS
US-08-483-528B-92
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OTHER INFORMATION: /product= "HYPERVARIABLE REGION 2"
                                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/483,528B
FILING DATE: 07-JUN-95
CLASSIFICATION: 536
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703)816-4000
INFORMATION FOR SEQ ID NO: 92:
SEQUENCE CHARACTERISTICS:
                                                         APPLICANT: HANAI, NOBUO
APPLICANT: KUWANA, YOSHTHISA
APPLICANT: HASEGAWA, WAMORU
TITLE OF INVENTION: HUMANIZED ANTIBODIES
NUMBER OF SEQUENCES: 103
CORRESPONDENCE ADDRESS:
                                                                                                                                                                         SSEE: NIXON & VANDERHYE P.C.
1100 NORTH GLEBE ROAD
ARLINGTON
                                                                                                                                                                                                                                                                  COUNTRY: U.S.A.
ZIP: 22201-4714
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DC
APPLICANT: NAKAMURA, KAZUYASU
APPLICANT: KOIKE, MASAMICHI
                                        SHITARA, KENYA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      : 129 amino acids amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME/KEY: sig_peptide
LOCATION: -22 -1
IDENTIFICATION METHOD:
IDENTIFICATION METHOD:
IDENTIFICATION METHOD:
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LDENTIFICATION METHOD: 1DENTIFICATION METHOD: 4
IDENTIFICATION METHOD: 4
IDENTIFICATION METHOD: 6
OTHER INFORMATION: /proc
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IDENTIFICATION METHOD:
IDENTIFICATION METHOD:
IDENTIFICATION METHOD:
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FEATURE:
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Best Local Similarity
Matches 10; Conserv
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Search completed: December 23, 2002, 07:33:14 Job time : 2.80233 secs
                                                                                                CLASSIFICATION:
CLASSIFICATION:
TELECOMUNICATION INFORMATION:
TELEPHONE: (703)816-4000
TELEFAX: (703)816-4100
INFORMATION FOR SEQ ID NO: 113:
SEQUENCE CHARACTERISTICS:
LENGTH: 130 amino acids
TYPE: amino acid
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                      , MOLECULE TYPE: protein US-09-393-385B-113
                                                                                                                                                                                                                                                                                       linear
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0.052;
hes 0; Indels
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/393,385B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 113, Application US/09393385B
Patent No. 6423511
GENERAL INFORMATION:
APPLICANT: NAKAMURA, KAZUYASU
APPLICANT: SHITARA, KENYA
APPLICANT: SHITARA, KENYA
APPLICANT: HANAI, NOBUO
APPLICANT: HASEGAWA, WAMORU
TITLE OF INVENTION: HUMANIZED ANTIBODIES
NUMBER OF SEQUENCES: 113
CORRESPONDENCE ADDRESS:
                                                                                            APPLICANT: NAKAWURA, KAZUYASU
APPLICANT: KOIKE, MASAMICHI
APPLICANT: SHITARA, KENYA
APPLICANT: HANAI, NOBUO
APPLICANT: HASEGAWA, YOSHIHISA
APPLICANT: HASEGAWA, MANORU
TITLE OF INVENTION: HUMANIZED ANTIBODIES
CORRESPONDENCES: 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     100.0%; Score 48; DB
100.0%; Pred. No. 0.0
iive 0; Mismatches
                                                                                                                                                                                                                                                                                 ADDRESSEE: NIXON & VANDERHYE P.C. STREET: 1100 NORTH GLEBE ROAD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADDRESSEE: NIXON & VANDERHYE P.C. STREET: 1100 NORTH GLEBE ROAD
                                   Sequence 111, Application US/09393385B Patent No. 6423511 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELECOMMUNICATION INFORMATION:
TELEPHONE: (703)816-4000
TELEPAX: (703)816-4100
INFORMATION FOR SEQ ID NO: 111:
SEQUENCE CHARACTERISTICS:
LENGTH: 130 anino acids
TYPE: amino acid
STRANDEDNESS: single
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
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Best Local Similarity 100.
Matches 10; Conservative
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MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         46 SASSSVSYMH 55
                                                                                                                                                                                                                                                                                                                         CITY: ARLINGTON STATE: VIRGINIA
                                                                                                                                                                                                                                                                                                                                                               COUNTRY: U.S.A.
ZIP: 22201-4714
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE: 2 CLASSIFICATION:
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US-09-393-385B-113
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                US-09-393-385B-111
RESULT 14
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PatentIn Release #1.0, Version #1.25
                 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/393,385B
FILING DATE: 27-JUN-96
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December 23, 2002, 07:20:23; Search time 1.26163 Seconds (without alignments) 163.250 Million cell updates/sec
GenCore version 5.1.3
Copyright (c) 1993 - 2002 Compugen Ltd.
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                                                                           OM protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                                                           Minimum DB seq length: 0
Maximum DB seq length: 2000000000
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31
1 STSNLAS 7
                                                                                                                                                                                         Title:
Perfect score:
Sequence:
                                                                                                                                                                                                                                                                      Scoring table:
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                                                                                                              Run on:
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Issued_Patents_AA:* Database :

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

1: /cgn2_6/ptodata/1/iaa/5A_COMB.pep:*
2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep:*
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4: /cgn2_6/ptodata/1/iaa/6B_COMB.pep:*
5: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
6: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Description	10,	10,	98,		ď,	15,	12,	12,	20,	61,	65,	71,	8,	o,	Sequence 2, Appli	7	92,	111,	Sequence 113, App	37, 1	37,		Se		8	Sequence 17, Appl	52,
ID	US-08-116-778E-10	US-08-438-562-10	US-08-483-528B-98	US-09-171-945-27	US-09-393-385B-109	US-08-308-494A-15	US-08-434-000A-12	US-09-312-157-12	US-09-171-945-50	US-09-171-945-61	US-09-171-945-65	US-09-171-945-71	US-08-483-749A-8	US-09-171-945-9	US-08-116-778E-2	US-08-438-562-2	US-08-483-528B-92	US-09-393-385B-111	-09-393-3	US-08-116-778E-37	US-08-438-562-37	US-08-483-528B-101	US-08-630-820-6	5455030-3	5455030-5	US-09-171-945-17	US-09-171-945-52
DB	~	~	~	4	4	~	٣	4	4	4	4	4	٣	4	7	~	~	4	4	~	7	~	m	9	9	4	4
% Query Match Length DB	7	7	7	7	7	100	105	105	107	107	107	107	108	108	129	129	129	130	130	133	133	133	213	215	225	235	235
% Query Match	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0
Score	31	31	31	31	31	31	31	31	31	31	31	31	31	31	31	31	31	31	31	31	31	31	31	31	31	31	31
Result No.	0	7	m, ·	4	S	9	7	8	6	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	56	27

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Sequence 97, Appl Sequence 99, Appl	۰. ک	Sequence 2, Appli Sequence 2, Appli	Patent No. 5455030	Sequence 2, Appli	Sequence 44, Appl	Sequence 16, Appl	Sequence 16, Appl	Sequence 16, Appl	Sequence 16, Appl	Sequence 51, Appl	Sequence 13, Appl	Sequence 14, Appl	13,	Sequence 21, Appl
US-09-171-945-97 US-09-171-945-99	5455030-7 rrs-08-230-843-2	US-08-636-936-2	5455030-3 5455030-11	US-08-652-507-2	US-09-423-439-44	US-08-661-052-16	US-09-188-082-16	US-09-364-088-16	US-09-102-716-16	US-09-423-439-51	US-08-783-853A-13	US-09-280-028-14	US-09-344-050-13	US-07-678-974D-21
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235	236	244	248	270	281	553	553	553	553	999	7	7	7	20
100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	90.3	90.3	90.3	90.3
31	31	31	31	31	31	31	31	31	31	33	58	28	28	28
28	30	35	34	35	36	37	38	39	40	41	42	43	44	45

ALIGNMENTS

SSULT 1	
Sequence 10, Application US/08116778E	
Patent No. 5830470 GENERAL INFORMATION:	
APPLICANT: NAKAMURA, KAZUYASU	
APPLICANT: SHITAKA, KENYA ADDIICANT: HANAT NOBIO	
à	
11	
NUMBER OF SEQUENCES: 49	
ADDRESSEE: NIXON & VANDERHYE P.C.	
GLEBE ROAD	
~	
STATE: VIRGINIA	
COUNTRY: U.S.A.	
ö	
COMPUTER: IBM PC compatible	
SYSTEM: PC-DOS/MS-DOS	
SOFTWARE: Patentin Release #1.0, Version #1.25	
CURRENT APPLICATION DATA:	
AFFLICATION NOMBER: 05/06/110,//65	
CLASSIFICATION 424	
ပ္	
NAME: WILSON, MARY J.	
, 955	
REFERENCE/DOCKET NUMBER: 249-59	
#ENERHONE: (/OS)810-4000	
INFORMATION OF THE TOTAL TO THE TOTAL THE TOTAL TO THE TOTAL THE TOTAL TO THE TOTAL	
LENGTH: 7 amino acids	
no acid	
ŗ	
MOLECULE TYPE: peptide	
Match. 100.0%; Score 31;	
Best Local Similarity 100.0%; Pred. No. 1.9e+05; Matches 7: Consormative O. Mismatches O. Indels O. Ca	מ
/; Colliservallive U; Mismalches U; inders U;	מ קמ ני

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APPLICANT: Emery, Stephen
APPLICANT: Emery, Clive Graham
APPLICANT: Emery, Clive Graham
APPLICANT: Emery, Clive Graham
APPLICANT: Expery, Clive Graham
APPLICANTON: Monoclonal Antibody to CEA
CURRENT APPLICATION NUMBER: US/09/171,945
CURRENT FILING DATE: 1998-10-29
FRIOR FILING DATE: 1997-02-14
FRIOR PAPLICATION NUMBER: GB9609405.7
FRIOR PAPLICATION NUMBER: PCT/GB97/01165
FRIOR APPLICATION NUMBER: PCT/GB97/01165
FRIOR APPLICATION NUMBER: PCT/GB97/01165
FRIOR FILING DATE: 1997-04-29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; OTHER INFORMATION: Description of Artificial Sequence: humanized US-09-171-945-27
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                   CITY:

STATE: VIRGIA...

COUNTRY: U.S.A.

ZIP: 22201-4714

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/483,528B

FILING DATE: 07-UN-95

CLASSIFICATION: SAGE

TELEPHONE: (703)816-4000

TELEPHONE: (703)816-4100

TELEPHONE: (703)816-4100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             100.0%; Score 31; DB 2; 100.0%; Pred. No. 1.9e+05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 27, Application US/09171945
Patent No. 6277599
GENERAL INFORMATION:
                       ADDRESSEE: NIXON & VANDERHYE E
STREET: 1100 NORTH GLEBE ROAD
CITY: ARLINGTON
STATE: VIRGINIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 27
LENGTH: 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 100.(
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY: linear

MOLECULE TYPE: peptide

US-08-483-528B-98
  CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 STSNLAS 7
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                                                                                                                                                                                                                                                                                                                                                                                                                                              STATE: FALLENDING
STATE: FALLENDING
COUNTRY: U.S.A.
ZIP: 22201-4714
COMPUTER: READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ouery Match
Best Local Similarity 100.0%; Pred. No. 1.9e+05;
Matches 77; Conservative 0; Mismatches 0;
                                                                                               Sequence 10, Application US/08438562
Patent No. 5874255
GENERAL INFORMATION:
APPLICANT:
ASSEGMA, MAMORU
TITLE OF INVENTION:
NUMBER OF SEQUENCES:
ADDRESSE:
ADDRESSE:
ADDRESSE:
ADDRESSE:
ANXON & VANDERYE P.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLIÇÂNT: NAKAMURA, KAZUYASU
APPLIÇÂNT: KOTKE, MASAMICHI
APPLIÇÂNT: SHITARA, KENYA
APPLIÇÂNT: HANAI, NOBUO
APPLICANT: KUMANA, YOSHIHISA
APPLICANT: HASEGANA, MAMORU
TITLEÂOF INVENTION: HUMANIZED ANTIBODIES
NUMBER OF SEQUENCES: 103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CARACH AFTLAND NUMBER: US/08/438,562
ETLING DATE: 10-MAY-95
CLASSIELCATION 1424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/116,778
FILINGEDATE: 07-SEP-93
CLASSIETCATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: #MILSON MARY J.
RECISTRATION NUMBER: 32,955
RECISTRATION NUMBER: 32,955
RECISTRATION NUMBER: 32,955
TELECOMMUNICATION INFORMATION:
TELECHOME: (703)816-4400
                                                                                                                                                                                                                                                                                                                                                                               SEE: NIXON & VANDERHYE P.C.:
** 1100 NORTH GLEBE ROAD
ARLINGTON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 98, Application US/08483528B Patent No. 5939532 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        INFORMATIÓN FOR SEÓ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 7 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TOPOLÕGY: linear
MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           amino acid
1 STSNLAS 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 STSNLAS 7
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                                                                                      US-08-438-562-10
                                                                                                                                                                                                                                                                                                                                                                                                      STREET: AR
CITY: AR
STATE: V
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                                                                   RESULT 2
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Sequence 12, Application US/08434000A

Patent No. 6046037

GENERAL INFORMATION

APPLICANT: ANDREW C. HIATT, JULIAN

APPLICANT: K.-C. MA, THOMAS LEHNER

TITLE OF INVENTION: IMMUNOGLOBULINS CONTAINING PROTECTION

TITLE OF INVENTION: PROTEINS IN PLANTS AND THEIR USES

NUMBER OF SEQUENCES: 19

CORRESPONDENCE ADDRESS:

ADDRESSEE: Lyon & Lyon

STREET: 633 West Fifth Street

STREET: G31 Let 470

CITY: Los Angeles

STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 100.0%; Score 31; DB 2; Length 100; Best Local Similarity 100.0%; Pred. No. 4.3; Matches 7; Conservative 0; Mismatches 0; Indels
SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/308,494A
FILING DATE: 21-SEP-1994
CLASSIFICATION: 424
                                                                                                              PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/891,739
FILING DATE: UJ-1092
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: DE P4118120.4
FILING DATE: UNFORMATION:
NAME: KOLIK, DAVIG J.
REGISTRATION NUMBER: 36,576
REFERENCE/DOCKET NUMBER: 05552-1186-02000
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-408-4400
INFORMATION FOR SEQ ID NO: 15:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
Including application
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/367,395
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: storage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  OPERATING SYSTEM: IBM P.C. DOS 5.0 SOFTWARE: Word Perfect 5.1 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/434,000A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME: Guise, Jeffrey W. REGISTRATION NUMBER: 34,613
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER: IBM Compatible OPERATING SYSTEM: IBM P.C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE: 12/30/94 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE CHARACTERISTICS:
LENGTH: 100 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TOPOLOGY: linear
MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-08-308-494A-15
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Patent No. 5559083
CENERAL INFORMATION:
CENERAL INFORMATION:
APPLICANT: Seeman, Gerhard
TITLE OF INVENTION: Tetravalent Bispecific Receptors, The
TITLE OF INVENTION: Preparation and Use Thereof
NUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADDRESSEE: Finnegan, Henderson, Farabow, Garrett & ADDRESSEE: Dunner
                                                                                                                                                                                                                                                                                                                                                                                                                                         COUNTRY: U.S.A.
2IP: 22201-4714
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      100.0%; Score 31; DB 4; 100.0%; Pred. No. 1.9e+05;
                                                                                                                                      APPLICANT: NAKAMURA, KAZUYASU
APPLICANT: KOIKE, MASAMICHI
APPLICANT: SHITARA, KENYA
APPLICANT: HANLI, NOBUO
APPLICANT: HASEGAWA, MAMORU
ITLLE OF INVENTION: HUMANIZED ANTIBODIES
NUMBER OF SEQUENCES: 113
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STREET: 1300 I Street, N.W., Suite 700 CITY: Washington STATE: D.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/393,385B
FILING DATE: 27-JUN-96
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                   ADDRESSEE: NIXON & VANDERHYE P.C. STREET: 1100 NORTH GLEBE ROAD CITY: ARLINGTON STATE: VIRGINIA
                                                                        Sequence 109, Application US/09393385B Patent No. 6423511 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELECOMMUNICATION INFORMATION:
TELEPHONE: (703)816-4000
TELEFAX: (703)816-4100
INFORMATION FOR SEQ ID NO: 109:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 100.
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LENGTH: 7 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
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                                                    JS-09-393-385B-109
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                          RESULT 5
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Gaps

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ORGANISM: Artificial Sequence
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                                                                                                                                                                   RESULT 9
US-09-171-945-50
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                   Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: ANDREW C. HIATT, JULIAN
K.-C. MA, THOMAS LEHNER
TITLE OF INVENTION: IMMUNOGLOBULINS CONTAINING PROTECTION
FOR
                                                                                                                                                                                                                                                    100.0%; Score 31; DB 3; Length 105; 100.0%; Pred. No. 4.6;
                                                                                                                                                                                                                                                                                       0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER: IBM Compatible
SOFWARE: WORD PERFORM: LBM P.C. DOS 5.0
CURRENT APPLICATION DATA:
                                                                                                                                                                                                     Guy's 13 Kappa
                                                                                                                                                                                                                                                                                       0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: US/09/312,157
FILING DATE: 14-May-1999
CLASSIFICATION: <UNKNOWN>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RAME: Guise, Jeffrey W.
REGISTRATION NUMBER: 312/127
REFERENCE/COKET NUMBER: 212/127
RELEPHONE: (619) 552-8400
TELEFAX: (619) 552-0159
TELEFAX: (619) 552-0159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; SEQUENCE DESCRIPTION: SEQ ID NO: 12:
US-09-312 $157-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRÃOR APPLICATION DATA:
APPLICATION NUMBER: 08/434,000
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
STREET: 613 West Fifth Street
Sulte 4700
REFERENCE/DOCKET NUMBER: 212/127
                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 12 Application US/09312157
Patent No. 6303341
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE LISTING INFORMATION FOR SEQ ID NO: 12: SEQUENCE CHARACTERISTICS:
            TELECOMMUNICATION INFORMATION:
TELEPHONE (619) 552-8400
TELEFAX: (619) 552-0159
TELEX: 67-3510
TELEX: SEQUENCE LISTING
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 105 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LENGTH: 105 amino acids
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STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CITY: Los Angeles
STATE: California
COUNTRY: U.S.A..
ZIP: 90071
COMPUTER READABLE FORM:
                                                                                                                                                                                linear
DESCRIPTION:
                                                                                                                                                                                                                                                                                       Conservative
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                                                                                                                                                                   single
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Matches 75 Conserva
                                                                                                                                                                   STRANDEDNESS:
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US-08-434-000A-12
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Sequence 61, Application US/09171945

Sequence 61, Application US/09171945

Patent No. 627759

GENERAL INFORMATION:

APPLICANT: Emery, Clive Graham

APPLICANT: Copley, Clive Graham

APPLICANT: Emery, Clive Graham

APPLICANT: Emery, Clive Graham

APPLICANT: Emery, Clive Graham

APPLICANT: Monoclonal Antibody to CEA, Conjugates Comprising Said

TITLE OF INVENTION: Antibody, and Their Therapeutic Use in an Adept System

TITLE OF INVENTION: Antibody, and Their Therapeutic Use in an Adept System

FILE REFERENCE: 1998-10-29

CURRENT FILING DATE: 1998-10-29

PRIOR APPLICATION NUMBER: GB9003405.7

PRIOR APPLICATION NUMBER: GB9003405.7

PRIOR APPLICATION NUMBER: POT/GB97/01165

PRIOR APPLICATION NUMBER: POT/GB97/01165

PRIOR APPLICATION NUMBER: POT/GB97/01165

SOFTWARE: PatentIn Ver. 2.1

SEQ ID NO 61

LENGTH: 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:

APPLICANT: Emery, Stephen

APPLICANT: Copley, Clive Graham

APPLICANT: Copley, Clive Graham

APPLICANT: Edge, Michael Derek

TITLE OF INVENTION: Monoclonal Antibody to CEA, Conjugates Comprising Said

TITLE OF INVENTION: Monoclonal Antibody to CEA

TITLE OF INVENTION: Monoclonal Antibody to CEA

TITLE OF INVENTION: Monoclonal Antibody to CEA

CURRENT APPLICATION NUMBER: US/09/171,945

CURRENT FILING DATE: 1998-10-29

PRIOR FILING DATE: 1997-02-14

PRIOR FILING DATE: 1997-02-14

PRIOR APPLICATION NUMBER: GE9609405.7

PRIOR FILING DATE: 1997-02-14

PRIOR FILING DATE: 1997-04-29

NUMBER OF SEQ ID NOS: 131

COPPURABE: DATE OF TAXABLE 
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; OTHER INFORMATION: Description of Artificial Sequence: humanized
US-09-171-945-50
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100.0%; Score 31; DB 4; Length 105; 100.0%; Pred. No. 4.6;
                                                                                                0; Indels
                                                                                                0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 50, Application US/09171945 Patent No. 6277599
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ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Patentin Ver. 2.1
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Best Local Similarity 100.
Matches 7; Conservative
                                             Best Local Similarity 100.
Matches 7; Conservative
                                                                                                                                                                                                                                                        49 STSNLAS 55
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49 STSNLAS 55
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ORGANISM: Artificial Sequence
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                                                                                                                                                                                                                  1 STSNLAS 7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY:
                                                                                                                                                                                                                                                                                                                    RESULT 13
US-08-483-749A-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 14
US-09-171-945-9
LENGTH: 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT:
                                                            FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   51
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APPLICANT: Emery, Stephen
APPLICANT: Emery, Stephen
APPLICANT: Copley, Cilve Graham
APPLICANTON: Moncolonal Antibody to CEA
TITLE OF INVENTION: And Their Therapeutic Use in an Adept System
FILE REPERENCE: Monocolonal Antibody to CEA
CURRENT APPLICATION NUMBER: US/09/171,945
CURRENT APPLICATION NUMBER: CB99703103.3
PRIOR FILING DATE: 1997-02-14
PRIOR FILING DATE: 1996-05-04
PRIOR FILING DATE: 1996-05-04
PRIOR FILING DATE: 1996-05-04
PRIOR APPLICATION NUMBER: POTT/CB97/01165
PRIOR FILING DATE: 1997-04-29
                                                                                                                                                                                                                                                                                                                                                                                                           TITLE OF INVENTION: Monoclonal Antibody to CEA, Conjugates Comprising Said
TITLE OF INVENTION: Monoclonal Antibody to CEA
TITLE OF INVENTION: Monoclonal Antibody to CEA
TITLE PEREBRENCE: Monoclonal Antibody to CEA
CURRENT APPLICATION NUMBER: 1998-10-29
PRIOR PELICATION NUMBER: GB95703103.3
PRIOR FILING DATE: 1997-02-14
PRIOR FILING DATE: 1997-02-04
PRIOR FILING DATE: 1997-04-29
PRIOR FILING DATE: 1997-04-29
NUMBER OF SEQ ID NOS: 131
SOFTWARE: PATENTIN VET: 2.1
SEQ ID NO 65
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; OTHER INFORMATION: Description of Artificial Sequence: humanized
US-09-171-945-65
            ; OTHER INFORMATION: Description of Artificial Sequence: humanized US-09-171-945-61
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                                                                        Length 107;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 31; DB 4; Length 107; Pred. No. 4.7;
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                                                                                                                  0; Indels
                                                                      100.0%; Score 31; DB 4;
100.0%; Pred. No. 4.7;
iive 0; Mismatches 0,
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                                                                                                                                                                                                                                                                                             Sequence 65, Application US/09171945
Patent No. 6277599
                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
APPLICANT: Emery, Stephen
APPLICANT: Copley, Clive Graham
APPLICANT: Edge, Michael Derek
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            100.0%;
100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: PRT ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Patentin Ver. 2.1
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Best Local Similarity 100.0
Matches 7; Conservative
                                                    Query Match
Best Local Similarity 100.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  49 STSNLAS 55
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                                                                                                                                                     1 STSNLAS 7
                                                                                                                                                                                                                                                       RESULT 11
US-09-171-945-65
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                                                                                             Gaps
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; OTHER INFORMATION: Description of Artificial Sequence: humanized US-09-171-945-71
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                                                                                                                                                                                                                                                                                                   GENERAL INCORNATION:
APPLICANT: RING, DAVID B.
TITLE OF INVENTION: MALECULES SPECIFIC FOR CANCER ANTIGENS
TITLE OF INVENTION: MOLECULES SPECIFIC FOR CANCER ANTIGENS
NUMBER OF SEQUENCES: 33
CORRESPONDENCE ADDRESS:
ADDRESSE: CHIRON CORPORATION
STREET: INTELLECTUAL PROPERTY - R440, PO BOX 8097
CITY: EMERYVILLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                100.0%; Score 31; DB 3; Length 108; 100.0%; Pred. No. 4.7; 0; Mismatches 0; Indels
                                                     100.0%; Score 31; DB 4; Length 107
100.0%; Pred. No. 4.7;
Live 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        07 VE US/08/483,749A 07-JUN-1995
                                                                                                                                                                                                                                                                 Sequence 8, Application US/08483749A Patent No. 6054561
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 9, Application US/09171945; Patent No. 6277599; GENERAL INFORMATION: APPLICANT: Emery, Stephen; APPLICANT: Copley, Clive Graham
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COUNTRY: USA
ZIP: 94662-8097
COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY disk
COMPUTER: IBM PC COMPATIBLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Emery, Stephen
Copley, Clive Graham
Edge, Michael Derek
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 36,914
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ATTORNEY/AGENT INFORMATION:
NAME: SAVEREIDE, PAUL B.
REGISTRATION NUMBER: 36,914
REFERENCE/DOCKET NUMBER: 05
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEPHONE: (510) 601-2585
TELEFAX: (510) 655-3542
INFORMATION FOR SEQ ID NO: 8:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LENGTH: 108 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 100.
Best Local Similarity 100.
Matches 7; Conservative
                                                   Query Match 100.
Best Local Similarity 100.
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     , MOLECULE TYPE: protein US-08-483-749A-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           linear
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Search completed: December 23, 2002, 07:33:14
Job time : 1.26163 secs
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        δ
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TITLE OF INVENTION: Monoclonal Antibody to CEA, Conjugates Comprising Said TITLE OF INVENTION: Antibody, and Their Therapeutic Use in an Adept System FILE REFERENCE: Monoclonal Antibody to CEA CURRENT APPLICATION NUMBER: US/09/171,945
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                    TYPE: PRT F
ORGANISM: Artificial Sequence
FEATURE: F
OTHER INFORMATION: Description of Artificial Sequence: humanized
US-09-171-945-9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ouery Match
100.0%; Score 31; DB 4; Length 108;
Best Local Similarity 100.0%; Pred. No. 4.7;
Matches 7; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/116,778E
FILING DATE: 07-SEP-93
: FILING DATE: 07-SEP-93
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: NAKAMURA, KAZUYASU
APPLICANT: KOIKE, MASANICHI
APPLICANT: HANAI, NOBUO
APPLICANT: HANAI, NOBUO
APPLICANT: HASEGARA, MANORU
TITLE OFFINENTION: HUMANIZED ANTIBODIES
NUMBER OF SEQUENCES: 49
CORRESPONDENCE ADDRESS:
ADDRESSEE: NIXON & VANDERHYE P. C.
STREET: 1100 NOP....
                                                                                    CURRENT FILING DATE: 1998-10-29
PRIOR APPLICATION NUMBER: GB9703103.3
PRIOR FILING DATE: 1997-02-14
PRIOR PILING DATE: 1997-02-14
PRIOR FILING DATE: 1996-05-04
PRIOR FILING DATE: 1996-05-04
PRIOR FILING DATE: 1997-04-29
NUMBER OF SEQ ID NOS: 131
SOFTWARE: Patentin Ver. 2.1
SEG ID NO 9
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PILING DATE: 07-5...
CLASSIFICATION: 424
ATORNEY/AGENT INFORMATION:
NAME: WILSON, MARY 3.
REGISTRATION NUMBER: 249-59
TELECOMUNICATION INFORMATION:
TELECHON INFORMATION:
TELECHON INFORMATION:
TELECHON INFORMATION:
TELECHON INFORMATION:
SEQUENCE CHARACTERISTICS:
LENGTH: 129 amino acids
TYPE: amino acid
TYPE: ... 11near
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49 STSNLAS 55
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US-08-116-778E-2
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Gaps
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OD: WITH KNOWN SEQUENCE OR TO AN ESTABLISHED
OD: CONSENSUS
/Product= "HYPERVARIABLE REGION 1"
                                                                                                                                                                                                                                                                                                                                          BY SIMILARITY WITH KNOWN SEQUENCE OR TO AN ESTABLISHED
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                                                                                                                                                                                                                                                                                                                                                                                         DD: CONSENSUS /product= "HYPERVARIABLE REGION 2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DENTIFICATION METHOD: CONSENSUS
OTHER INFORMATION: /Product- "HYPERVARIABLE REGION 3"
US-08-116-778E-2
                                                                                                                                 NAME/KEY: domain
LOCATION: 24..33
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OTHER INFORMATION: /proc
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NAME/KEY: domain
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OTHER INFORMATION: /Proc
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LOCATION: 88..96
IDENTIFICATION METHOD:
IDENTIFICATION METHOD:
                                     IDENTIFICATION METHOD:
IDENTIFICATION METHOD:
IDENTIFICATION METHOD:
sig_peptide
-22..-1
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Anti-CEA antibody; carcinoembryonic antigen; 806.077 Ab; cancer therapy; cancer diagnosis; complementarity determining region; light chain.
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                                                                                                                                                                                                                                               AAB10021
AAY90815
AAY53591
AAY59306
AAB82710
                                                                              AAB62264
AAW03182
AAE13144
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AAW41390
AAB83159
AAB83167
AAG63987
AAR21294
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AAG80318
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AAW41397
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AAR79884
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                    AAG80315
                              AAW89175
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                97GB-0003103
96GB-0009405
  (first entry)
(ZENE ) ZENECA LTD.
 02-JUN-1998
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Synthetic.
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CDR2 of light chai
Peptide fragment f
Complementary dete
H. pylori 26 kDa p
Humanised antibody
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248.221 Million cell updates/sec
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2. /SIDSZ/gcgdata/geneseq/geneseqp-embl/AA1981.DAT:*
3. /SIDSZ/gcgdata/geneseqp-embl/AA1981.DAT:*
4: /SIDSZ/gcgdata/geneseqp-embl/AA1981.DAT:*
5: /SIDSZ/gcgdata/geneseqy-embl/AA1981.DAT:*
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121: /SIDSZ/gcgdata/geneseqy/geneseqp-embl/AA1991.DAT:*
122: /SIDSZ/gcgdata/geneseqy/geneseqp-embl/AA2001.DAT:*
                                                                   December 23, 2002, 07:16:08; Search time 3.75775 Seconds
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          GenCore version 5.1.3
Copyright (c) 1993 - 2002 Compugen Ltd.
                                                                                                                                                                                                     Total number of hits satisfying chosen parameters:
                                                                                                                                                                                   908470 seqs, 133250620 residues
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                                                                                                                                                                                                                                                                    Maximum Match 100%
Listing first 45 summaries
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AAW73170
AAY28391
AAX297233
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AAB81368
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Murine VL kappa gr Murine VL kappa gr Anti-EGFR antibody Anti-CEA antibody Variable light cha H. pylori 26 kDa p 33F8 hybridoma VL

Anti-CEA antibody Mouse ganglioside Ganglioside GM2 an Amino acid sequenc

VK domain of antib Monoclonal antibod Monoclonal antibod

Light chain comple Anti-human TNF-alp Anti-p53 monoclona Human ORFX protein Light chain constr Guy's 13 anti-Stre Humanised antibody

Antigen-binding pr Anti-CEA antibody Humanised antibody Humanised antibody

Title: Perfect score:

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Database

Antigen-binding pr Antigen-binding pr Anti-human TNF-alp Ganglioside GD2 sp Ganglioside GD2 sp Murine trkC antibo Murine VL kappa gr

Anti-carcinoembryonic antigen antibody 806.077 Ab - used for diagnosis and therapy of cancer

VEGF antagonist an Ganglioside GD2 sp Mouse ganglioside Complementarity de

Score

Result Š. 3377777777

Emery SC

Copley CG, Edge MD, WPI; 1997-558987/51.

Light chain from a DCB light chain va VEGF antagonist an

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Page 196; 208pp; English

8 × 5 5 5 5 5 5 5 5 5 5 8 8

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Peptide fragment from the human anti-GM2 light chain in REI.
                                                                                                                                                                                   antibody; REI; complementarity determining region; CDR;
chimeric; light chain; heavy chain.
                                          AAY28391 standard; Protein; 7
                                                                                                             04-NOV-1999 (first entry)
                                                                                                                                                                                                                                        Homo sapiens
                                                                            AAY28391;
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          RESULT 3
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This sequence represents a complementarity determining region (CDR) of the light chain of the antibody of the invention. The antibody is an anti-CEA (carcinoembryonic antigen) antibody (806.077 Ab). Host cells or transpented organisms transformed with DNA encoding the antibody, are used to make the antibody or conjugate. The conjugate is used in a medicament suitable for intravenous administration. The conjugate can be used for cancer therappy, selectively killing tumour cells. The antibody can be used for used for in vitro diagnosis of cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This sequence represents a complementarity determining region (CDR) from the heavy chain of the antibody of the invention. The antibody of the invention is a human CDR transplanted antibody that reacts specifically with ginglioside GM2. DNA encoding the antibody, and vectors and transformants containing it, can be used for the recombinant production of the fantibody. The antibody itself can be used as an anti-tumour agent or as a diagnostic tool for related cancers. The antibody has antitumour
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ganglios de GM2; antibody; complementarity determining region; cancer;
                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A human type complementarity determining region transplanted antibody, against ganglioside GM2 - useful as an anti-tumour agent and as & diagnostic for related cancers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ight chain of ganglioside GM2 targeting antibody.
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                                                                                                                                                                                                 Score 31; DB 18;
Pred. No. 7.8e+05;
Mismatches 0;
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100.0%; Pred. No.7.8e+05;
iive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     activity against ganglioside GM2 positive cells.
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Best Local Similarity 100.
Matches 7; Conservative
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                                                                                                                                                                                 Query Match | Best Local Similarity | 7 | Conserva
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                                                                                                                                                                  Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CDR2 of
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                                                                                                                                                                                                                                                                                                                                                             RESULT 2
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The sequences AAY28390 to AAY28392 replace the CDR regions of the NEWM DNA and they produce AAY28394, the hKM796L human anti-GM2 antibody light
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Chimeric human antibodies of the invention are useful in the treatment of cancer, especially that which is of neural ectodermal origin. In contrast to prior art constructs based on mouse monoclonal antibodies, the chimeric human antibodies do not cause anti-mouse
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Immunoglobulin production. The chimeric human antibodies have a prolonged half-life and a reduced frequency of adverse effects when compared to mouse monoclonal
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                                                                                                                                                                                                                                                      Hasegawa M, Koike M,
                                                                                                                                                                                                         (KYOW ) KYOWA HAKKO KOGYO KK
                                                                                                                                       95US-0483528.
93US-0116778.
                                                                                          95US-0483528
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Best Local Similarity
Matches 7; Conserv
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JS5939532-A.
                                             17-AUG-1999.
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Gaps

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Indels

STSNLAS 7 STSNLAS

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                                                                                                                                                                                                                                                                                                                                                                            Novel immunoglobulin molecules binding kinase insert domain-containing receptor with the same affinity as vascular endothelial growth factor,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Acid-resistant microorganism; detection; faecal; intestine; infection; monoclonal antibody; light chain; complementarity determining region;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
humanised antibody; chimeric antibody; tumour; diabody; triabody; glioblastoma multiforme; hemandicolastoma; AIDS; central nervous system neoplasms; AIDS associated Karposi's sarcoma; acquired immune deficiency syndrome; AIDS; human.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      H. pylori 26 kDa protein-binding antibody light chain CDR2 peptide.
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Pred. No. 7.8e+05;
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100.0%; Pred. No. 7.8
tive 0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                            used to reduce tumour growth
                                                                                                                                                                                      28-JAN-2000; 2000WO-US02180
                                                                                                                                                                                                                     99US-0117726.
                                                                                                                                                                                                                                                                  (IMCL-) IMCLONE SYSTEMS INC
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                                                                                                                         WO200044777-A1.
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                                                                                                                                                                                                                   29-JAN-1999;
29-JAN-1999;
                                                                            Homo sapiens.
Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Unidentified
                                                                                                                                                        03-AUG-2000.
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infection by an acid-resistant microorganism (A) by treating a faccal sample with at least two different monoclonal antibodies (MAb) (or their fragments or derivatives) or aptamers (collectively (I)) and detecting formation of a complex (C) between (I) and the corresponding antigen of formation of a complex (C) between (I) and the corresponding antigen of (A). The first and second (I) bind to epitopes of different antigens of (A). The first and second (I) bind to epitopes of different antigens of at least some mammals, and have either: (I) their native structure; or (ii) a structure against which an antibody is produced by an animal infection by acid-fast bacteria, particularly of the genera Helicobacter, or fragment, or with a synthetic peptide. Practically all mammals display at least one of the specified epitopes. The method is used to detect infection by acid-fast bacteria, particularly of the genera Helicobacter, Mycobacterium and Campylobacter, specifically H. Pylori, H. hepaticus, who therepensive and easily standardizable diagnosis, despite possible degradation of antigens during passage through the intestines. This sequence represents a fragment of a H. Pylori 26 kba protein-binding antibody light chain complementarity determining region CDR2 which is used to illustrate the method of the invention.
                                                                                                                                                                                                                                                                                                                               Detecting infection by acid-fast microbes for diagnosis of Helicobacter pylori, comprises reacting a faecal sample with two binding reagents for antigens that survive intestinal passage -
                                                                                                                                                                                                                                                                                                                                                                                                                                                   This invention describes a novel method for the detection of a mammalian
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Vascular endothelial growth factor receptor; VEGFR; antagonist; tumour; cytostatic; light chain hypervariable region; VL; myelocytic leukaemia; lymphocytic; erythrocytic; monocytic; multiple myeloma; lymphoid cell; fodgkin's disease; complementarity determining region 2; CDR-2; mouse.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Humanised antibody murine light chain hypervariable region (VL) CDR2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                               Friedrichs U, Heppner P, Lakner M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        100.0%; Score 31; DB 21;
100.0%; Pred. No. 7.8e+05;
iive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAE13141 standard; peptide; 7 AA.
                                                                                                                                                                                                                                                                                                                                                                                                          Claim 24; Page 21; 84pp; German.
                                                                         99WO-EP08212
                                                                                                               98EP-0120517
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     28-JAN-2002 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   7; Conservative
                                                                                                                                                                                                               Reiter C, Cullmann G,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ouery Match
Best Local Similarity
                                                                                                                                                                        (CONN-) CONNEX GMBH.
                                                                                                                                                                                                                                                                      WPI; 2000-365747/31
                                                                                                                                                                                                                                                                                            N-PSDB; AAA40161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      7 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 STSNLAS 7
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                                                                                                               29-OCT-1998;
06-NOV-1998;
                                                                         29-OCT-1999;
                                    11-MAY-2000
                                                                                                                                                                                                                                   Ringeis A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAE13141;
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29-JAN-2001; 2001WO-US02839
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        30-SEP-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    05-APR-2001
                                                                                                                                          Kerbel R;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAB81968;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence
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                                                                                                                                                                                                                                                                                                                                                                                The invention relates to a method for inhibiting the growth of non-solid tumour ceils that are stimulated by a ligand of vascular endothelial growth factor receptor (VEGFR) in mammals particularly humans. The method involves Ereating the mammals with humanised VEGFR monoclonal antibodies (antagonists) Humanised monoclonal antibody comprises humanised mouse variable fegion joined to human constant region, where the humanised mouse variable region contains mouse complementarity determining region (CDR) grafted into human variable region. The method is useful for treating jeukaemias such as acute or chronic myelocytic leukaemia, acute or chronic lymphocytic leukaemia, erythrocytic or monocytic leukaemia, multiple myelomas and lymphoid cells, particularly those related to non-Hodgful's and Hodgful's and Hodgful's disease. The present sequence is humanised antibody murine light chain hypervariable region (VL) CDR-2 used in the exemplification of the invention.
                                                                                                                                                                                                                                                                              Inhibiting growth of non-solid tumor cells useful to treat bone marrow tumors such as leukemias or multiple myeloma comprises treatment with an antagonist of a vascular endothelial growth factor receptor -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 IMC-LC11; chimeric antibody; mouse; human; antagonist; VEGF; vascular endothelial growth factor; angiogenesis; antianglogenic; antitumiour; neoplasm; collagen-vascular disease; autoimmune disease; tumour; breast carcinoma; lung carcinoma; prostate carcinoma; colon carcinoma; neuroblastoma; glioblastoma multiforme; melanoma; therapy; light chain; CDR;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 7;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match: 100.0%; Score 31; DB 22; Best Local Similarity 100.0%; Pred. No. 7.8e+05; Matches 7; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      VEGF antagonist antibody IMC-1C11 VL CDR-2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             complementarity determining region.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAB82707 standard; Peptide; 7 AA
                                                                                                                                                                                                                                                                                                                                                     laim 8; Page 15; 68pp; English.
                                                                                                                                        (IMCL-) IMÉLONE SYSTEMS INC. (CORR ) CORREL RES FOUND INC.
                                                                   30-MAR-2001 2001WO-US10504
                                                                                                      31-MAR-2000; 2000US-0540770.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Chimeric - Mus sp.
Chimeric - Homo sapiens.
                                                                                                                                                                                                                              WPI; 2001-662942/76.
N-PSDB; AAD21667.
                                                                                                                                                                                             Rafii S;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   7 AA;
WO200174296-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 STSNLAS 7
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                                  11-OCT-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence
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The present sequence is that of complementarity determining region 2 of the light chain variable region (see also AAB82702) of 2 of the light chain variable region (see also AAB82702) of 2 of the light chain variable region (see also AAB82702) of 2 of MC-1011, a mouse-human chimeric antibody that has vascular endothelial growth factor (VEGF) antagonist activity. The antibody, or a fragment of it, can be used as an anti-angiogenic molecule, cogether with a chemotherapeutic acid, for the treatment of an angiogenic dependent condition in a mammal, especially a human. The invention relates generally to a method of treating or controlling an angiogenic dependent condition by administering an anti-angiogenic molecule and a chemotherapeutic agent. The preventing significant toxicity of the chemotherapeutic agent. The anti-angiogenic molecule inhibits or blocks the action of a vascular endothelium survival factor such as VEGF or its receptor, and is especially IMC-1011. Conditions that can be treated include a neoplasm, a collagen-vascular disease or an autoimmune disease,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ganglioside; GD2; complementation determining region; CDR; antibody;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        especially a solid tumour, including breast carcinoma, lung carcinoma, prostate carcinoma, colon carcinoma, prostate carcinoma, ovarian carcinoma, neuroblastoma, central nervous system tumour, neuroblastoma, ultiforme or melanoma (all claimed).
                                                                                                                                                                                                                                                                                                                                                                                                                            Treating or controlling an angiogenic dependent condition (e.g. neoplasm, collagen-vascular or autoimmune disease) in mammal by administering a combination of an antiangiogenic molecule and a chemotherapeutic agent.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ganglioside GD2 specific antibody related peptide SEQ ID NO: 7.
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                                                                                                                       (SUNN-) SUNNYBROOK HEALTH SCI CENT. (IMCL-) IMCLONE SYSTEMS INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Disclosure; Page 37; 42pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAB81968 standard; Peptide; 7 AA.
28-JAN-2000; 2000US-0178791.
31-MAR-2000; 2000US-0539692.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      29-SEP-2000; 2000WO-JP06773.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          99JP-0278290.
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                                                                                                                                                                                                                                                                                                                                                WPI; 2001-514531/56
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Matches 7; Conserv
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Monoclonal antibody 2C4; sialoadhesin factor-2; SAF-2; allergic rhinitis; allergy; asthma; anemia; eczema; lymphoma; systemic mastocytosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Novel monoclonal antibody specific for human sialoadhesin factor-2 for diagnosis, prevention, treatment of allergy, asthma, eczema or diseases such as lymphoma, leukemia or systemic mastocytosis, in a mammal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAG63991-93 represent the complementarity determining regions (CDRs) of the light chain variable region of murine monoclonal antibody 2C4. This antibody binds to human sialoadhesin factor-2 (SAF-2). The antibody is useful for treating or preventing allergic rhinitis, allergies, asthma, anemia, eczema or diseases such as lymphoma, leukemia or systemic mastocytosis in a mammal. It is also useful for detecting the presence of a cell, especially eosinophil in a sample, by detecting binding of the antibody to SAF-2. The antibody can be coupled to toxins, antiproliferative drugs or radionuclides to kill cells in areas of excessive SAF-2 expression.
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                                              Gaps
                                                                                                                                                                                                                                                                                                                                                       Complementarity determining region of light chain of antibody 2C4.
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                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Match 100.0%; Score 31; DB 22; Local Similarity 100.0%; Pred. No. 7.8e+05; es 7; Conservative 0; Mismatches 0;
h 100.0%; Score 31; DB 22; Similarity 100.0%; Pred. No. 7.8e+05; 7; Conservative 0; Mismatches 0;
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                                                                                                                                                                                                                                AAG63992 standard; peptide; 7 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 10; Page 34; 35pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (SMIK ) SMITHKLINE BEECHAM CORP. (SMIK ) SMITHKLINE BEECHAM PLC. (UYJO ) UNIV JOHNS HOPKINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         07-MAR-2000; 2000US-0187595.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   05-MAR-2001; 2001WO-US07193
                                                                                                                                                                                                                                                                                                             26-NOV-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                        Leukemia; eosinophil
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 2001-570749/64.
      Query Match
Best Local Similarity
Matches 7; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   7 AA;
                                                                                                          STSNLAS 7
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                                                                                    STSNLAS 7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           13-SEP-2001.
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Best Local 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mus sp.
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AAU81254
ID AAU813
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                                                                                                                                                                                                                                                                                        The present invention describes an antibody, which can react specifically with ganglioside GD2, and is transplanted with a human type complementation-determining domain (CDR), or its fragments. The antibody and its derivatives are useful in diagnosis and therapy of tumours, particularly cancer diagnosis. The present sequence is a peptide used in the exemplification of the invention.
                                                                                                                                              Human type complementation-determining domain transplanted antibody and derivatives against ganglioside GD2, useful in diagnosis and therapy of e.g. tumours, has low antigenicity, little side effects but potent
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The present invention relates to derivatives of an antibody against agaquicaide GMZ. The antibody may be a monoclonal antibody or its fragments. The antibody is combined with a radioactive isotope, protein or small drug in the treatment and diagnosis of cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Monoclonal antibodies against ganglioside GM2 combined with drugs, radioisotopes or proteins for treatment and diagnosis of cancer -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mouse; ganglioside; GM2; antibody; cytostatic; cytotoxic; cancer; complementarity determining region; CDR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mouse ganglioside GM2 antibody light chain variable region CDR2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        100.0%; Score 31; DB 22;
llarity 100.0%; Pred. No. 7.8e+05;
Conservative 0; Mismatches 0;
                                                                   я;
                                                                   Niwa
                                                                                                                                                                                                                                                    Claim 6; Page 100; 123pp; Japanese.
                                                                   Nakamura K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 4; Page 72; 80pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAB83164 standard; peptide; 7 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Niwa R;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (KYOW ) KYOWA HAKKO KOGYO KK
                           (KYOW ) KYOWA HAKKO KOGYO KK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            99JP-0278292.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    29-SEP-2000; 2000WO-JP06775.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Nakamura K,
                                                                 Shitara K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 2001-266142/27.
                                                                                                       WPI; 2001-266163/27
                                                                                                                                                                                                           activity in cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
Matches 7; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   7 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                  7 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   02-JUL-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              05-APR-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                      Seguence
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                                                               Hanai N,
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RESULT 9 AAB83164

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Zhu Z;
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                                                                                                   trka; trkB; cisplatin-induced neuropathy; pyridoxine-induced neuropathy; peripheral neuropathy; diabetic neuropathy; neurodegenerative disease; large-fibre sensory neuropathy; amyotrophic lateral sclerosis; tumour; nerve cell injury; blood cell disorder; leukopaenia; eosinopaenia; wound; basopaenia; lymphopaenia; monocytopaenia; neutropaenia; cancer; ulcer; alzheimer's disease; Parkinson's disease; Huntington's disease; diabetes; sickle cell disorder; cerebrovascular disorder;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The invention relates to an anti-trkC agonist monoclonal antibody which shows no significant cross-reactivity with trkA or trkB, and recognizes an epitôpe in domain 5 of trKC. The antibodies of the invention are effective in the treatment of cisplatin- or pyridoxine-induced neuropathy, peripheral neuropathy, diabetic neuropathy and large-fibre sensory meuropathy, neurodegenerative disease including amyotrophic lateral sclerosis, nerve cell injuries, disorders of insufficient blood cells such as leukopaenia including eosinopaenia, basopaenia, lymphopäenia, monocytopaenia, neutropaenia, Alzheimer's disease, Parkinsön's disease, muntington's disease and tumours. The sequences are also useell for inducing angiogenesis for treating wounds, ulcers and diabetic complications of sickle cell disease, for treating cardiac
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    diabetic complications of signatures. It is trained with the diagnosis of diseases is the diagnosis of diseases involving cellular degeneration. Sequences AAU81229-AAU81284 represent human and mouse anti-trKC agonist monoclonal antibodies and antibody fragments of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                              Novel and 1-trkC agonist monoclonal antibody useful for treating neurodegenerative disease, shows no significant cross-reactivity with trkA/trkB, and recognizes epitope in domain 5 of trkC
                                                                                        Human; mouse; anti-trkC agonist monoclonal antibody; trkC; antibody;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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                                                              antibody light chain CDR2 of variable region #2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 7;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            100.0%; Score 31; DB 23;
100.0%; Pred. No. 7.8e+05;
ive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                Shelton DL;
                                                                                                                                                                                                degeneration; gene therapy
                                                                                                                                                                                                                                                                                                                                                                                             Devaux B; Hongo JS, Presta LG,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 13; Fig 11; 121pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAU74410 standard; peptide; 7 AA.
                                                                                                                                                                                                                                                                                                    22-JUN-2001; 2001WO-US20153.
                                                                                                                                                                                                                                                                                                                             22-JUN-2000; 2000US-213141P.
05-OCT-2000; 2000US-238319P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      7; Conservative
                                                                                                                                                                                                                                                                                                                                                                     (GETH ) GENENTECH INC
                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 2002:-130790/17.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local Similarity
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                                                                                                                                                                                                                                                 WO200198361-A2.
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                                                              Murine trkC
                                    09-APR-2002
                                                                                                                                                                                                                                                                           27-DEC-2000
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                                                                                                                                                                                                cellular
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AAU74410
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The invention describes an antigen-binding protein (I) comprising a complex of two polypeptides (P1) and two second polypeptides (P2) which are stably associated in an immunoglobulin like complex. Pl has an antigen-binding site located to the N terminus of immunoglobulin (Ig) (Ight chain constant domain (CL domain), and P2 has an antigen-binding site located to the N terminus of immunoglobulin (Ig) (Ight chain constant domain (CL domain), and P2 has an antigen-binding constant domain to day associate and proving the activation of a vascular endothelial growth factor (VEGF) receptor; reducing tumour growth; inhibiting angiogenesis, constrain of human leukaemia cells; blocking interaction of a protein and its ligand; promoting interactions between immune cells and target cells; and in vivo and in vitro for investigative, diagnostic or treatment continued continued in the design of (I) provides for efficient production so that substantially all of the antigen-binding proteins production so that cand in tetrament form. The heavy chain constant domains which constitute the Er region (e.g., CH2 and CH3 for an IgG molecule) of a natural cantibody and which provide other antibody functions can be present. There is no requirement for processing in vitro to obtain the complete product.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New bispecific immunoglobulin-like antigen-binding protein for reducing tumour growth and for inhibiting angiogenesis, comprises a complex of two polypeptides and two second polypeptides
                                                                                                                                                                    Complementarity determining region, CDR; CDRL2; antigen; cytostatic; angiogenesis inhibitor; vascular endothelial growth factor receptor; VBGF; tumour; leukaemia; antibody; cell proliferation inhibitor; antibody light chain variable domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           complementarity determining region L2 (CDRL2) incorporated into an antigen-binding protein described in the method of the invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ;
0
                                                                                    Light chain complementarity determining region L2 (CDRL2).
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llarity 100.0%; Pred. No. 7.8e+05;
Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 55; Page 57; 64pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  24-MAY-2001; 2001WO-US16924.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  24-MAY-2000; 2000US-206749P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (IMCL-) IMCLONE SYSTEMS INC.
26-MAR-2002 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 2002-106189/14.
N-PSDB; AAS20281.
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Best Local Similarity
Matches 7; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WO200190192-A2.
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/note= "unspecified"

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Best Loca
Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                               This invention describes novel heavy chain and light chain polypeptides or their fragments of a recombinant antibody to human TWR-alpha which contain complementarity determining region (CDR) sequences. The products of the invention have vasotropic, antiarchic, neuroprotective and protozoacide activity. The antibodies act by neutralising TWR-alpha in vivo. The antibodies are used for producing chimaric and humanised antibodies that may be used for the treatment and prevention of TWR-alpha associated diseases such as toxic shock syndrome, rheumatoid arthritis, malaria and multiple sclerosis. The antibodies have low immunogenicity in humans. This sequence represents the anti-human tunnour necrosis
                                                     INF-alpha; tumour necrosis factor-alpha; antibody; anti-human; CDR; heavy chalin; light chain; complementarity determining region; vasotropic; antiarthritic; neuroprotective; protozoacide; toxic shock syndrome; rheumatoid arthritis; malaria; multiple sclerosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Anti-p53; monoclonal antibody 240; immunogen; anti-tumour; immunity; immune response; tumour associated antigen; metastatic cancer.
                                                                                                                                                                                                                                                                                                                                                 Novel heavy and light-chain polypeptides of chimeric and humanised antibodies against human tumour necrosis factor alpha for low-immunogenicity treatment of TNF-related diseases such as toxic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Anti-p53 monoclonal antibody 246 variable light chain sequence.
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0
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100.0%; Pred. No. 7.8e+05;
iive 0; Mismatches 0;
                           Anti-human TNF-alpha CDR-L2 peptide.
                                                                                                                                                                                                                                                                                             Nakanishi T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Key Location/Qualifiers
Misc-difference 53
                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 3b; Page 26; 36pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAW89175 standard; peptide; 92 AA.
                                                                                                                                                                                                          18-APR-2001; 2001WO-JP03308.
                                                                                                                                                                                                                                      19-APR-2000; 2000JP-0117394
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18-FEB-2002 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            7; Conservative
                                                                                                                                                                                                                                                                                            Fukuda Y, Nagahira K,
                                                                                                                                                                                                                                                                 (SUNR ) SUNTORY LID
                                                                                                                                                                                                                                                                                                                       WPI; 2002-066345/09
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      8 AA;
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                                                                                                                                                     WO200179298-A1
                                                                                                                                                                                                                                                                                                                                                                                           shock syndrome
                                                                                                                            Homo sapiens.
                                                                                                                                                                                25-OCT-2001
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Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence
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The present invention describes the use of an immunogen (A) to induce anti-tumour immunity; to elicit an increased immune response to tumour associated antigen (TAA) and/or to induce an immune response to tumour associated antigen (TAA) ind/or to induce an immune response to mutant or wild-type forms of TAA in mammals. (A) is: (I) a monoclonal antibody (MAb) to TAA, or its fragment; (ii) a peptide based on a CDR (complementarity determining region) on the heavy or light chain of MAb (able to elicit antibodies to TAA); or (iii) a DNA that encodes the variable (V) region of MAb, in a gene delivery vehicle. The present sequence represents the variable light chain sequence-from anti-p53 MAb 246. Also described is a method for generating sequence-specific, anti-DNA antibodies (Ab) by immunising a mammal with a MAb directed to a noti-DNA antibodies (Ab) by immunising a mammal with a MAb directed to a companion containing a DNA-binding site of a DNA-binding protent. (A) is used to treat a wide variety of primary and metastatic cancers, particularly those where p53 is involved. Ab are used for diagnosis (e.g to determine critical sequences in animmal or plant breeding); to identify bacteria and other parasites; to determine parentage; in forensis cachence; to isolate specific genes for DNA vaccination; in gene sequencing and cloning; also possibly for activation of selected therapeutic genes in plants, animmals and humans. (A) induce an effective anti-tumour response without causing harm to the patient. The method uses (A) to generate anti-TAA by exploiting the anti-idiotype network.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Use of a monoclonal antibody to a tumour-associated antigen - to induce anti-tumour immunity or elicit an increased immune response
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100.0%; Pred. No. 11;
tive 0; Mismatches 0;
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                               'note= "unspecified"
                                                                                                     /note= "unspecified"
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                                                                                                                                                                                                                                                                                                                                                                                                               97IL-0121041.
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to the antiqen
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The present invention describes substantially purified human proteins (referred to as open reading frame, ORFX, where X is 1-11491 (see Table 1) in the specification). ABN15762 to ABN27252 encode the human ORFX proteins are useful for treating or preventing a pathology associated with an ORFX postated for treating or preventing a pathology associated with an ORFX-associated disorder in humans, and in the manufacture of a medicament for treating a syndrome (associated with ORFX-associated disorder. ORFX polynucleotide syndrome (associated in gene therapy. ORFX sequences can be used in the treatments of cancer, hyperproliferative disorders, cirrhosis of liver, psoriasis, benign tumours, keloid, degenerative disorders, hemorrhage, osteoarthitis, neurodegenerative disorders, disorders related to organ transplantation, cardiovascular diseases, disorders related to organ transplantation, and the manument of ficiencies and disorders, infectious storage diseases, various immune deficiencies and disorders, rheumatoid arthritis, autoimmune disorders such as multiple sclerosis, rheumatoid arthritis, autoimmune infammatory eye disease. ORFX proteins are also more, if the properties of the part of th
cardiovascujar disease; diabetes mellitus; systemic lupus erythematosus; hypertension; hypothyroidism; cholesterol ester storage disease; fimune defficiency; immune disorder; infectious disease; autoimmune disorder; rheumatoid arthritis; autoimmune thyroiditis; myasthenia gravis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          N.B. The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         disease and autoimmune inflammatory eye disease. ORFX proteins are also useful for treating burns, incisions, ulcers, for treating osteoporosis, bone degenerative disorders, or periodontal disease, and for gut protection or regeneration and treatment of lung or liver fibrosis, reperfugion injury in various tissues and conditions resulting from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Novel human polypeptides and polynucleotides useful for diagnosing, preventing and treating cardiovascular disease, neurodegenerative, hyperproliferative disorders and autoimmune disorders
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                                                                                                                                                                                                                                                                                                                                                                                                                                  2000US-206132P.
2000US-228716P.
                                                                                                                                                                                                                                                                                                                                                                           29-MAY-2001; 2001WO-US10836
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 systemic cytokine damage.
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Best Local Similarity
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N-PSDB; ABN17903.
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STSNLAS 21 STŠNLAS 7 QQ

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Gaps

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Search completed: December 23, 2002, 07:25:06 Job time : 4%75775 secs

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GenCore version 5.1.3 CVpyright (c) 1993 - 2002 Compugen Ltd.
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OM protein - protein search, using sw model

December 23, 2002, 07:17:57; Search time 1.38372 Seconds (without alignments) 486.327 Million cell updates/sec Run on:

US-09-865-198-5 31 1 STSNLAS 7 Title: Perfect score: Sequence:

Scoring table:

BLOSUM62 Gapop 10.0 , Gapext 0.5

Total number of hits satisfying chosen parameters: 283224 seqs, 96134422 residues Searched:

283224

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

PIR_73:* Database :

pir1:* pir2:* pir3:* pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Description	Ig kappa chain V r	ם י	ь	Б	ь	ь	Б	ь	ь	g light	ь	g light	Ig light chain V r	g kappa	a chain	l protein	finger protein neu		Ig heavy chain V r	Ig kappa chain V r	Ig light chain V r	О	major capsid prote	hypothetical prote		hypothetical prote	hypothetical prote	hypothetical prote	F-3
	ID	S17626	S17630	S17623	S17640	S17641	S17642	C33730	D38601	PH1058	PH1059	PH1060	PT0404	PT0405	A32513	PL0013	AH3513	S35371	S61667	S20651	PL0082	A42848	548376	PIWLHS	AG1812	T11653	B82881	T37738	571	B70524
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Ig kappa chain V region - mouse

Ig kappa chain V region - mouse

Ig kappa chain V region - mouse

C; Species: Mus musculus (house mouse)

C; Species: Musuculus (house mouse)

C; Accession: \$17630

R; Clackson, T: Hoogenboom, H.R.; Griffiths, A.D.; Winter, G.

R; Clackson, T: Hoogenboom, H.R.; Griffiths, A.D.; Winter, G.

R; Reference number: \$17930

R; Reference number: \$17230; MUD: 91326098; PMID: 1907718

A; Recassion: \$17630

A; Restaus: preliminary

A; Molecule type: nucleic acid

A; Residues: 1-91 <CLA>

C; Superfamily: immunoglobulin V region; immunoglobulin homology

C; Reywords: heterotetramer; immunoglobulin

F; 8-81/Domain: immunoglobulin homology <IMM>

RESULT 2

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Query Match 100.0%; Score 31; DB 2; Length 91; Best Local Similarity 100.0%; Pred. No. 2.3; Matches 7; Conservative 0; Mismatches 0; Indels

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90.3	87.1	87.1	87.1	87.1	87.1	87.1	87.1	87.1	87.1	87.1	87.1	87.1	87.1	87.1		
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21-7	<u>.</u>		0;	
RESULT 1 \$17626 C.Species: Mus musculus (house mouse) C.Species: Mus maculus (house mouse) C.Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 21-Jan-2000	Chroceston: 517.020 R.Clackson, T.; Hoogenboom, H.R.; Griffiths, A.D.; Winter, G. Nature 352, 624-628, 1991 A;Title: Making antibody fragments using phage display libraries. A;Reference number: S17230; MUID:91326098; PMID:1907718 A;Accession: S17626 A;Status: preliminary	A;Molecule type: nucleic acid A;Residues: 1-91 <cla> A;Residues: 1-91 <cla> C;Superfamily: immunoglobulin V region; immunoglobulin homology C;Keywords: heterotetramer; immunoglobulin F;8-81/Domain: immunoglobulin homology <imm></imm></cla></cla>	Query Match 100.0%; Score 31; DB 2; Length 91; Best Local Similarity 100.0%; Pred. No. 2.3; Matches 7; Conservative 0; Mismatches 0; Indels	Oy 1 STSNLAS 7 1 1 1 1 1 1 1 1 1 1

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S17641
Ig kappa chain V region - mouse
C; Species: Mis musculus (house mouse)
C; Date: 22-NÖv-1993 #sequence_revision 10-Nov-1995 #text_change 21-Jan-2000
C; Accession: PS17641
R; Clackson, M: Hoogenboom, H.R.; Griffiths, A.D.; Winter, G.
Nature 352, 1624-628, 1991
A; Title: Making antibody fragments using phage display libraries.
A; Reference flumber: S17230; MUID:91326098; PMID:1907718
A; Accession: S17641
A; Residues: Preliminary
A; Molecule fype: nucleic acid
A; Residues: A; Beliminary
A; Molecule fype: nucleic acid
A; Residues: A; Beliminary
C; Superfamily: immunoglobulin V region; immunoglobulin homology
C; Keyvords: freterotetramer; immunoglobulin
F; 8-83/Domain: munoglobulin homology < LWA>
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Cispecies: Mus musculus (house mouse)
Cispecies: Nov-1993 #sequence_revision 10-Nov-1995 #text_change 21-Jan-2000
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Nature 352, 624,628, 1991
A;Title: Making antibody fragments using phage display libraries.
A;Reference number: S17230; MUID:91326098; PMID:1907718
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A.Status: preliminary
A.Molecule type; nucleic acid
A.Residues: 1-93 ACLA>
C.Superfamily: immunoglobulin V region; immunoglobulin homology
C.Superfamily: immunoglobulin V region; immunoglobulin
F:8-83/Domain: immunoglobulin homology AIMM>
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Pred. No. 2.3;
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R.Lawler, A.M.; Kearney, J.F.; Kuehl, M.; Gearhart, P.J.
Proc. Natl. Acad. Sci. U.S.A. 86, 6744-6747, 1989
A.Title: Barly rearrangements of genes encoding murine immunoglobulin kappa-chains, u
A;Reference number: A33730; MUID:89367325; PMID:2505260
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C;Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 21-Jan-2000
C;Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 21-Jan-2000
C;Accession: S17642
R;Clackson, T.; Hoogenboom, H.R.; Griffiths, A.D.; Winter, G.
Nature 352, 624-628, 1991
A;Title: Making antibody fragments using phage display libraries.
A;Title: Making antibody fragments using phage display libraries.
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C.bacte: 30-Aug-1991 #sequence_revision 30-Aug-1991 #text_change 21-Jan-2000
C.Accession: D38601
R.Goshorn, S.C.; Retzel, E.; Jemmerson, R.
                                                       Gaps
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A Molecule type: DNA
A Molecule type: DNA
A Residues: 1-96 CLAM>
A Residues: 1-96 CLAM>
A Residues: 1-96 CLAM>
A Residues: 1-96 CLAM>
A Note: the authors translated the codon TTG for residue 34 as Phe
C; Superfamily: immunoglobulin V region; immunoglobulin homology
C; Keywords: heterotetramer; immunoglobulin
F;16-91/Domain: immunoglobulin homology <IMM>
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A; Residues: 1-93 < CLA>
C; Superfamily: immunoglobulin V region; immunoglobulin homology
C; Keywords: heterotetramer; immunoglobulin
  Length 93;
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  Score 31; DB Pred. No. 2.3;
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100.0%;
ilarity 100.0%;
Conservative 0;
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Best Local Similarity 100.0
Matches 7; Conservative
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Query Match
Best Local Similarity
Matches 7; Conserv
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Matches 7; Conserv
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A; Status: preliminary
                                                                                                                                          43 STSNLAS 49
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43 STSNLAS 49
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51 STSNLAS 57
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A; Accession: PT0404
A; Molecule type: DNA
A; Residues: 1-109 <BEH>
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Matches 7; Conserv
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Ig light chain V region (clone 163.72) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Species: Mus musculus (house mouse)
C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 21-Jan-2000
C;Accession: PH1058
R;Tillman, D.M.; Jou, N.T.; Hill, R.J.; Marion, T.N.
J. Exp. Med. 176, 761-779, 1992
A;Title: Both IgM and IgG anti-DNA antibodies are the products of clonally selective B G
A;Reference number: PH0971; MUD:92381444; PMID:1512540
A;Retence number: PH0971; MUD:92381444; PMID:1512540
A;Retence number: PH0971; MUD:92381444; PMID:1512540
A;Rocession: PH1058
A;Retus: nucleic acid sequence not shown
A;Molecule type: mRNA
A;Residues: 1-99 <TILL
A;Experimental source: B cell, strain [NZB x NZW]F1
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Reywords: immunoglobulin
F;16-91/Domain: immunoglobulin
                          figures: Mus musculus (house mouse)
C;Species: Mus musculus (house mouse)
C;Species: Mus musculus (house mouse)
C;Species: Mus musculus (house mouse)
C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 21-Jan-2000
C;Accession: PH1059
R;Tillman, D.M.; Jou, N.T.; Hill, R.J.; Marion, T.N.
J. Exp. Med. 176, 761-779, 1992
A;Tille: Both IgM and IgG anti-DNA antibodies are the products of clonally selective B A;Reference number: PH0971; MUID:92381444; PMID:1512540
A;Accession: PH1059
A;Accession:
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C; Superfamily: immunoglobulin V region; immunoglobulin homology
C; Keywords: immunoglobulin
F;16-91/Domain: immunoglobulin homology <IMM>
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100.0%; Pred. No. 2.5;
Live 0; Mismatches
Biol. Chem. 266, 2134-2142, 1991
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Best Local Similarity 100.
Matches 7; Conservative
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RiBehar, S.M.; Lustgarten, D.L.; Corbet, S.; Scharff, M.D.
J. Exp. Med. 173, 731-741, 1991
A;Title: Characterization of somatically mutated S107 VH11-encoded anti-DNA autoantib A;Reference number: Pr0376; MUID:91147903; PMID:1900082
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R;Behar, S.M.; Lustgarten, D.L.; Corbet, S.; Scharff, M.D.
J. Exp. Med. 173, 731-741, 1991
A;Title: Characterization of somatically mutated S107 VH11-encoded anti-DNA autoantib A;Reference number: PT0376; MUID:91147903; PMID:1900082
Ig light chain V region (clone 74-cl) - mouse (fragment)
C; Species: Mus musculus (house mouse)
C; Species: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 21-Jan-2000
C; Accession: PH1060
R; Tillman, D.M.; Jou, N.T.; Hill, R.J.; Marion, T.N.
J. Exp. Med. 176, 761-779, 1992
A; Title: Both IgM and IgG anti-DNA antibodies are the products of clonally selective A; Reference number: PH0971; MUID:92381444; PMID:1512540
A; Accession: PH1060
A; Molecule type: mRNA
A; Residues: 1-99 < TIL>
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C;Species: Mus musculus (house mouse)
C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 16-Jul-1999
C;Accession: PT0404
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C;Species: Mus musculus (house mouse)
C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 16-Jul-1999
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A; Residues: 1-109 <BBH>
C; Superfamily: immunoglobulin V region; immunoglobulin homology C; Keywords: immunoglobulin
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C; Superfamily: immunoglobulin V region; immunoglobulin homology
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F;16-91/Domain: immunoglobulin homology <IMM>
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A; Residues: 1440 < CHE>
A; Residues: 1440 < CHE
A; Residues: 1440 < CHE
C; Comment: This protein is an anti-idiotypic antibody that induces an anti-phosphorylche
C; Superfamily immunoglobulin V region; immunoglobulin homology
C; Superfamily immunoglobulin V region; Ribitatus predicted < SIG>
F; 23-129/Product: Iq heavy chain V region (4CII) #status predicted < CMAT>
F; 38-111/Domain; immunoglobulin homology < IMM>
F; 46-55/Region; complementarity-determining 1
F; 71-77/Region; complementarity-determining 2
F; 110-118/Region; complementarity-determining 3
F; 130-140/Domāin: constant region (fragment) #status predicted < COR>
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R;Kofler, R.; Strohal, R.; Balderas, R.S.; Johnson, M.E.; Noonan, D.J.; Duchosal, M.A.; Clin. Invest, 82, 852-860, 1988
A;Title: Immunoglobulin kappa 11ght chain variable region gene complex organization and A;Reference number: A94689; MUID:88331394; PMID:3138286
A;Accession: A32513
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                                                                                                                                                                                                                                                                                                                                                       Ig Kappa chain precursor V region (MRL22) - mouse
C;Species: Mus musculus (house mouse)
C;Date: 21-May-1990 #sequence_revision 31-Dec-1990 #text_change 21-Jan-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       musculus (house mouse)
1992 #sequence_revision 30-Jun-1992 #text_change 21-Jan-2000
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A;Residues: 1-130 <KOF>
A;Cross-referefices: GB:M20834; NID:g196943; PIDN:AAA38846.1; PID:g196944
C;Superfamily: Ammunoglobulin v region; immunoglobulin homology
C;Reywords: heterotetramer; immunoglobulin
F;38-113/Domain; immunoglobulin homology <IMM>
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A.Title: Structural basis of stimulatory anti-idiotypic antibodies. A: Reference number: PL0011; MUID: 88142863; PMID: 3125424
A: Accession: PL0013
                                                      100.0%; Score 31; DB 2; Length 109; 100.0%; Pred. No. 2.8; tive 0; Mismatches 0; Indels
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F;16-91/Domain: immunoglobulin homology <IMM>
                                                   Ouery Match 100.
Best Local Similarity 100.
Matches 7; Conservative
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71 STSNLAS 77
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December 23, 2002, 07:31:36

Search completer

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December 23, 2002, 07:30:08; Search time 0.651163 Seconds (without alignments) 180.208 Million cell updates/sec
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Compugen Ltd.
                                                                                                                                                    Total number of hits satisfying chosen parameters:
                                                                                                                                     106657 seqs, 16763532 residues
GenCore version
Copyright (c) 1993 - 2002
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Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                                                            Published_Applications_AA:*
                                protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 200000000
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SEQ ID NO 5
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                                                                                                                                                             Sequence 50, Appl
Sequence 61, Appl
Sequence 65, Appl
Sequence 71, Appl
Sequence 8, Appli
Sequence 9, Appli
Sequence 17, Appl
Sequence 52, Appl
Sequence 52, Appl
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Sequence 5, Appli
Sequence 27, Appl
Sequence 12, Appl
Sequence 24, Appl
Sequence 23, Appl
Sequence 76, Appl
Sequence 76, Appl
                                                                US-09-976-787-5

US-09-8165-198-5

US-09-910-059-27

US-09-976-787-124

US-09-976-787-24

US-09-976-787-24

US-09-10-059-50

US-09-11-059-61

US-09-910-059-61

US-09-910-059-61

US-09-910-059-61

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US-09-910-059-17 US-09-910-059-52 US-09-910-059-97

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Sequence 5, Application US/09865198
Patent No. US20020103345A1
GENERAL INFORMATION:
APPLICANT: Zhu, Zhenping
TITLE OF INVENTION: Bispecific Immunoglobulin-Like Antigen Binding Proteins and Me
TITLE OF INVENTION: Production
FILE REFERENCE: 11245/47102
CURRENT APPLICATION NUMBER: US/09/865,198
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                                                                                                       Gaps
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Sequence 5, Application US/09976787

Sequence 5, Application US/09976787

Sequence 5, Application US2000064528A1

GENERAL INFORMATION

APPLICANT: Zhu, Zhenping

APPLICANT: Witte, Larry

TITLE OF INVENTION: Antibodies Specific to KDR and Uses Thereof

FILE REFERENCE: 11245/46505

CURRENT APPLICATION NUMBER: US/09/976,787

CURRENT FILING DATE: 2000-11-28

PRIOR PLILING DATE: 2000-01-28

PRIOR PLILING DATE: 1999-01-29

PRIOR PLILING DATE: 1999-01-29

NUMBER OF SEQ ID NOS: 40

SOFTWARE: WordPerfect 8.0 for Windows
                                                                                                                                                                                                                                                                                                                     Sequence Sequence Sequence Sequence Sequence
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0 US-09-976-787-29

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US-09-865-198-27

US-09-865-198-27

US-09-865-108-28

US-09-965-099-13

US-09-965-099-55

US-09-965-099-55

US-09-965-099-65

US-10-051-852-66

US-09-965-099-67

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US-09-965-099-67

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        Best Local Similarity 100.
Matches 7; Conservative
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      RESULT 1
US-09-976-787-5
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Sequence 23, Application US/09865198
Sequence 23, Application US/09865198
Patent No. US20020103345a1
GENERAL INFORMATION:
GENERAL INFORMATION:
FAPLICANT: Zhu, Zhenping
TITLE OF INVENTION: Bispecific Immunoglobulin-Like Antigen Binding Proteins and Me
TITLE OF INVENTION: Production
TITLE OF INVENTION: Production
CURRENT APPLICATION NUMBER: US/09/865,198
CURRENT FILING DATE: 2001-05-24
PRIOR FILING DATE: 2000-05-24
NUMBER OF SEQ ID NOS: 34
SOFTWARE: WordPerfect 8.0 for Windows
SEQ ID NO 23
LENGTH: 106
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                                                                                                   ; OTHER INFORMATION: Description of Unknown Organism: Guy's 13 Kappa US-09-982-107-12
                                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
APPLICANT: Zhu, Zhenping
APPLICANT: Zhu, Zhenping
TITLE OF INVENTION: Antibodies Specific to KDR and Uses Thereof
FILE REFERENCE: 11245/46505
CURRENT APPLICATION NUMBER: US/09/976,787
CURRENT FILING DATE: 2000-10-12
PRIOR FILING DATE: 2000-01-28
PRIOR FILING DATE: 1999-01-29
NUMBER OF SEQ ID NOS: 40
SOFTWARE: WordPerfect 8.0 for Windows
SEQ ID NO 24
LENGTH: 106
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100.0%; Score 31; DB 10; Length 106;
Best Local Similarity 100.0%; Pred. No. 2.4;
Matches 7; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                100.0%; Score 31; DB 9; Length 105; 100.0%; Pred. No. 2.4;
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100.0%; Pred. No. 2.4;
ive 0; Mismatches 0;
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                                       TYPE: PRT
ORGANISM: Unknown Organism
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Best Local Similarity luv..
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Matches 7; Conservative
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STSNLAS 55
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US-09-976-787-24
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US-09-865-198-23
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               LENGTH: 105
                                                                                                                                                                Query Match
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APPLICANT: Gobley, Clive G
APPLICANT: Gobley, Clive G
APPLICANT: Gobley, Clive G
APPLICANT: Edge, Michael Derek
APPLICANT: Emery Stephen Charles
TITLE OF INVENTION: Moncolonal Antibody to CEA, Conjugates Comprising Said Antibody,
TITLE OF INVENTION: Moncolonal Antibody to CEA, Conjugates Comprising Said Antibody,
TITLE OF INVENTION: MONBER: US 09/171,945
FILE REFRENCE: 1991-299
CURRENT APPLICATION NUMBER: US 09/171,945
PRIOR FILING DATE: 1997-04-29
PRIOR FILING DATE: 1997-04-29
PRIOR FILING DATE: 1997-02-14
PRIOR FILING DATE: 1997-02-14
PRIOR FILING DATE: 1997-02-14
PRIOR FILING DATE: 1997-02-14
PRIOR FILING DATE: 1996-05-04
SOFTWARE: PARCH ONCOS: 131
SOFTWARE: PARCH ONCOS: 131
SOFTWARE: PARCH ONCOS: 131
SOFTWARE: PARCH ONCOS: 131
SEQ. ID NO 27;
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Patent No. US2002015995841
GENERAL INGENARION:
APPLICANT: HATT, ANDREW C.
APPLICANT: HEIN, MICH B.
TITLE OF INVENTION: PROFECTION PROTEINS IN PLANTS AND THEIR USE
TITLE OF INVENTION: NUMBER: US/09/982,107
CURRENT APPLICATION NUMBER: US/09/982,107
NUMBER OF SEQ ID NOS: 19
SOFTWARE: Patentin Ver: 2.1
SEQ ID NO 12
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100.0%; Pred. No. 8.8e+04;
iive 0; Mismatches 0;
CURRENT FILING DATE: 2001-05-24
PRIOR APPLICATION NUMBER: US 60/206,749
PRIOR FILING PATE: 2000-05-24
NUMBER OF SEQ ID NOS: 34
SOFTWARE: Worddperfect 8.0 for Windows
SEQ ID NO 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 27, Application US/09910059
Patent No. U$20020142359A1
GENERAL INFORMATION:
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Best Local Similarity 100.
Matches 7; Conservative
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CRGANISM: Mus musculus
US-09-910-059$27
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; ORGANISM: Mouse
US-09-865-198-5
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ORGANISM: Artificial Sequence
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Best Local Similarity 100.C
Matches 7; Conservative
  GENERAL INFORMATION:
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LENGTH: 107
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                                                                                                                                              Sequence 76, Application US/09144886
| Patent No. US2002155114A1
| GENERAL INFORMATION:
| APPLICANT: Marks, James D
| APPLICANT: Amersdorfer, Peter
| TILE OF INVENTION: Therapeutic Monoclonal Antibodies That Neutralize
| TILE OF INVENTION: Detailnum Neurotoxins
| FILE REFERENCE: 2500.117050
| CURRENT APPLICATION NUMBER: US/09/144,886
| CURRENT FILING DATE: 1998-08-31
| NUMBER OF SEQ ID NOS: 98
| SOFTWARE: PatentIn Ver. 2.0
| SEQ ID NO 76
| LENGTH: 107
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APPLICANT: Marks, James D
APPLICANT: Marks, James D
APPLICANT: Amersdorfer, Peter
TITLE OF INVENTION: Therapeutic Monoclonal Antibodies That Neutralize
TITLE OF INVENTION: Botulinum Neurotoxins
FILE REFERENCE: 2500.1170SO
CURRENT APPLICATION UNMBER: US/09/144,886
CURRENT FILING DATE: 1998-08-31
NUMBER OF SEQ ID NOS: 98
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 88
LENGTH: 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; OTHER INFORMATION: Description of Artificial Sequence: BONT/A clone; OTHER INFORMATION: C9 region VL epitope 1 US-09-144-886-76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; OTHER INFORMATION: Description of Artificial Sequence: BONT/a clone; OTHER INFORMATION: 2G5 region VL epitope 2
US-09-144-886-88
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US-09-910-059-50
Sequence 50, Application US/09910059
Patent No. US20020142359A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 88, Application US/09144886 Patent No. US20020155114A1 GENERAL INFORMATION:
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ORGANISM: Artificial Sequence
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49 STSNLAS 55
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APPLICANT: Copley, Clive G
APPLICANT: Edge, Michael Derek
APPLICANT: Edge, Michael Derek
APPLICANT: Edge, Michael Derek
TITLE OF INVENTION: Stephen Charles
TITLE OF INVENTION: Monoclonal Antibody to CEA, Conjugates Comprising Said Antibod
TITLE OF INVENTION: Their Therapeutic use in an Adept System
FILE REPERENCE: 1991-209
CURRENT APPLICATION WUMBER: US 09/171,945
PRIOR FILING DATE: 1998-10-29
PRIOR FILING DATE: 1998-10-29
PRIOR PPLICATION NUMBER: PCT/GB97/01165
PRIOR PPLICATION NUMBER: GB 9703103.3
PRIOR FILING DATE: 1997-02-14
PRIOR FILING DATE: 1997-02-14
PRIOR FILING DATE: 1996-05-04
SPRIOR FILING DATE: 1996-05-04
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SOFTWARE: PATENTHARE: PATENTHAR
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Fatent No. US2002014235941
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Edge, Michael Derek
APPLICANT: Emery, Stephen Charles
TITLE OF INVENTION: Monoclonal Antibody to CEA, Conjugates Comprising Said Antibod
TITLE OF INVENTION: Monoclonal Antibody to CEA, Conjugates Comprising Said Antibod
TITLE OF INVENTION: Monoclonal Antibody to CEA, Conjugates Comprising Said Antibod
TITLE OF INVENTION: Monoclonal Antibody
CURRENT APPLICATION NUMBER: US/09/910,059
CURRENT FILING DATE: 1991-029
FRIOR FILING DATE: 1997-04-29
FRIOR FILING DATE: 1997-04-29
FRIOR FILING DATE: 1997-04-29
FRIOR FILING DATE: 1996-05-04
NUMBER OF SEQ ID NOS: 131
SEQ ID NO 61
LENGTH: 107
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100.0%; Score 31; DB 10;
Best Local Similarity. 100.0%; Pred. No. 2.4;
Matches 7; Conservative 0; Mismatches 0;
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GENERAL INFORMATION:
APPLICANT: Zhu, Zhenping
TITLE OF INVENTION:
Bispecific Immunoglobulin-Like Antigen Binding Proteins and Me
TITLE OF INVENTION:
FILE REFERENCE: 11245/47102
CURRENT APPLICATION NUMBER: US/09/865,198
CURRENT FILING DATE: 2001-05-24
PRIOR PILING DATE: 2000-05-24
NUMBER OF SEQ ID NOS: 34
SOFTWARE: WordPerfect 8:0 for Windows
SEQ ID NO 8
LENGTH: 108
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Fatent No. US20020064528A1

GENERAL INFORMATION:

APPLICANT: Zhu, Zhenping

APPLICANT: Witte, Larry

TITLE OF INVENTION: Antibodies Specific to KDR and Uses Thereof

TITLE OF INVENTION: Antibodies Specific to KDR and Uses Thereof

CURRENT APPLICATION NUMBER: US/09/976,787

CURRENT FILING DATE: 2001-10-12

FRIOR APPLICATION NUMBER: US 60/413,539

PRIOR APPLICATION NUMBER: US 60/117,726

PRIOR APPLICATION NUMBER: US 60/117,726

FRIOR FILING DATE: 1999-01-29

NUMBER OF SEQ ID NOS: 40

SOFTWARE: WordPerfect 8.0 for Windows
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               ; Score 31; DB 10; Length 107; Pred. No. 2.4;
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Patent No. US20020103345A1
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ilarity 100.0%;
Conservative (
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                                 Query Match
Best Local Similarity
Matches 7; Conserv
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                        RESULT 11

US-09-910-059-65

Sequence 65, Application US/09910059

Sequence 65, Application US/09910059

Patent No. US200201423591

GENERAL INFORMATION:

APPLICANT: George, Michael Derek

APPLICANT: George, Michael Derek

APPLICANT: George, Michael Derek

APPLICANT: George, Michael Derek

TITLE OF INVENTION: Monoclonal Antibody to CEA, Conjugates Comprising Said Antibody,

TITLE OF INVENTION: Their Their Theoremic use in an Adept System

TITLE OF INVENTION: WOMBER: US/09/910,059

CURRENT APPLICATION NUMBER: US/09/910,059

CURRENT FILING DATE: 1998-10-29

PRIOR PELLING DATE: 1998-10-29

PRIOR APPLICATION NUMBER: CE 9703103.3

PRIOR PELLING DATE: 1997-02-14

PRIOR FILING DATE: 1997-02-14

PRIOR FILING DATE: 1996-05-04

NUMBER OF SEQ ID NOS: 131

SEQ ID NO 65

LENGTHARE: PERCENCE:

LENGTHARE: LOSE AND ASSET AND AS
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GENERAL INC. 02.002.014.2.5.9.4.1.

APPLICANT: Copley, Clive G
APPLICANT: Enge, Michael Derek
APPLICANT: Enge, Michael Derek
APPLICANT: Engery, Stephen Charles
TITLE OF INVENTION: Their Therapeutic use in an Ad
TITLE OF INVENTION: Their Therapeutic use in an Ad
FILE REFERENCE: 1991-209
CURRENT FIGHTON NUMBER: US/09/910,059
CURRENT FIGHED DATE: 1991-029
PRIOR PLING DATE: 1998-10-29
PRIOR PLING DATE: 1997-04-29
PRIOR FILING DATE: 1997-04-29
PRIOR FILING DATE: 1997-02-14
PRIOR FILING DATE: 1997-02-14
PRIOR FILING DATE: 1996-05-04
NUMBER OF SEQ ID NOS: 131
SOFWARE: Patentin version 3.1
LENGTH: LO7
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ORGANISM: Artificial Sequence
49 STSNLAS 55
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49 STSNLAS 55
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Best Local Similarity 100.0%; Pred. No. 2.5;
Matches 7; Conservative 0; Mismatches 0; Indels (
US-09-910-059-9
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C; Acces:	sion: S0	5268; J	L0062;	S03	1846	
submitted to	ed to the	e EMBL	Data Li 5267	bra	Submitted to the EMBL Data Library, February 1989 A:Reference number: 805267	
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J. Exp. A;Title	Med. 16 : Altern	8, 1607 ative V	-1620, r kappa	198 gen	18 1e rearrangements in a mur	ine B cell lymphoma. An expl
A; Refer	ence num	ber: JL 0062	,0061; N	UIC):89035985; PMID:3141553	
A; Moleci	ule type	E MRNA	۵			
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S17641 Ig kapp	S17641 Ig kappa chain V	V region	esnow - uc	ıse		
C;Speci C;Date:	es: Mus 22-Nov-	musculu 1993 #s	is (hous	e n	nouse) evision 10-Nov-1995 #text_	change 21-Jan-2000
C; Acces	sion: S1	.7641 Hooger	boom, F	<u>ب</u>	C; Accession: S17641 R; Clackson, T.; Hoogenboom, H.R.; Griffiths, A.D.; Winter, G.	. 5
Nature	352, 624 Making	1-628, 1	1991 Idv frac	9	ots using phage display li	hraries
A; Refer	ence num	ber: S1	7230; N		0:91326098; PMID:1907718	
A; Status: preliminary A: Molecule type: nucleic a	s: preli	minary	ביטה טיים	_		
A; Resid	ues: 1-9	3 <cla></cla>	7			

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Gaps

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Indels

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Ig kappa chain V region (14D2) - mouse (fragment)
C; Species: Mus musculus (house mouse)
C; Date: 30-Aug-1991 #sequence_revision 30-Aug-1991 #text_change 23-Jul-1999
C; Accession: E38601
R; Goshorn, S.C.; Retzel, E.; Jemmerson, R.
J. Biol. Chem. 266, 2134-2214, 1991
A; Title: Common structural features among monoclonal antibodies binding the same anti A; Reference number: A38601; MUD: 91115823; PMID: 1703527
A; Status: preliminary
A; Molecule type: mRNA
A; Residues: 1-35 <GGSS
A; Residues: 1-35 <GGSS
A; Cssession: E38601
A; Residues: 1-35 <GGSS
C; Superfemally: Immunoglobulin V region; Immunoglobulin homology
C; Keywords: heterotetramer; Immunoglobulin
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C;Species: Mus musculus (house mouse)
C;Date: 30-Aug-1991 #sequence_revision 30-Aug-1991 #text_change 21-Jan-2000
C;Accession: D38601
R;Goshorn, S.C.; Retzel, E.; Jemmerson, R.
J. Biol. Chem. 266, 2134-2142, 1991
A;Title: Common structural features among monoclonal antibodies binding the same anti
A;Reference number: A38601; MUID:91115823; PMID:1703527
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Ig kappa chain V region - mouse
C;Species: Mus musculus (house mouse)
C;Species: Mus musculus (house mouse)
C;Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 21-Jan-2000
C;Accession: S17626
R;Clackson, T; Hoogenboom, H.R.; Griffiths, A.D.; Winter, G.
Nature: Making antibody fragments using phage display libraries.
A;Feference number: S17230; MUID:91326098; PMID:1907718
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A;Residues: 1-91 <CLA>
CLA>
CS.Superfamily: immunoglobulin V region; immunoglobulin homology
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Reywords: heterotetramer; immunoglobulin
F;8-81/Domain: immunoglobulin homology <IMM>
                                                                                                                                                                                                                                                                                                                                                                                                             Length 35;
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Pred. No. 0.26;
1; Mismatches
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Pred. No. 0.7;
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Pred. No. 1.6;
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Local Similarity 87.5%;
nes 7; Conservative 1
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88.9%;
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Best Local Similarity
7; Conserve
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Best Local Similarity
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A; Molecule type: mRNA
A; Residues: 1-99 <GOS>
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Matches
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                                                                                                                                                                                                                                                                                                                                                                    19 light chain y region anti-triplex DNA - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Species: Mus musculus (house mouse)
C:Date: 06-oct=1904 #sequence_revision 18-Nov-1994 #text_change 21-Jan-2000
C:Accession: B54378
B:Agazie, Y.M. Lee, J.S.; Burkholder, G.D.
J. Biol. Chan. 269, 7019-7023, 1994
A:Title: Characterization of a new monoclonal antibody to triplex DNA and immunofluoresc
A:Reference number: A54378; MulD:94165109; PMID:7509814
A:Accession: B54378
A:Reference number: A54378; MulD:945546; PIDN:AAB30096.1; PID:95545747
A:Residues: 1-106 cAGAS
A:Residues: 1-106 cAGAS
A:Residues: GB:S68985; NID:9545746; PIDN:AAB30096.1; PID:9545747
A:Resperimental source: spleen and myeloma cell line MOPC 315.43
A:Note: sequence extracted from NCBI backbone (NCBIN:144174, NCBIP:144175)
C:Superfamily:immunoglobulin V region; immunoglobulin homology
C:Reywords: immunoglobulin homology <IMM>
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19 kappa chain V region (38C13.V6.1) - mouse
C.Species: Mus musculus (house mouse)
C.Species: Mus musculus (house mouse)
C.Accession: PSOG70
C.Accession: PSOG70
C.Accession: PSOG70
C.Accession: Mod. 170, 1-13, 1989
A.Title: Functional immunoglobulin light chain genes are replaced by ongoing rearrangeme A; Reference number: A92781; MUID:89310348; PMID:2501443
A.Accession: PSOG70
A.Accession: PSOG70
A.Stelus: translation not shown
A; Mesidues: 1%106 < LEVA.
C.Superfamily: Immunoglobulin V region; immunoglobulin homology
C; Keywords: héterotetramer: immunoglobulin
F:16-89/Domain: immunoglobulin homology <IMM>
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C;Superfamily: immunoglobulin V region; immunoglobulin homology C;Keywords: heterotetramer; immunoglobulin F;8-83/Domain: immunoglobulin homology <IMM>
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Pred. No. 0.29;
0; Mismatches
                                                                                                     Score 42; DB 2;
Pred. No. 0.26;
0; Mismatches
                                                                                                     87.5%;
88.9%;
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8; Conservative
                                                                                             Ouery Match
Best Local Similarity 88.9
Matches 8% Conservative
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les 8; Conserv
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Matches 8; Conserv
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E38601
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A; Residues: 1-106 <CAT>
A; Estdues: 1-106 <CAT>
A; Estdues: 1-106 <CAT>
A; Experimental source: strain Balb/c
A; Note: this sequence was determined from the germline gene
C; Comment: This chain was isolated from a hybridoma protein that binds influenza viru
C; Superfamily: immunoglobulin V region; immunoglobulin homology
C; Keywords: heterotetramer; immunoglobulin
F; 16-89/Domain: immunoglobulin homology <IMM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Type chain precursor V region (MRL22) - mouse C; Species: Mus musculus (house mouse) C; Species: Mus musculus (house mouse) C; Species: 10. May 1990 #sequence_revision 31-Dec-1990 #text_change 21-Jan-2000 C; Accession: A32213 R; A2213 R; A2213 R; A2213 R; A2213 R; A2213 R; A2213 R; A2214 R;
                                Ricaton, A.J.; Brownlee, G.G.; Staudt, L.M.; Gerhard, W.
EMBO J. 5, 1577-1587, 1986
A;Title: Structural and functional implications of a restricted antibody response to A;Reference number: A91043; WIID:86300658; PMID:2427335
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A;Residues: 1-130 <KOF>
A;Cross-references: GB:M20834; NID:g196943; PIDN:AAA38846.1; PID:g196944
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;38-113/Domain: immunoglobulin homology <IMM>
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C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
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Pred. No. 3.6;
0; Mismatches
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Pred. No. 3.7;
1; Mismatches
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Pred. No.
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77.8%;
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87.5%;
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77.8%;
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Best Local Similarity 87.5.
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A; Residues: 1-132 <KLE>
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89 QRSSYPLT 96
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A.Residues: 1-140 <CHE>
A.Residues: 1-140 <CHE>
A.Residues: 1-140 <CHE>
C.Comment: This protein is an anti-idiotypic antibody that induces an anti-phosphorylchd (C.Comment: This protein is an anti-idiotypic antibody that induced an anti-phosphorylchd (S.Superfamily: immunoglobulin V region; immunoglobulin homology (C.Keywords: heterotetramer; immunoglobulin predicted <SIG>
F.12.2/Domain: signal sequence #status predicted <SIG>
F.23-129/Product: Ig heavy chain V region (4C11) #status predicted <MAT>
F.38-111/Domain: immunoglobulin homology <CHM)
F.38-51/Region: complementarity-determining 1
F.71-77/Region: complementarity-determining 2
F.71-77/Region: complementarity-determining 2
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C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 21-Jan-2000
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C;Species: Mus musculus (house mouse)
C;Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 21-Jan-2000
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C;Date: 15-Dec-1988 #sequence_revision 15-Dec-1988 #text_change 21-Jan-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                               C; Accession: S42466
R; Shiyanov, P.A.; Bespalov, I.A.; Terletskaya, H.N.; Deyev, S.M.
submitted to the RMBL Data Library, March 1994
A; Reference number: S42466
A; Residues: 1-117 < SHI>
A; Ross references: EMBL: X78108; NID:9460824; PIDN:CAA54998.1; PID:9460825
C; Superfamily: immunoglobulin V region; immunoglobulin homology
C; Reyvords: heteroctetramer; immunoglobulin
F; 26-100/Domain: immunoglobulin homology < IMM>
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F;130-140/Domain: constant region (fragment) #status predicted <COR>
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R:Cheng, H.L.; Scod, A.K.; Ward, R.E.; Kieber-Emmons, T.; Kohler, H Mol. Immunol. 25, 33-40, 1988
A;Title: Structural basis of stimulatory anti-idiotypic antibodies. A;Reference number: PL0011; MUID:88142863; PMID:3125424
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2.4;
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Pred. No. 2.1;
1; Mismatches
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Mismatches
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Pred. No. 2
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88.9%;
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Best Local Similarity 77.8%;
Matches 7; Conservative
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Best Local Similarity
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A; Accession: F83862
A; Status: preliminary -
A; Molecule type: DNA
A; Residues: 1-886 <STO>
A; Resirences: GB:AP001512; GB:BA000004; NID:g10174030; PIDN:BAB05421.1; GSPDB:G
A; Experimental source: strain C-125
C; Genetics:
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Matches 6; Conserv
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       C; Accession: F83862
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A; Gene: FlyBase.ninaC
A; Cross-references: FlyBase: FBgn0002938
A; Gene: FlyBase.ninaC
C; Superfamily: ninaC protein: myosin motor domain homology; protein kinase homology
C; Superfamily: ninaC protein kinase homology < KIN>
F; 14-282, Tomain: protein kinase homology < KIN>
F; 14-282, Tomain: myosin motor domain homology < MMOT>
F; 315-1022, Domain: myosin motor domain homology < MMOT>
F; 315-102, Domain: myosin motor domain predicted
F; 1054-1501, Domain: carboxyl-terminal < CGBT>
F; 1054-1501, Domain: carboxyl-terminal < CGBT>
F; 455, 60, 145, Active site: Lys, Glu, Asp **status predicted
F; 431/Binding **status predicted
                                                                                                                                                                    174K ninaC protein - fruit fly (Drosophila melanogaster)
N;Contains: protein kinase (EC 2.7.1.-)
C;Species - Drosophila melanogaster
C;Decies - Drosophila melanogaster
C;Date: 31-Decino 93 #sequence_revision 31-Dec-1993 #text_change 19-Jan-2001
C;Accession: B29813
E;Montall, C.;Enblin, G.M.
Cell 52, 755-772, 1988
A;Title: The Drosophila ninaC locus encodes two photoreceptor cell specific proteins with A;Reference number: A90898; MUID:88151067; PMID:2449973
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C; Species: Nus musculus (house mouse)
C; Date: 01-Dec-1989 #sequence_revision 01-Dec-1989 #text_change 09-May-1997
C; Accession: 628195
R; Sherman, M.A.; Deans, R.J.; Bolger, M.B.
B; Sherman, M.A.; Deans, R.J.; Bolger, M.B.
A; Title: Haloperidol binding to monoclonal antibodies. Hypervariable region amino acid A; Reference number: A28195; MuID:88153717; PMID:3267217
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A; Molecule: 1-1501 <MON>
A; Cross-references: GB:M20230; NID:9157967; PIDN:AAA28721.1; PID:9157968
C; Genetics:
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C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
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66.7%; Pred. No. 3.9;
Live 2; Mismatches 1; Indels
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Matches 6; Conservative
                            110 QOFNSYPFT 118
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Best Local Similarity
Matches 7; Conserv
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A; Residues: 1586 <SHE>
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1 QORSSYPFT
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C28195
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C;Date: 01-Dec-2000 #sequence_revision 01-Dec-2000 #text_change 15-Jun-2001
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R;Takami, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Masui, N.; Fuji, F.; H Nuclear Acids Res. 28, 4317-4331, 2000 A;Title: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans a A;Reference number: A83650; MUID:20512582; PMID:11058132

Gaps ô Length 886; Indels DB 2; 36; 1; Mismatches Score 36; Pred. No. 75.0%; 75.0%; 6; Conservative

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Search completed: December 23, 2002, 07:31:37 Job time : 2.77907 secs